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The trade-off between feed efficiency, methane production and reproduction in sheep

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Executive summary

Selecting sheep that eat less and are more feed efficient will decrease methane and carbon dioxide. Carbon dioxide can be used as an indicator trait for intake because they are closely correlated and carbon dioxide has a strong heritability. Also, there is high repeatability between ages so sheep can be selected to eat less, produce less methane and be more feed efficient younger. This means that intake can be measured cheap and fast making it a viable option for commercial breeders. Also, the most efficient and environmentally friendly animals can be selected early. This is important because sheep can be made efficient faster. For Australian agriculture it will change the way farmers think about breeding for resilience and efficiency with many new opportunities. It is difficult to breed fast growing sheep without increasing intake and methane but it's easier to breed sheep that are feed efficient and grow fast. Wool and reproduction can be improved without effecting methane and intake. Therefore, farmers can improve production and efficiency simultaneously. Finally, methane produced per kg of product can be decreased by selecting more productive sheep.

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1. Background

There has been a significant knowledge gap in the understanding of the correlations between feed use efficiency, methane production and reproduction, how the relationships between these traits are influenced by ewe age and breed, and most important, how changing these traits in sheep translates into changes in whole farm emissions and profits. Improving feed efficiency and reproduction are both promoted as means to reduce methane emissions, but recent evidence suggests that feed efficiency and reproduction may be negatively correlated. If so, the net effects of improved feed efficiency or reproduction on emissions may be less than expected. More important perhaps, is that the impacts of improving feed efficiency and reproduction on emissions would only be realised if farmers maintained the same number of more efficient animals, or reduced the number of adult ewes to maintain the amount of lamb produced per hectare, which reduces production potential and consequent farm profit. The objective of this project was to determine the genetic correlations between feed efficiency, methane production and reproduction and use whole-farm modelling to re-evaluate the scope for sheep selection strategies that reduce methane emissions but also improve whole-farm profitability. This will enable a more informed position for policy makers to develop methods that allow farmers to participate in the Emission Reduction Fund. The project worked at two sites on Merino (WA) or non-Merino sheep (VIC). In this report we describe the methodology, results and discussion for both sites separately. We discuss both sites together in a combined discussion at the end.

Merinos in Western Australia

We tested the hypothesis that breeding sheep that eat less and have a lower residual feed intake will produce less methane. In other words, more efficient sheep will be better for the environment. If sheep that have a lower residual feed intake eat less based on their size and production, it was also reasonable to expect that these animals will produce less methane per unit of production. Finally we tested if intake, residual feed intake and methane are the same trait across ages.

2. Methodology

During years 2010 to 2016 we measured feed intake, gas, live weight, fat, muscle, reproduction, wrinkle and wool traits from Merino sheep. We measured these sheep at post weaning (mean 223 days old), hogget (607 days old), and adult ages (1080 days old). We recorded 1,816 post weaners, 1,051 hoggest and 444 adults. Of these records, 975 had post-weaning and hogget records and 406 had post-weaning, hogget and adult records. The sheep were from 116 sires and 1,452 dams and managed at the University of Western Australia, Ridgefield research farm (32° 32'S, 117° 05'E).

The sheep were transported in groups of approximately 225 to the Department of Agriculture and Food Research Station at Medina, Perth (32⁰13'S, 115⁰48'E). At Medina, they were randomised in outdoor pens and fed oaten hay *ad libitum* and 100g/hd/day with pellets with 17% crude protein 17% and 12.3 MJ metabolisable energy. This pellet ration was increased by 100-200g/day for at least 15 days or until intake was *ad libitum*. After adaptation to the pellet diet outside, we randomized sheep by sire into 15 indoor pens (approximately 15 sheep per pen), except at post-weaning age they were grouped by live weight so that there was less than 5 kg difference between the heaviest and lightest sheep in each pen. We regrouped the post-weaners by weight to reduce bullying and shy feeding. Additionally, the chutes leading to the feeders could be adjusted to the size of the sheep in the pen so that only one sheep entered the feeder at a time. Individual feed intake was recorded using electronic identification and weighing daily intake. Each pen had a feeder set up to allow only one sheep to feed at a time. To access the feeder sheep walked past a radio-frequency identification aerial that recorded their electronic tag. The duration of feeding and the weight of feed eaten was automatically recorded through electronic scales and weigh bars. Feed intake was measured across 35 days.

During the last 14 to 21 days of the feed intake test, sheep put into individual portable accumulation chambers (PACs) at least twice. Methane was measured using a modified version of the technique described by Goopy *et al.* (2013). Methane (CH_4), carbon dioxide (CO_2) and oxygen (O_2) were measured at 10 minute intervals for 40 minutes. Records were removed if the methane accumulation

over the 40 minutes was not linear. We analysed methane, carbon dioxide and oxygen recorded at 40 minutes. The portable accumulation chambers are made of polycarbonate. They are 1.23m long, 1.24m high and 0.53m wide. They are open at the bottom and have $0.795m^3$ volume. Methane was measured by putting 16 sheep into two races with portable accumulation chambers suspended over them. The chambers were lowered over the sheep from front to the back of each race. The chambers were sealed against 5-mm industrial rubber belting on the floor of the race using elastic straps. The lower edges of the chambers were covered with medium density foam rubber tape to help seal the chambers completely. After each 10 minute interval, methane concentration (CH₄ µL/L) was measured using a flame ionization detector (MX100053; ENVCO, Wellington, New Zealand). CO₂ µL/L was measured using a Foxbox gas analysis system (Sable Instruments, Las Vegas, NV). The measurements were made via a tube attached to the machines and pushed through a 3mm hole in the chambers. When measurements were not taken the port was sealed with tape.

Genetic analysis

A description of each trait is in Table 1. Residual feed intake was the unexplained part of the average intake over 35 to 42 days, corrected for mean live weight and growth over the 35 to 42 days. Residual feed intake was estimated for each group. Some early measurements of feed intake were unreliable so only groups with significant effects of live weight and growth were included. These groups were measured from the second half of 2013 to 2015. We included three traits for methane adjusted for intake (CH4_{intake}), live weight (CH4_{weight}) and growth (CH4_{growth}). These traits indicate the amount of methane produced per kg intake, live weight or growth, with these traits fitted as covariates to methane. Fitting these traits as covariates means that issues related to ratios traits, such as non-normal distributions and screwed means, are avoided (Allison et al. 1995). Extreme outliers were removed from traits, if they were more than six times the standard deviation. For methane, oxygen and carbon dioxide traits that were measured 2 or 3 times per sheep, we included a weighting for the number of records.

Trait	Units	Description
Intake	kg DM/day	Average intake over 45 days
Intake ₂₄	kg DM/day	Intake 24 hours before methane measurement
Intake ₄₈	kg DM/day	Intake 48 hours before methane measurement
RFI	kg DM/day	Residual feed intake
CH₄	g/day	Methane (standard temperature and pressure)
CO ₂	g/day	Carbon dioxide
O ₂	g/day	Oxygen
LW	kg	Average live weight over 45 days
Growth	kg/day	Average daily growth over 45 days
EMD1	mm	Eye muscle depth at start of 45 days
EMD2	mm	Eye muscle depth at end of 45 days
CF₁	mm	C site fat at start of 45 days
CF ₂	mm	C site fat at end of 45 days
NLS	lambs	Number of lambs scanned
NLB	lambs	Number of lambs born
NLW	lambs	Number of lambs weaned
TBWT	kg	Total weight of lambs born
TWWT	kg	Total weight of lambs weaned
Wrinkle body	score	Wrinkle score on body
Winkle breach	score	Wrinkle score at breach
CFW	kg	Clean fleece weight
FD	μm	Fibre diameter
CVFD	%	Coefficient of variation of fibre diameter
SS	nkt	Straple strength (newtons per kilotex)
SL	mm	Staple length

Table 1 Description of traits with their units

The heritability of traits was estimated using univariate models;

$$\mathbf{y} = \mathbf{X}\mathbf{b} + \mathbf{Z}_{\mathbf{a}}\mathbf{a} + \mathbf{e} \tag{1}$$

where **y** are the observations for the traits, **b** is the vector of fixed effects, **a** is the vector of animal genetic effects, **g** are the genetic group effects, and **e** is the vector of error effects. **X** and **Z** are the incidence matrices, and \mathbf{ZQ}_g is the matrix which describes the proportion of genes in each animal that originate from each genetic group. The random effects of **e** are normally distributed with a mean of zero.

To test if fitting genetic groups significantly improved the fit of the traits, we used likelihood-ratio-tests. None of the traits had significant effects for genetic groups. Genetic groups were not significant because only 4% of sheep had contributions from genes of breeds other than Merino more than 25%. Therefore, it was difficult to find significant variance in traits due to genetic groups.

All other models tested excluded genetic groups. The other models used were;

$$y = Xb + Z_aa + Z_mm + e$$

(3)

(2)

where \mathbf{m} are the maternal genetic due to the dam, and $\mathbf{Z}_{\mathbf{m}}$ relate the \mathbf{m} vectors to the traits (y).

We tested model 3 against model 1 to see if adding maternal genetic effects significantly improved the fit of the traits. We did these tests using likelihood-ratio-tests. There were no significant permanent environmental effects caused by the dam in all traits, but maternal genetic effects were significant for most traits.

The genetic correlations (r_g) between traits were estimated using a bivariate model, estimating the variance of traits and the covariance between trait 1 (tr1) and trait 2 (tr2);

$$\begin{bmatrix} \mathbf{y}_{tr1} \\ \mathbf{y}_{tr2} \end{bmatrix} = \begin{bmatrix} \mathbf{X}_{tr1} & \mathbf{0} \\ \mathbf{0} & \mathbf{X}_{tr2} \end{bmatrix} \begin{bmatrix} \mathbf{b}_{tr1} \\ \mathbf{b}_{tr2} \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{a\,tr1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{a\,tr2} \end{bmatrix} \begin{bmatrix} \mathbf{a}_{tr1} \\ \mathbf{a}_{tr2} \end{bmatrix} + \begin{bmatrix} \mathbf{Z}_{m\,tr1} & \mathbf{0} \\ \mathbf{0} & \mathbf{Z}_{m\,tr2} \end{bmatrix} \begin{bmatrix} \mathbf{m}_{tr1} \\ \mathbf{m}_{tr2} \end{bmatrix} + \begin{bmatrix} \mathbf{e}_{tr1} \\ \mathbf{e}_{tr2} \end{bmatrix}$$

where y_{tr1} and y_{tr2} are the observations for the first and second trait in the analysis, \mathbf{b}_i is the vector of fixed effects, \mathbf{a}_i is the vector of additive genetic effects, \mathbf{m}_i is the vector of maternal genetic effects and \mathbf{e}_i is the vector of error effects. \mathbf{X}_i and $\mathbf{Z}_{a\,i}$ and $\mathbf{Z}_{m\,1}$ are the incidence matrices (i = tr1 and tr2). The random effects \mathbf{a}_i , \mathbf{m}_i and \mathbf{e}_i are bivariate and normally distributed with mean zero and variance:

$$\operatorname{var} \begin{bmatrix} \mathbf{e}_{tr1} \\ \mathbf{e}_{tr2} \end{bmatrix} = \mathbf{R} \otimes \mathbf{I} \text{ where } \mathbf{R} = \begin{bmatrix} \sigma_{e\ tr1}^2 & \sigma_{e\ tr1\ tr2} \\ \sigma_{e\ tr1\ tr2} & \sigma_{e\ tr2}^2 \end{bmatrix},$$
$$\operatorname{var} \begin{bmatrix} \mathbf{a}_{tr1} \\ \mathbf{a}_{tr2} \end{bmatrix} = \mathbf{G} \otimes \mathbf{A} \text{ where } \mathbf{G} = \begin{bmatrix} \sigma_{a\ tr1}^2 & \sigma_{a\ tr2\ tr1} \\ \sigma_{a\ tr1\ tr2} & \sigma_{a\ tr2}^2 \end{bmatrix} \text{ and}$$
$$\operatorname{var} \begin{bmatrix} \mathbf{m}_{tr1} \\ \mathbf{m}_{tr2} \end{bmatrix} = \mathbf{N} \otimes \mathbf{M} \text{ where } \mathbf{N} = \begin{bmatrix} \sigma_{m\ tr1\ tr2}^2 & \sigma_{m\ tr2\ tr1} \\ \sigma_{m\ tr1\ tr2} & \sigma_{m\ tr2\ tr1}^2 \end{bmatrix}.$$

I is the identity matrix, A is the additive genetic relationship matrix between animals and M is the maternal genetic relationship matrix between animals.

Variance components and their standard errors were estimated using ASRemI (Gilmour *et al.*, 2006). When maternal genetic effects were significant for both traits, we included the variance for each trait. When only one of the traits in the bivariate model had significant maternal genetic effects, we included maternal genetic effects for that trait only.

Variance components for each trait were estimated first with a univariate model. The results of these univariate models were used as starting values in the bivariate analysis. To test if the genetic correlations between traits were significantly greater magnitude than zero we used likelihood ratio tests to compare the fit of two models. The first model was with no restrictions on the estimates for

variance and covariance and the second model restricted the covariance between the two traits to zero. The second model therefore reflects our null hypothesis that the genetic correlation is equal to zero. We also tested if genetic correlations were significantly different to 1 or -1 using likelihood ration tests.

We estimated the genetic parameters for how much fat and muscle changes in the sheep between the start and finish of the feed intake period. These new traits are change in muscle ($\Delta EMD = EMD2 - EMD1$) and change in fat ($\Delta CF = CF2 - CF1$).

The variance components of these muscle and fat change traits were calculated by estimating the covariance between both measurements. For example the additive genetic variance of change in muscle ΔEMD ($\sigma^2_{a(\Delta EMD)}$) is;

$$\sigma^{2}_{a (\Delta EMD)} = \sigma^{2}_{a EMD2} + \sigma^{2}_{a EMD1} - 2 x \text{ cov}_{a}(EMD2, EMD1)$$

where $\sigma_{a EMD2}^2$ is the additive genetic variance of EMD2, $\sigma_{a WEMD1}^2$ is the additive genetic variance of EMD1 and $cov_a(EMD2, EMD1)$ is the additive genetic covariance between EMD2 and EMD1.

The genetic correlations between fat and muscle change with intake and gas traits were calculated from the covariances between the two fat or muscle traits and the intake and gas traits and the variances of all three traits. For example, the genetic correlation between muscle change and Intake ($r_{g \ \Delta EMD,Intake}$) is;

$$r_{g \Delta EMD,Intake} = \frac{cov_{a}(EMD2,Intake) - cov_{a}(EMD1,Intake)}{\sigma_{a Intake} \times \sqrt{\sigma_{a EMD2}^{2} + \sigma_{a EMD1}^{2} - 2 \times cov_{a}(EMD1,EMD2)}}$$

To test if this genetic correlation was significantly greater magnitude than zero a likelihood ratio test was used to compare the fit of two models. The first model was with no restrictions on the estimates for variance and covariance and the second model required the covariance between EMD2 and Intake to be equal to the covariance between EMD1 and NLB. Making the covariances between each muscle and Intake equal makes the numerator for the correlation zero. The second model therefore reflects our null hypothesis that the genetic correlation is equal to zero.

For all traits we fitted fixed effects for group, birth and rear type, sex, pen, age of measurement. Significant fixed effects are in. For methane adjusted for intake, live weight and growth, we fit these covariates as second order polynomials, because it significantly improved the fit of the model. All significant interactions between significant fixed effects were also included.

We also used random regression to estimate the genetic correlations between feed intake measured for different durations. The length of feed intake measurement was a continuous function days of measurement from the first day to the 35th day. For example, feed intake measured for 1 day, the first 2 days, until all 35 days. This random regression analysis was done separately for post weaners, hoggets and adults.

 $Y = Xb + \theta_a k_a + \theta_p k_p + e,$

where **y** is a vector of observations for feed intake of individual sheep; **X** is the incidence matrix for the vector of the fixed effects **b**; θ_a and θ_p are the matrices with orthogonal polynomial coefficients of j x i dimensions where j is the number of polynomial coefficients and i is the number of days feed intake was measured (35) standardized to the first and last days. θ_a and θ_p correspond to the matrices with additive genetic and permanent environmental random regression coefficients \mathbf{k}_a and \mathbf{k}_p , and \mathbf{e} is the random residual. Permanent environmental effects were estimated to account for non-genetic effects common to repeated feed intake measurements.

We fitted the fixed curve of average live weight as a polynomial nested within year. We chose the order of polynomial using Maximum likelihood ratio tests. We also included the same fixed effects as for the feed intake averaged over 35 days. We then selected the order of fit for the random effects, additive genetic and permanent environmental by using Bayesian Information Criterion. We first

estimated the best fit for additive genetic effects up to 6th order and then for permanent environmental effects. The order of polynomial is in **Error! Reference source not found.**.

We included 35 separate residual variance classes along the duration of measurement x-axis, one for each duration because the residual variance for each separate live weight measurement estimated using the multivariate analysis was different.

Table 2. Order of polynomial used for fixed effect, additive genetic and permanent environmental random effects

Age	Fixed curve	Additive genetic	Permanent environment	
Post weaners	2	5	5	
Hoggets	3	5	4	
Adults	3	5	2	

Estimates of economic values

<u>MIDAS</u>

The analysis was done using the Great Southern version of the MIDAS suite of models. This model represents a typical farm in the Darkan/Kojonup region in the 500-600mm rainfall zone in the Great Southern of WA. The farm represented is mixed livestock and cropping with animals eating the crop stubbles as a feed source during summer and autumn. The base production levels were based on the top 25% of the Icon Agriculture farm benchmarking database (Ritchie *pers. comm.*).

The animal production system evaluated was a Merino wool system where Merino ewes are mated to merino rams. The model optimised flock structure by selecting the sale age of CFA ewes (5.5yo or 6.5yo), the sale age of surplus young ewes (either as lambs at 5mo or as hoggets at 18 mo) and the sale age of wethers (5mo through to 6.5yo). The flock structure was not re-optimised for the subsequent evaluation of each trait and the base case flock structure was used in each case. The nutrition of the ewes followed the Lifetime Ewe Management guidelines.

A standard set of prices reflecting a medium term outlook for agriculture was used for the analysis (Table 3). The prices are lower than the current wool and meat prices being received by producers and include a higher premium for fine wool than the current market. We used a medium term outlook because breeding objectives are selecting the best animals for the future. Therefore, they need to represent expected future prices for a region.

Parameter	Units	Standard
Wool price		
20µ	\$/kg (fleece wool)	9.50
FD premium	Price change per micron	5%
	3 1	
Animal sale price		
Store Lamb	\$/kg DW	3.75 (47)
Ewe Hogget	\$/ka DW / (\$/hd)	3.70 (75)
CFA Ewe 5.5vo	\$/kg DW / (\$/hd)	3.20 (69)
CFA Ewe 6.5vo	\$/kg DW / (\$/hd)	2.60 (59)
Wether Hogget	\$/kg DW / (\$/hd)	4 00 (75)
Older Wethers	\$/kg DW / (\$/hd)	1 40 (75)
		1.40 (70)
Supplementary Feed	Prices	
	\$/t DM fed out	315
Mothono		515
emissions		
CO ₂ equivalents	\$/t of CO ₂ -e	14

Table 3. Prices used in this analysis

¹ The 100 year global warming potential for methane (38/kg of CO_2 -e / kg of CH_4) was used to calculate the value of a tonne of CH_4 emissions. Therefore, the value of methane was \$476/t.

Modelling the Economic Values

Two changes were made to the model when calculating relative economic values:

- I. All fixed costs associated with animal production were changed to variable costs
- II. A cost on the land asset was introduced into the profit function to reflect 'normal profit' as a cost and result in a profit value that is close to zero.

Use of the MIDAS suite of optimisation models ensures that all management variables are optimised and this reduces any inaccuracies caused by scale variables. The calculation of the economic value of a trait should be done when other traits that are included in the breeding objective are held constant i.e. only the correlated change in traits that aren't in the breeding objective are valued. The rational for this is that the (genetically) correlated change in the other traits will be valued because of the change in that traits breeding value. An implication of this is that the economic value of a trait will change depending on the list of other traits included in the breeding objective.

The relative economic values were calculated as the increase in profit per hectare for a change in each trait. The change in each trait that was valued was based on the estimated genetic variance, except for NLW and intake for which the genetic variance was large and the change in profit may not have been linear over the specified range. In these instances a smaller value was used.

Traits Valued

Traits have been valued from the perspective of the commercial producer assuming that there is no effect on prices received for produce from improving any of the traits. This assumption is valid if decisions on breeding objectives are made independently by individual producers and they select diverse indices, however, it may not be valid for some traits if a majority of the industry follow a similar index.

This analysis has been done for a breeding objective that includes clean fleece weight (CFW), fibre diameter (FD), liveweight traits (WT), number of lambs weaned (NLW), intake and also daily methane production (DMP). These traits are expressed multiple times during the animal's lifetime (eg animals are shorn each year and therefore express CFW & FD each year) and they have been divided into

separate traits and each expression has been valued. The age groups were split on an annual time step to be consistent with the SelAction program that will be used to calculate the response to selection from the relative economic values generated in this analysis.

The traits were named using A# so the numeral was the age of the animal at the end of the period. The animals moved from one group to the next on their birthdays i.e. 1yo, 2yo, 3yo etc. This doesn't align with on-farm management where animals are sold based on shearing date, and therefore the shearing and selling events occur in the middle of the age group. This doesn't alter the calculation but it does make reporting of the results confusing. For example, the A3 age group includes the animals between 2 and 3 years of age and ends with the ewe having a lamb as a 3 year old. The confusion may occur because it includes the shearing of the 2yo animals that is occurring at 2 ½ years of age.

Table 4	. Traits	that	were	valued	in t	this	analysis	and	the	mechanism	through	which	the	trait
alters p	rofit						-				-			

Trait	The mechanism relating the trait to profit
CFW	Higher fleece value
FD	Higher fleece value
A1WT	Higher value for animals sold as lambs
A2WT	Higher sale value for surplus ewe hoggets
	Higher sale value for wether hoggets sold as export wethers
A3WT	Higher sale value of wethers sold as export wethers at this age
A4WT	Higher sale value of wethers sold as export wethers at this age
A5WT	Higher sale value of wethers sold as export wethers at this age
A6WT	Higher sale value of wethers sold as export wethers at this age
	Higher sale value of ewes sold CFA after 4 lambing opportunities
A7WT	Higher sale value of wethers sold as export wethers at this age
	Higher sale value of ewes sold CFA after 5 lambing opportunities
NLW	Increased number of animals for sale and alters the age structure of the flock
Intake	Reduced feed consumption throughout the whole year and the increased number of
	stock that can be carried or the reduced level of grain feeding required.
DMP	Generation of ACCUs for sale.

CFW = clean flece weight, FD = fibre diameter, A1WT = weight between birth and 1 yo, A2WT = weight between 1 and 2 years of age and includes hogget weight, AWT = adult weight during the 12 months prior to the specified age, NLW = number of lambs weaned, DMP = daily methane production.

The increase in CFW was assumed to result in a proportionate increase in fleece wool and oddments so the average wool price remains constant. A value wasn't calculated for the A1 age group because this is a minor shearing with the wool growth period being much less than 1 year. The correlation between CFW and body composition has not been included in this analysis.

The reduction in FD was valued assuming that it was not associated with a change in staple length or staple strength. There is, however, a small correlated change in the estimated hauteur of the wool which was calculated using the TEAM1 equation.

It was assumed that the weight increased for any sales that occurred during the 12 month period and, that ewe and wether liveweight were genetically the same trait and therefore changed by the same amount. The increases in A1 weight (animals sold as lambs) was utilised by selling the animals at the same age but at heavier weights rather than selling earlier at the same weight.

There is a phenotypic correlation between weaning weight and weaner survival. However, this was not represented and it was assumed that there was no genetic relationship between weaning weight and weaner survival during their first summer.

The mechanism for the increased number of lambs weaned (fertility, fecundity or survival) did not need to be included in this analysis because the traits that this affects (CFW, FD, PWWT & intake) are all traits for which relative economic values are being calculated in this analysis. This trait was only

calculated up to 6 years of age because 6 years of age is the last lambing opportunity that is represented in the MIDAS model.

The reduction in intake (kg/hd/d) was modelled as the reduction in the potential intake of the animals on high quality abundant feed. The reduction in intake on a poor quality or sparsely available feed was modelled as a proportion of the potential. This is consistent with the trait that was measured in the trials which was intake of a high quality pelleted diet. It is possible that intake of a high quality diet could be a different trait to intake of a poor quality diet but this has not been quantified in this analysis.

The reduction in methane was calculated based on a reduction in daily methane production (g/hd/d) multiplied by the number of sheep days for each age group during the year.

Results

Activity #1 and 2: Feed efficiency and methane production in relation to reproductive performance of ewe lambs and adult ewes

The total number of records for each trait and the mean with standard deviation of each trait at postweaning, hogget and adult age is summarised in Table 5. Sheep ate more over 24 hours, 48 hours and 35 to 42 days as they got older. Residual feed intake also increased as the sheep aged. Hoggets on average produced more methane, carbon dioxide and oxygen than adults and post weaners.

	post weaning			hogget	adult		
Trait	no	mean	no	mean	no	mean	
Intake	1476	1.4 (.302)	1046	2.03 (0.313)	443	2.17 (0.386)	
Intake24	1318	1.9 (.951)	676	2.2 (0.395)	361	2.34 (0.53)	
Intake48	1291	4.22 (2.22)	602	4.71 (0.887)	269	5.35 (1.31)	
RFI	1470	-0.009 (0.206)	1046	-0.000 (0.182)	443	0.0006 (0.238)	
CH4	2665	31.7 (10.3)	964	37.1 -12	436	32.7 (8.43)	
CO2	753	2.49 (0.375)	969	3.31 (0.508)	439	3.18 (0.417)	
02	755	18.8 (0.382)	970	17.9 (0.511)	439	17.8 (0.415)	
LW	2717	40.6 (9.12)	1046	59 (7.85)	443	71.1 (7.76)	
Growth	2714	0.226 (0.0565)	1043	0.27 (0.0824)	442	0.282 (0.0803)	
EMD1	1936	21.9 (4.64)	973	24.4 (3.58)	443	27.4 (3.66)	
EMD2	2032	26.9 (3.33)	996	31.1 (2.46)	442	33.3 (2.3)	
CF1	1934	2.17 (1.08)	972	2.21 (0.974)	443	2.87 (1.07)	
CF2	2024	3.69 (1.14)	995	4.63 (1.29)	442	5.26 (1.55)	
NLS	1532	0.561 (0.645)	991	1.01 (0.707)	437	1.43 (0.669)	
NLB	1531	0.48 (0.615)	782	0.849 (0.759)			
NLW	1530	0.37 (0.544)	782	0.708 (0.692)			
TBWT	1519	2.09 (2.76)	779	3.95 (3.45)			
TWWT	1528	8.45 (12.6)	780	17.9 (17.2)			
Wrinklebody	1179	1.9 (0.979)					
Winklebreach	1412	1.83 (0.999)					
CFW	2198	2.33 (0.87)	960	2.88 (0.76)	437	3.21 (0.82)	
FD	1833	17.6 (1.36)	897	17.4 (1.38)	318	17.3 (1.43)	
CVFD	1833	19.9 (2.44)	897	30.4 (28.8)			
SS	1615	42.9 (34.3)	815	25.5 (6.95)			
CI	1615	5Q 2 (21 5)	Q15	7/ 6 (10 2)			

Table 5. The total number of records for each trait and the mean with standard deviation in brackets for post weaning, hogget and adult ages

The phenotypic variance, heritability and maternal heritability for each trait across ages groups is summarised in Table 6. Maternal genetic effects were mostly not significant or low in all traits. Hoggets had the highest heritability for all traits. Feed intake measured across 35 days was the most heritable (range 0.31 to 0.49). Feed intake across 24 hours (range 0.15 to 0.19) and 48 hours (range 0.18 to 0.20) was less heritable than feed intake measured across 35 to 42 days. Residual feed intake had low to moderate heritability (range 0.07 to 0.29). Oxygen (range 0.10 to 0.20) and carbon dioxide (range 0.08 to 0.28) had similar heritabilities and were more heritable than methane (range 0.11 to 0.14).

Traits	Age'	$\sigma_{ m p}^2$	h ²	m²
Intake	pw	0.055 (0.00266)	0.31 (0.09)	-
	h	0.072 (0.00382)	0.49 (0.09)	-
	а	0.129 (0.00955)	0.42 (0.14)	-
Intake24	pw	0.444 (0.0241)	0.15 (0.04)	0.2 (0.03)
	h	0.239 (0.0177)	0.19 (0.07)	-
	а	0.421 (0.0433)	0.17 (0.09)	-
Intake48	pw	1.33 (0.0842)	0.18 (0.06)	0.03 (0.04)
	h	1.19 (0.101)	0.20 (0.09)	0.00 (0.00)
	а	2.26 (0.335)	0.20 (0.11)	0.00 (0.00)
RFI	pw	0.0345 (0.00155)	0.17 (0.07)	-
	h	0.0333 (0.00156)	0.29 (0.08)	-
	а	0.0566 (0.00383)	0.07 (0.08)	-
CH₄	pw	91.5 (3.59)	0.11 (0.03)	0.00 (0.00)
	h	114 (7.95)	0.14 (0.05)	0.02 (0.03)
	а	109 (9.56)	0.10 (0.06)	-
CO ₂	pw	0.119 (0.00909)	0.18 (0.08)	0.00 (0.00)
	h	0.234 (0.018)	0.28 (0.09)	0.03 (0.04)
	а	0.335 (0.0294)	0.08 (0.06)	-
O ₂	pw	0.123 (0.00928)	0.20 (0.08)	0.00 (0.00)
	h	0.271 (0.0169)	0.20 (0.06)	-
	а	0.293 (0.0308)	0.10 (0.08)	-

Table 3. Phenotypic variance (σ_p^2), heritability (h^2) and maternal heritability (m^2) with standard errors in brackets. Missing maternal heritabilities (-) were not significant

¹ pw = post weaning, h = hogget, a = adult

Correlations between traits

Genetic correlations between feed intake measured across 24 hours, 48 hours and 35 to 42 days was higher than phenotypic correlations apart for adults (Table 4). All genetic correlations between feed intake traits were significantly higher than zero and significantly different from 1 (p < 0.01). Genetic correlations between intake traits were higher in post weaners (range 0.94 to 0.99) than hoggets (range 0.70-0.97) and adults (range 0.46-0.98). Genetic correlations (range 0.62 to 0.99) between feed intake traits and residual feed intake were higher than phenotypic correlations (range 0.28 to 0.83) for post weaners and hoggets. Correlations between feed intake traits and residual feed intake were higher than phenotypic correlations (range 0.28 to 0.83) for post weaners. All genetic correlations between feed intake traits and residual feed intake in post weaners and hoggets were significantly greater than zero (p < 0.01).

Table 4 Phenotypic and genetic correlations between feed intake averaged across 35 days and feed intake measured 24 hours and 48 hours before methane measurements. Phenotypic correlations are above diagonal and genetic correlations are below diagonal. NC means the model did not converge because of singularity problems. Bold genetic correlations are significantly different magnitude to zero.

Post weaning	Intake	Intake24	Intake48	RFI
Intake	-	0.67 (0.01)	0.73 (0.01)	0.83 (0.00)
Intake24	0.94 (0.08)	-	0.90 (0.00)	0.49 (0.02)
Intake48	0.99 (0.06)	0.94 (0.04)	-	0.54 (0.02)
RFI	0.87 (0.05)	0.99 (0.16)	0.84 (0.13)	
Hogget				
Intake	-	0.56 (0.02)	0.60 (0.02)	0.64 (0.01)
Intake24	0.70 (0.26)	-	0.81 (0,01)	0.28 (0.03)
Intake48	0.73 (0.18)	0.97 (0.08)	-	0.30 (0.03)
RFI	0.82 (0.06)	0.66 (0.24)	0.62 (0.24)	
Adult				
Intake	-	0.82 (0.01)	0.82 (0.01)	0.65 (0.02)
Intake24	0.46 (0.68)	-	NC	0.47 (0.04)
Intake48	0.98 (0.07)	NC	-	0.45 (0.04)
RFI	0.33 (0.89)	0.42 (0.81)	0.74 (0.49)	. ,

At all ages' methane and carbon dioxide had strong phenotypic (range 0.71 to 0.74) and genetic correlations (range 0.34 to 0.86; **Error! Reference source not found.**). Genetic correlations between methane and carbon dioxide were not significantly different to 1 (p < 0.05). At all ages oxygen had mostly strong negative phenotypic (range -0.62 to -0.90) and genetic (range -0.13 to -0.98) correlations with carbon dioxide and methane. The genetic correlations between carbon dioxide and oxygen were significantly different from zero in post weaners and adults (p < 0.05). The bivariate analysis between carbon dioxide and oxygen in hogget's did not converge. It probably did not converge because the traits are too similar.

Table 5. Phenotypic and genetic correlations between methane, carbon dioxide and oxygen. Phenotypic correlations are above diagonal and genetic correlations are below diagonal. Bold genetic correlations are significantly different magnitude to zero. Genetic correlations with * are not significantly different to 1.

Post weaning	CH.	0.0	0.
	0114		
	-	0.78 (0.01)	-0.66 (0.02)
CO_2	0.76 (0.12)*	-	-0.71 (0.01)
O ₂	-0.48 (0.19)	-0.93 (0.07)	-
Hoggot			
nogget			
CH ₄	-	0.74 (0.01)	-0.59 (0.02)
CO_2	0.86 (0.07)*	-	NC
O ₂	-0.71 (0.16)	-NC	-
Adult			
CH ₄	-	0.71 (0.02)	-0.62 (0.03)
CO ₂	0.34 (0.60)	-	-0.90 (0.00)
O ₂	-0.13 (0.67)	-0.98 (0.07)	-

Intake traits had positive phenotypic correlations with methane, methane yield traits and carbon dioxide (range 0.24 to 0.74; Table 9). Some of these correlations in adults were close to zero. Most of the phenotypic correlations between intake traits and oxygen were medium to high negative (range - 0.48 to -0.70) with adults having mostly low positive correlations. Residual feed intake had phenotypic

correlations with methane, methane yield traits, oxygen and methane in the same direction as intake but not as strong. These residual feed intake correlations with methane, methane yield and carbon dioxide ranged from 0.08 to 0.30 and with oxygen ranged between -0.25 to -0.27. Intake traits and residual feed intake in adults had inconsistent phenotypic correlations in the opposite direction than in post weaners and hoggets apart for oxygen, methane produced per kg eaten and methane produced per kg growth.

	CH_4	CO ₂	O ₂	CH₄/LW	CH₄/Intake	CH₄/growth		
Post weaning								
Intake	0.46 (0.02)	0.74 (0.01)	-0.70 (0.02)	0.48 (0.02)	0.20 (0.02)	0.32 (0.02)		
Intake24	0.49 (0.02)	0.57 (0.02)	-0.55 (0.02)	0.48 (0.02)	0.33 (0.02)	0.37 (0.02)		
Intake48	0.52 (0.02)	0.57 (0.02)	-0.56 (0.02)	0.51 (0.02)	0.32 (0.02)	0.38 (0.02)		
RFI	0.16 (0.02)	0.30 (0.04)	-0.25 (0.04)	0.11 (0.03)	0.08 (0.03)	0.14 (0.02)		
Hogget								
Intake	0.54 (0.02)	0.71 (0.01)	-0.67 (0.01)	0.24 (0.04)	0.45 (0.02)	0.44 (0.03)		
Intake24	0.49 (0.02)	0.57 (0.02)	-0.48 (0.03)	0.29 (0.03)	0.37 (0.03)	0.39 (0.03)		
Intake48	0.43 (0.03)	0.52 (0.03)	-0.48 (0.03)	0.20 (0.04)	0.30 (0.03)	0.31 (0.03)		
RFI	0.18 (0.03)	0.29 (0.03)	-0.27 (0.03)	-0.34 (0.03)	0.21 (0.03)	0.18 (0.03)		
Adult								
Intake	0.57 (0.03)	0.01 (0.07)	-0.00 (0.07)	0.00 (0.07)	0.52 (0.03)	0.47 (0.04)		
Intake24	0.61 (0.03)	0.51 (0.04)	0.25 (0.04)	0.37 (0.05)	0.55 (0.03)	0.50 (0.04)		
Intake48	0.01 (0.07)	0.68 (0.03)	0.00 (0.05)	-0.00 (0.07)	0.39 (0.05)	0.24 (0.06)		
RFI	-0.70 (0.02)	-0.00 (0.07)	-0.32 (0.04)	-0.30 (0.05)	0.28 (0.04)	0.28 (0.04)		

Table 9. Phenotypic correlations between intake and gas traits.

Intake and residual feed intake had genetic correlations with gas traits mostly in the same direction as the phenotypic correlations (Table 10). All intake and residual feed intake traits in hoggets had significant positive genetic correlations with methane (p < 0.01; range 0.76 to 0.90). All intake and residual feed intake traits in post weaners and hoggets had significant positive genetic correlations with carbon dioxide (p < 0.01; range 0.65 to 0.96). All intake and residual feed intake traits in post weaners and hoggets had significant negative genetic correlations with oxygen (r < 0.01; range -0.95 to -0.62) apart from residual feed intake in post weaners. All intake and residual feed intake traits in hoggets had significant genetic correlations with methane produced per kg growth (p < 0.05; range 0.66 to 0.89). The only other significant correlation was between intake and methane produced per kg intake in hoggets (p < 0.01; 0.90).

	CH_4	CO ₂	O ₂	CH ₄ /LW	CH₄/Intake	CH₄/growth		
Post weaning								
Intake	0.42 (0.18)	0.86 (0.07)	-0.82 (0.09)	0.44 (0.18)	0.16 (0.21)	0.20 (0.22)		
Intake24	0.53 (0.21)	0.71 (0.16)	-0.76 (0.13)	0.51 (0.21)	0.23 (0.24)	0.35 (0.25)		
Intake48	0.51 (0.19)	0.79 (0.12)	-0.74 (0.13)	0.47 (0.20)	0.14 (0.23)	0.32 (0.23)		
RFI	0.17 (0.25)	0.68 (0.22)	-0.40 (0.25)	0.14 (0.25)	0.07 (0.24)	0.06 (0.26)		
Hogget								
Intake	0.77 (0.13)	0.96 (0.03)	-0.95 (0.03)	0.44 (010)	0.90 (0.10)	0.71 (0.17)		
Intake24	0.88 (0.13)*	0.86 (0.10)	-0.62 (0.20)	0.21 (0.55)	0.65 (0.25)	0.66 (0.25)		
Intake48	0.90 (0.14)	0.62 (0.19)	-0.63 (0.20)	0.22 (0.71)	0.60 (0.28)	0.78 (0.26)		
RFI	0.76 (0.18)	0.65 (0.14)	-0.62 (0.15)	-0.87 (3.60)	0.46 (0.24)	0.89 (0.27)		
Adult								
Intake	0.69 (0.21)*	0.35 (0.32)	-0.23 (5.52)	-0.28 (0.42)	0.47 (0.27)	0.65 (0.26)		
Intake24	0.64 (0.28)*	0.20 (4.27)	-0.88 (0.18)	0.27 (0.51)	0.37 (0.37)	0.64 (0.34)		
Intake48	0.51 (0.34)	0.49 (1.64)	-0.12 (4.50)	-0.31 (0.49)	0.12 (0.40)	0.28 (0.47)		
RFI	0.21 (0.73)	0.06 (2.40)	-0.09 (1.00)	-0.04 (0.71)	0.36 (0.55)	0.81 (0.88)		

Table 10. Genetic correlations between intake and gas traits. Bold correlations are significantly different magnitude to zero. Correlations with * are not significantly different to 1.

Correlations between ages

All correlations for each trait between ages were positive (Table 11). All genetic correlations between ages were significantly lower than 1. Genetic correlations were higher than phenotypic correlations (**Error! Reference source not found.**). Most the genetic correlations between hoggets and adults (range 0.62 to 0.90) were higher than between post weaners and hoggets (range 0.36 to 0.81) and post weaners and adults (range 0.00 to 0.64). Residual feed intake was generally not correlated phenotypically or genetically between ages. Intake (range 0.64 to 0.78) and methane (range 0.62 to 0.86) had consistently high correlations between ages. Residual feed intake had the lowest genetic correlations between ages (range 0.00 to 0.75) with high errors. Oxygen and carbon dioxide had high genetic correlations between post weaners and hoggets (range 0.72 to 0.76) and between hoggets and adults (range 0.69 to 0.90). Oxygen and carbon dioxide have low genetic correlations between post weaners and adults (range 0.03 to 0.16).

Phenotypic	Post weaning/ hogget	Post weaning /adult	Hogget / adult
Intake	0.48 (0.03)	0.25 (0.05)	0.58 (0.03)
RFI	0.15 (0.03)	0.04 (0.05)	0.33 (0.04)
CH_4	0.40 (0.03)	0.38 (0.04)	0.32 (0.04)
CO ₂	0.43 (0.03)	0.32 (0.05)	0,46 (0,03)
O ₂	0.38 (0.04)	0.25 (0.06)	0.45 (0.03)
Genetic	Post weaning/ hogget	Post weaning /adult	Hogget / adult
Intake	0.74 (0.09)	0.64 (0.17)	0.78 (0.12)
RFI	0.36 (0.22)	0.00 (0.53)	0.75 (0.74)
CH₄	0.81 (0.14)	0.86 (0.15)	0.62 (0.26)
CO ₂	0.76 (0.16)	0.03 (0.56)	0.90 (0,22)
O ₂	0.72 (0.17)	0.16 (0.50)	0.69 (0.40)

Table 11. Phenotypic and genetic correlations between ages for feed intake, residual feed intake, methane, carbon dioxide and oxygen. Phenotypic correlations are on top. Bold genetic correlations are significantly different magnitude to zero.

All traits had genetic correlations significantly higher than zero between post weaners and hoggets (p < 0.01;Table 11) apart from residual feed intake. Only intake and methane had significant genetic correlations (p < 0.01) between post weaning and adults. All traits had genetic correlations significantly higher than zero between hoggets and adults (p < 0.01) apart from methane *Correlations between intake, gas and production traits*

Live weight and growth had moderate to high positive phenotypic correlations with intake, carbon dioxide and methane (range 0.33 to 0.67), low with residual feed intake (range -0.02 to 0.12) and moderate to high with oxygen (range -0.46 to -0.61; Table 12). Live weight and growth had significant positive genetic correlations with intake at all ages (range 0.50 to 0.94). Growth rate and intake had significant positive genetic correlations with residual feed intake at hogget age only (range 0.42 to 0.48). Growth rate and intake had significant positive genetic correlations with residual feed intake at hogget age only (range 0.42 to 0.48). Growth rate and intake had significant positive genetic correlations with carbon dioxide and methane (range 0.45 to 0.85) and significant negative genetic correlations with oxygen (range -0.44 to -0.71) at post weaning and hogget ages. All other genetic correlations were not significantly different from zero.

Table 12. Phenotypic (top half) and genetic (bottom half) correlations between growth and live weight traits with intake, residual feed intake, methane, carbon dioxide and oxygen traits. Bold genetic correlations are significantly different to zero.

Phenotypic	Intake	RFI	CH_4	CO ₂	O ₂
Post weaners					
LW	0.52 (0.02)	0.12 (0.02)	0.40 (0.01)	0.67 (0.02)	-0.64 (0.02)
Growth	0.46 (0.02)	0.09 (0.02)	0.41 (0.01)	0.53 (0.02)	-0.46 (0.02)
Hoggets					
LW	0.61 (0.02)	-0.00 (0.03)	0.48 (0.02)	0.54 (0.02)	-0.51 (0.02)
Growth	0.61 (0.02)	0.04 (0.03)	0.49 (0.02)	0.56 (0.02)	-0.54 (0.02)
Adults					
LW	0.47 (0.03)	-0.02 (0.04)	0.33 (0.04)	0.46 (0.03)	-0.52 (0.03)
Growth	0.67 (0.02)	0.01 (0.04)	0.50 (0.03)	0.63 (0.02)	-0.61 (0.03)
	(· · · ·	(
Genetic					
Post weaners					
LW	0.50 (0.10)	0.12 (0.17)	0.62 (0.09)	0.85 (0.06)	-0.80 (0.07)
Growth	0.61 (0.13)	0.35 (0.20)	0.63 (0.12)	0.45 (0.18)	-0.44 (0.18)
	· · · ·	(<i>, ,</i>	· · · ·	· · · ·	
Hoggets					
LW	0.76 (0.06)	0.42 (0.16)	0.71 (0.10)	0.72 (0.08)	-0.71 (0.08)
Growth	0.74 (0.07)	0.48 (0.16)	0.84 (0.09)	0.78 (0.08)	-0.83 (0.07)
	· · · ·	· · /	· · · ·	· · · ·	
Adults					
LW	0.94 (0.09)	0.37 (0.51)	-0.01 (0.41)	0.30 (1.67)	-0.16 (3.18)
Growth	0.83 (0.12)	0.58 (0.51)	0.55 (0.29)	0.79 (0.33)	-0.60 (0.30)

Fat and muscle had generally low negative phenotypic correlations with intake, residual feed intake, methane and oxygen (range -0.53 to 0.16) and low positive correlations with oxygen (range -0.20 to 0.42; 13). Phenotypic correlations between muscle and fat measured at the end of the feed intake period (EMD2 and FAT2) with intake, residual feed intake, methane and oxygen were almost always more positive than fat and muscle measured at the start of the feed intake measurement period. This relationship was opposite for oxygen.

The genetic correlations between fat and muscle with intake, residual feed intake, methane, carbon dioxide and oxygen followed similar patterns to the phenotypic correlations. Muscle measured at the start had significant negative genetic correlations with intake (post weaners and adults), residual feed intake and carbon dioxide (post weaners only; Table 13). Muscle measured at the end had significant negative genetic correlations with intake (post weaners and hoggets) and methane (post weaners) but significant negative with intake in adults. Fat measured at the start had significant negative genetic correlations with intake (post weaners and hoggets), residual feed intake (post weaners), methane (post weaners and hoggets) and carbon dioxide (post weaners) but a significant positive genetic correlation with oxygen (post weaners). Fat measured at the end only had a significantly negative genetic correlation with methane in post weaners.

Table 13. Phenotypic (top half) and genetic (bottom half) correlations between muscle and fat traits corrected for live weight with intake, residual feed intake, methane, carbon dioxide and oxygen. Bold genetic correlations are significantly different to zero.

	1 4 1				
Phenotypic	Intake	RFI	CH_4	CO_2	0 ₂
Post weaners					
EMD1	-0.13 (0.03)	-0.09 (0.02)	-0.06 (0.02)	-0.12 (0.04)	0.09 (0.04)
EMD2	-0.02 (0.03)	-0.04 (0.02)	-0.04 (0.02)	-0.00 (0.04)	0.03 (0.04)
CF1	-0.37 (0.02)	-0.18 (0.03)	-0.12 (0.02)	-0.37 (0.03)	0.38 (0.03)
CF2	-0.05 (0.03)	0.08 (0.03)	-0.12 (0.02)	-0.13 (0.04)	0.17 (0.04)
Hoggets					
EMD1	-0.18 (0.03)	-0.24 (0.03)	-0.17 (0.03)	-0.13 (0.03)	0.07 (0.03)
EMD2	-0.24 (0.03)	-0.17 (0.03)	-0.11 (0.03)	-0.12 (0.03)	0.05 (0.03)
CF1	-0.27 (0.03)	-0.22 (0.03)	-0.19 (0.03)	-0.21 (0.03)	0.19 (0.03)
CF2	-0.13 (0.03)	-0.13 (0.03)	-0.04 (0.03)	-0.11 (0.03)	0.06 (0.03)
		· · /		· · /	· · /
Adults					
EMD1	-0.53 (0.03)	-0.47 (0.03)	-0.38 (0.04)	-0.39 (0.04)	0.36 (0.04)
EMD2	0.13 (0.04)	-0.17 (0.04)	0.07 (0.04)	0.16 (0.04)	-0.20 (0.04)
CF1	-0.53 (0.03)	-0.51 (0.03)	-0.33 (0.04)	-0.00 (0.05)	0.42 (0.04)
CF2	-0.37 (0.04)	-0.25 (0.04)	-0.20 (0.05)	-0.33 (0.04)	0.31 (0.05)
	(()				
Genetic					
Post weaners					
EMD1	-0.49 (0.15)	-0.57 (0.17)	-0.22 (0.17)	-0.60 (0.17)	0.30 (0.19)
EMD2	-0.37 (0.17)	-0.38 (0.19)	-0.38 (0.17)	-0.13 (0.23)	-0.05 (0.20)
CF1	-0.63 (0.11)	-0.50 (0.15)	-0.29 (0.13)	-0.62 (0.14)	0.46 (0.14)
CF2	-0.16 (0.16)	-0.14 (0.18)	-0.46 (0.13)	-0.35 (0.20)	0.33 (0.18)
		· · /	. ,	· · /	. ,
Hoggets					
EMD1	-0.24 (0.18)	-0.19 (0.23)	-0.33 (0.24)	0.00 (0.22)	0.01 (0.22)
EMD2	-0.39 (0.16)	-0.06 (0.25)	-0.35 (0.25)	-0.19 (0.22)	0.09 (0.23)
CF1	-0.34 (0.14)	-0.21 (0.18)	-0.43 (0.19)	-0.18 (0.17)	0.30 (0.16)
CF2	-0.17 (0.13)	-0.06 (0.17)	0.01 (0.20)	-0.06 (0.16)	-0.01 (0.16)
	(0			(0	
Adults					
EMD1	-0.69 (0.19)	-0.17 (0.64)	-0.73 (0.32)	-0.92 (0.59)	0.65 (0.35)
EMD2	0.89 (0.29)	0.04 (0.71)	0.08(0.63)	0.68 (0.67)	-0.84 (0.43)
CF1	-0.41 (0.29)	0.02 (0.77)	-0.29 (0.45)	-0.08 (3.35)	0.89 (0.32)
CF2	-0.23 (0.22)	-0.00 (0.47)	-0.03 (0.34)	-0.60 (0.29)	0.53(0.26)

Change in fat and muscle had positive correlations with intake (Table 14). This is because when the covariance between the first measurement and intake is lower than the covariance between the second measurement and intake, the correlation became positive.

Table 14. Phenotypic (top half) and genetic (bottom half) correlations between change in muscle (Δ EMD) and change in fat (Δ CF) from the start to the finish of the feed intake period and live weight traits with intake, residual feed intake, methane, carbon dioxide and oxygen traits. Bold genetic correlations are significantly different to zero.

Phenotypic	Intake	RFI	CH_4	CO ₂	O ₂
Post weaners					
ΔEMD	0.22 (0.02)	0.05 (0.03)	0.14 (0.02)	0.24 (0.03)	-0.17 (0.03)
ΔCF	0.35 (0.02)	0.25 (0.03)	0.07 (0.02)	0.25 (0.04)	-0.20 (0.04)
Hoggets					
ΔEMD	0.18 (0.03)	0.16 (0.03)	0.21 (0.03)	0.16 (0.03)	-0.14 (0.03)
ΔCF	0.22 (0.03)	0.06 (0.03)	0.22 (0.03)	0.19 (0.03)	-0.21 (0.03)
Adults					
ΔEMD	0.52 (0.03)	0.35 (0.04)	0.35 (0.04)	0.40 (0.04)	-0.36 (0.04)
ΔCF	0.24 (0.05)	0.08 (0.04)	0.17 (0.05)	0.19 (0.04)	-0.18 (0.05)
Genetic					
Post weaners					
ΔEMD	0.84 (0.22)	0.68 (0.30)	-0.04 (0.33)	0.71 (0.23)	-0.59 (0.26)
ΔCF	0.54 (0.12)	0.49 (0.16)	0.08 (0.16)	0.24 (0.18)	-0.03 (0.17)
		. ,	. ,		. ,
Hoggets					
ΔEMD	0.42 (0.23)	0.43 (0.29)	0.48 (0.28)	0.13 (0.28)	-0.23 (0.27)
ΔCF	0.34 (0.15)	0.29 (0.20)	0.69 (0.17)	0.37 (0.17)	-0.55 (0.15)
	. ,	ζ, γ	. ,	()	. ,
Adults					
ΔEMD	0.73 (0.20)	0.50 (0.60)	0.83 (0.35)	0.55 (0.59)	-0.55 (0.40)
ΔCF	0.26 (0.23)	0.12 (0.44)	0.28 (0.34)	0.07 (0.59)	0.00 (0.43)

All reproduction traits had mostly low positive phenotypic correlations with intake, residual feed intake, methane and carbon dioxide (range -0.04 to 0.14) and low negative correlations with oxygen (range - 0.15 to -0.03). Reproduction had negative genetic correlations with intake and gas traits. However these correlations had very high errors and none were significantly different from zero.

All phenotypic correlations between wool traits and intake, residual feed intake, methane, carbon dioxide and oxygen were low (range -0.18 to 0.23). There was only two genetic correlations significantly different to zero between intake and fibre diameter in post weaners (0.31) and between methane and wrinkle body score in post weaners (-0.39).

Genetic correlations between feed intake measured over different periods

Post weaners had more accurate genetic correlations than hoggets and adults (Fig. 1). Post weaners had genetic correlations with 35 day measurements above 0.90 around 15 days. Hoggets and adults had different curves than post weaners and did not reach genetic correlations above 0.9 until 20 days (hoggets) and 25 days (adults), respectively. There were fewer measurements at hogget and adult age than post-weaning age which contributed to the higher error. The low genetic correlations and the high error between measurements between 1 and 10 days could be because animals had just entered the feed intake facility. Therefore, they were still adjusting to the pen and their pen mates.



Figure 1. Genetic correlations between feed intake measured for 1 to 35 days with feed intake measured for 35 days. Correlations are for post weaners, hoggets and adults.

Activity #3: Whole farm systems modelling and development of methane selection indices and potential CFI methodologies

The base case farm is presented in Table 15. It is a 2130 ha property running 9560 DSE on 1099 ha at 8.7 DSE/ha. The optimum flock structure is selling cast-for-age ewes (CFA) at 5.5 years and, selling surplus young ewes and the wethers after hogget shearing at 17 months of age. The lambing percentage is 82% and this results in a flock that has 69% of the total DSE as ewes.

	Units	
Profit ¹	\$/farm	40
	\$/ha	0.02
Farm size	ha	2130
Area of Pasture	ha	1099
	% of farm	52%
Stocking rate	DSE/WG ha	8.5
Number of ewes	hd	3808
No. of ewe hoggets	hd	1081
Lambing %	Lambs/ewe joined	82
Flock structure	% ewes	69
	Sale age ewes (yr)	5.5
	Sale age wethers (yr)	1.5
Grain feeding	kg/DSE	19.2
Grazing days	Sheep.d/ha	
A1		523
A2		330
A3		171
A4		162
A5		154
A6		69
A7		0

Table 15	The standard	farm	production	profile
	i ine stanuaru	am	production	prome

¹ Profit includes an extra cost on assets to scale the profit to a level close to zero which represents long term normal profit (after Goddard 1998).

Clean fleece weight (\$12.5/ha/genetic standard deviation) was relatively more important than live weight (\$9.9), number of lambs weaned (\$7.0), feed intake (-\$6.1), methane (-\$2.28) and fibre diameter (-\$2.3). Production traits, particularly live weight, had a high economic value because feed intake was included in the breeding objective and hence changes in energy requirements for increasing the production traits were not included in the calculation of their relative economic value.

The relative economic value of each trait has a higher magnitude for the younger expressions of the trait (Table 16). The main driver of this result is the greater number of animals on the farm in the younger age groups, however, for some traits there is also a change in value per head with age. The REV of FD reduces with age because of the lower clean fleece weight of older animals. The value of liveweight is zero for most age groups because no animals are being sold at these ages and hence there is no value of being heavier except at the hogget age and at 5.5 years when animals are being sold. The variation in the REV of intake also varies with the diet quality required by each age group. Younger growing animals require a higher quality and more expensive diet than older animals so the REV of intake is higher per grazing day for the younger animals. The A6Intake has a very low REV because the animals are only the farm for half the year and it is mostly during the spring period when pasture is abundant and has a low value.

The REVs for liveweight would vary markedly if the flock structure (being the sale age of the ewes and wethers) evaluated in the modelling analysis was changed. The overall impact of this in a breeding programme will depend on the correlation between liveweight at different ages and how closely the actual sale age aligns with the sale age used in the calculation of the REVs.

The relative economic values that have been calculated in this analysis can be used in conjunction with heritability, variance and correlations to calculate the response to selection. These calculations would indicate the optimum breeding outcome for breeders producing rams for this environment.

Trait & Age	Units	Trait change	Change in Profit	REV	REV
-		evaluated	(\$/ha)	(\$/ha/unit)	(\$/ha/sd)
Clean Fleece Weig	ght				
A2	kg CFW/yr	0.47	6.44	13.70	6.44
A3	kg CFW/yr	0.44	1.78	4.04	1.78
A4	kg CFW/yr	0.44	1.52	3.46	1.52
A5	kg CFW/yr	0.44	1.44	3.28	1.44
A6	kg CFW/yr	0.44	1.38	3.14	1.38
A7	kg CFW/yr	0.44	0.00	0.00	0.00
Fibre Diameter					
A2	μ	-0.93	-0.88	-0.942	-0.88
A3	μ	-0.84	-0.37	-0.443	-0.37
A4	μ	-0.84	-0.42	-0.502	-0.42
A5	μ	-0.84	-0.37	-0.443	-0.37
A6	μ	-0.84	-0.32	-0.386	-0.32
A7	μ	-0.84	0.00	0.000	0.00
Liveweight (Growt	h Rate)				
A1	kg	3.2	0.00	0.000	0.00
A2	kg	4.8	7.24	1.508	7.24
A3	kġ	5.3	0.00	0.000	0.00
A4	kg	5.3	0.00	0.000	0.00
A5	kg	5.3	0.00	0.000	0.00
A6	kg	5.3	2.66	0.502	2.66
A7	kg	5.3	0.00	0.000	0.00
Number of Lambs	Weaned				
A2	lambs/ewe	0.11	1.51	13.7	1.88
A3	lambs/ewe	0.11	1.44	13.1	1.79
A4	lambs/ewe	0.11	1.37	12.4	1.71
A5	lambs/ewe	0.11	1.31	11.9	1.63
A6	lambs/ewe	0.11	0.00	0.0	0.00

Table 16. Change in profit for the change in each trait the economic value (EV) for a 1 unit change in each trait (\$/ha), and the Relative Economic values (REV) which is the change per genetic standard deviation and the unit of change evaluated.

Intake					
A1	kg/d	-0.1	-1.97	-19.72	-2.56
A2	kg/d	-0.1	-0.62	-6.18	-1.16
A3	kg/d	-0.1	-0.34	-3.42	-0.78
A4	kg/d	-0.1	-0.32	-3.25	-0.74
A5	kg/d	-0.1	-0.31	-3.09	-0.71
A6	kg/d	-0.1	-0.04	-0.41	-0.09
A7	kg/d	-0.1	0.00	0.00	0.00
Daily Methane	e Production				
A1	g/d	-1	0.25	-0.249	-0.79
A2	g/d	-1	0.16	-0.157	-0.64
A3	g/d	-1	0.08	-0.082	-0.26
A4	g/d	-1	0.08	-0.077	-0.26
A5	g/d	-1	0.07	-0.073	-0.23
A6	g/d	-1	0.03	-0.033	-0.10
A7	g/d	-1	0.00	0.000	0.00

Discussion

Merino sheep that eat less and are more feed efficient and produce less methane. Therefore, we accepted our hypothesis that breeding sheep that eat less and have a lower residual feed intake produce less methane. More efficient sheep are therefore better for the environment. More efficient animals produce less methane because less energy is lost from methane production. Additionally, selecting for intake and gas traits in post weaners and hoggets will also select the best performing adults.

The phenotypic and genetic correlations between intake, residual feed intake with methane ratio traits were positive but weaker than just methane. Most genetic correlations were not significant, although hoggets that eat more and are inefficient produce more methane per kg of growth. Also hoggets that eat more also produce more methane per kg of feed they eat. Sheep that have a lower residual feed intake eat less, but this relationship gets weaker as the sheep age. This may be because post weaners, hoggets and adults have different requirements for growth and maintenance.

Feed intake and residual feed intake are important traits for increasing the efficiency of production. Feed intake, however, is expensive and impractical to measure in large numbers and unlikely to be used commercially by Australian sheep breeders. Genetic correlations between feed intake measured over different periods indicated that at post-weaning age after 15 days there was a genetic correlation above 0.90 with intake measured over 35 to 52 days. Hoggets and adults needed intake to be measured over 20-25 days to achieve a genetic correlation exceeding 0.90 with intake measured over 35-42 days. Hoggets and adults had fewer measurements which contributed to the higher error. With more measurements, perhaps the curve would be more similar to the curve for post weaners. Also, with random regression using polynomials, sometimes the curves can be erratic when there is high error from lack of records. Therefore, more measurements or lower order polynomials might reduce the uncertainty of these curves. In conclusion, it is possible to measure feed intake for less days. This will make feed intake cheaper to measure with less labour and feed required.

Feed intake had strong genetic correlations between methane, carbon dioxide and oxygen. Therefore, these traits are good alternatives traits for measuring feed intake. These gas traits were measured with portable respiration chambers over 40 minutes. They are therefore a lot cheaper and faster to measure than feed intake. Therefore genetic improvement of methane production is one way to get a permanent and continuous reduction in methane production and potentially improve efficiency.

Oxygen and carbon dioxide were more heritable than methane so are better candidate traits for feed intake. Also, phenotypically and genetically, feed intake is most closely explained by carbon dioxide and oxygen. Methane also has medium to strong phenotypic and genetic correlations with intake but not as strong as carbon dioxide and oxygen. Because of these close relationships between intake and gas traits, sheep that are more efficient with lower residual feed intake also produce less methane and carbon dioxide.

Some studies suggested that genotype by environment interactions are important if the genetic correlation is below 0.8. Therefore, selecting for low methane in post weaners will also select the hoggets and adults with the lowest methane. Also, selecting for low carbon dioxide in hoggets will also select the adults with low carbon dioxide. Alternatively, other studies suggested that optimal breeding strategies are affected when genetic correlations between environments are below 0.61. Therefore, breeders can select for intake in post weaners and residual feed intake, oxygen, and carbon dioxide in hoggets without having to select again in adults. This is important for breeding programs because it decreases the generation interval and increases response to selection. In other words, the best animals can be identified earlier and used earlier for mating. Therefore, their genes are passed on earlier making the breeding program more effective.

If methane were to be included into a selection index then it may be best to include methane instead of methane yield. Some researchers suggested that methane produced per kg of product produced should be used instead of including methane alone. Methane yields, however, involve traits that often have high phenotypic or genetic correlations which makes it difficult to control the direction of change for both traits in the yield. Our results suggest that decreases in methane yield also decreases feed intake. Therefore, for this to happen, the decrease in methane production needs to be more than feed intake. Therefore, including yield in breeding programs for sheep would not be more effective than selecting for lower methane and intake simultaneously. Additionally, the differences in heritability and additive genetic variance between intake and methane suggest that response to selection would be easier for feed intake compared to methane. Therefore, more selection pressure would be needed for methane than intake to decrease it compared to feed intake. In conclusion, to have a more transparent selection strategy, methane should be in an index with other production traits and feed intake.

It is difficult to select for high growth in sheep and decrease feed intake and methane production. This is easier to do in post weaners where growth is potentially more important. Residual feed intake had lower genetic correlations with live weight and growth than intake that were not significantly different to zero for post weaners and adults. Therefore, it is easier to make animals more feed efficient whilst growing faster. Therefore, we accepted our hypothesis that more efficient animals can produce less methane per unit of production because the genetic correlations between residual feed intake and growth were not too high and generally not significantly different to zero.

Sheep that were fatter and musclier at the start and finish of the feed intake periods ate less genetically and phenotypically than skinnier and less muscular at the same live weight. Perhaps animals that were skinnier ate more to compensate on the high quality diet. The genetic correlations between fat and muscle and intake are more negative at the start of the period than the finish. Therefore, change in fat and muscle had positive correlations with intake. This is because when the covariance between the first measurement and intake is lower than the covariance between the second measurement and intake, the correlation becomes positive. Therefore, skinnier and less muscular sheep ate more and gained more fat and muscle than fatter and more muscular sheep.

Wool and reproduction traits had very low genetic and phenotypic correlations with intake, residual feed intake and gas traits. This means that breeders can select for more wool, lambs and improve the quality of wool whilst simultaneously selecting for lower intake, methane and carbon dioxide.

Clean fleece weight (\$12.5/ha/genetic standard deviation) was relatively more important than live weight (\$9.9), number of lambs weaned (\$7.0), feed intake (-\$6.1), methane (-\$2.28) and fibre diameter (-\$2.3). Production traits had a high economic value, particularly live weight, because feed intake was included in the breeding objective. Therefore, changes in energy requirements for increasing live weight were not included to avoid double counting.

The main antagonistic relationships were between methane, feed intake and live weight, they have moderate positive genetic correlations (ranging from 0.50 to 0.94) and opposing economic values. Because of the antagonism between these traits it is expected that the optimal breeding objective for merinos will slow the rate of increase in methane and feed intake as was found in other research for meat sheep.

In conclusion, selecting for lower feed intake and residual feed intake will reduce methane and carbon dioxide production in Merino sheep eating high quality pellets. Additionally, carbon dioxide could be used as an indicator trait for feed intake. Carbon dioxide is a good indicator trait because it has high genetic and phenotypic correlations with feed intake and a higher accuracy than methane and oxygen. Therefore, it can be measured cheap and quickly in portable accumulation chambers providing a good alternative to expensive feed intake measurements. Also, sheep can be selected for feed intake, residual feed intake or gas traits either as post weaners or hoggets. Farmers and breeders can select to improve most production traits, decrease intake and methane and improve feed efficiently simultaneously. It is difficult to make sheep grow faster without also increasing intake and methane production, although it seems that it is possible in some sheep to grow fast whilst being more feed efficient.

Non Merinos in Victoria

Methodology

Experimental Animals

We measured feed intake between 2014 and 2016 in Maternal Composite (predominantly Coopworth base) ewes (n= 505) born in 2013 and 2014. Feed intake was measured at two ages for the 2014, and three ages for the 2013 drop, all ages represented the same group of sheep. For the 2014 drop ewes, post weaning and hogget ages were 311 days (209 ewes) and 533 Days (210 ewes) respectively. For the 2013 drop ewes, post weaning age was 322 days (94 ewes) hogget age 536 days (208 ewes) and adult age was 859 days (232 ewes) (Table 17). We measured the sheep at the automatic feeding facility at Agriculture Victoria (Department of Economic Development, Jobs, Transport and Resources) Hamilton, Victoria.

Status	Number	Age at Start	Start LWT	Start CS	Start EMD	Start C2
		(days)	(kg)	(units)		Fat Depth
Post Weaning		314 <i>± 15</i>	39.3 ±4.2			
2013 Drop	94	322 ± 24	39.1 ± 4.7			
2014 Drop	209	311 ± 5	39.4 ± 4.0		38.8 ± 3.3	2.6 ± 0.5
Hogget		534 ± 19	54.0 ± 6.8	2.97 ± 0.32	27.3 ± 3.8	3.8 ± 0.9
2013 Drop	208	536 ± 26	51.7 ± 6.2	2.96 ± 0.35	26.4 ± 3.9	2.0 ± 0.9
2014 Drop	210	533 ± 5	56.3 ± 6.6	2.99 ± 0.29	28.2 ± 3.5	2.4 ± 0.7
Adult (2013 Drop)	232	859 ± 23	62.0 ± 6.8	3.05 ± 0.42	30.8 ± 3.3	3.3 ± 1.5

Table 17. Characteristics of Ewes at the start of each feed intake test period

Feed Intake Facility and Management

The automatic feed intake facility records individual feed intake of group housed sheep. The facility has 10 pens, each fitted with two feed units. Feed units allow a single sheep to feed at a time, with the feeding sheep separated from other sheep by an electronically locking gate. Individual feed intake was recorded using electronic identification and weighing daily intake (Zi-argus Australia). The duration of feeding and the weight of feed eaten was automatically recorded using electronic scales and weigh bars. The data was recorded and managed using specially designed software (FMS, Zi-argus Australia).

Ewes were adapted to the pelleted ration for 10 to 14 days. The ewes were fed the pellets *ad libitum* from self-feeders in a small holding paddock with minimal pasture cover. After adaptation to the diet we randomised the ewes by sire (or sire syndicate) and weight into the 10 pens (not greater than 24 ewes/ pen). Sheep were grouped by live weight to reduce bullying and shy feeding. Additionally, the chutes leading to the feeders could be adjusted to the size of the sheep in the pen so that only one sheep entered the feeder at a time.

Sheep were allowed up to 14 days to adapt to the feed units and feed intake was recorded for a minimum of 35 days following adaptation (indicated by consistent use of feed intake units by all sheep). Mean number of days with intake recorded was 42 for post weaning age, 41 for hogget age and 47 for adult age ewes. These test periods are in accordance with Cockrum *et al.* (2013) who found a 42 day test was required to determine RFI in sheep. Sheep were allowed ad libitum access to the feed during the intake testing period, the number of visits to the feeder were restricted only by the dynamics of ewes in the pen.

Outside of feed intake test periods, sheep were managed in two age based mobs at the DEDJTR Hamilton farm. Ewes were managed with common farming practices including joining, crutching and shearing.

Rations

During feed intake testing, all sheep were fed cereal straw based 9mm pelleted ration (Heywood Stockfeeds, Victoria, Australia; Table 18). Pellets were analysed by NIR to have a digestibility (DMD) of 65 (\pm 2.4) %, metabolisable energy content of 9.8 (\pm 1.6) MJ/kg DM, crude protein content of 9.6 (\pm 0.58) % and neutral detergent fibre content (NDF) of 48 (\pm 3.18) %.

Table 18.	Typical	Ingredient	composition	n of ration fe	ed durina	feed intake testing.
	i ypioui	ingreatent	oompositioi		sa aaring	recu mane testing.

Ingredient	Percentage
Cereal Straw	40
Cereal Grain (barley/ wheat)	20
Legume Grains (beans/lupins/lentils)	15
Oathulls	15
Almond Hulls	7
Lime	1
Bentonite	1.5
Gypsum	0.5

Between feed intake test periods, sheep were offered supplementary feed based on available pasture and animal requirements (pregnancy/lactation). Supplementary feeds included pasture hay, straw based pellets (as fed during feed intake test periods) and barley grain.

Animal Measurements- Live weight and body condition change

During feed intake measurements, live weight was measured 3 times a week (Monday, Wednesday and Friday). Live weight was recorded using a weigh crate (Pratley 3 way manual drafter S03300L – Pratley Industries Ltd, Temuka, New Zealand) and scales (Tru-Test MP600, Tru-Test Livestock Management, Shepparton, Victoria, Australia) connected to an electronic weigh head (Tru-Test XR3000, Tru-Test Livestock Management, 12 Joseph Baldwin Place, Shepparton, Victoria 3630, Australia). Ewe body condition was measured at the start and end of the feed intake period. Body condition was assessed as the amount of muscle and fat coverage over the spine and short ribs of the sheep on a 1.0 to 5.0 scale (http://www.lifetimewool.com.au/conditionscore.aspx). Eye muscle area and C2 fat depth were measured by ultrasound scanning before and after each feed intake test period (Advanced Livestock Services, Hamilton, Victoria).

Methane Measurements

Methane was measured twice for each feed intake test period, after ewes had been on feed for approximately 4 weeks. Methane measurements were at least 10 days apart for each animal. Methane was measured using the portable accumulation chamber (PAC) technique described by Goopy et al. (2011) with modifications. The primary modification was that chambers were sealed using a water bath. Gas was sampled from the sealed chambers at the commencement of the methane test, and at 15 minute intervals for 45 minutes. The concentration of CH_4 was measured using a laser detector (Gazomat Inspectra Laser, Bischheim, France), whilst CO_2 and O_2 concentration were measured using an infra-red gas analyser (Gas Data GFM Series, Coventry, United Kingdom).

Sampling protocols were designed to limit the effect of diurnal eating patterns on methane emissions. Time and amount of last meal were recorded using the automatic feeders allowing these factors to be accounted for in the estimation of total daily methane emissions.

Reproductive Measurements

Ewes were syndicate mated (ram ratio 3% for maiden ewes and 2 % for older ewes) for 6 weeks outside of the feed intake facility (between February and April). Ultrasound pregnancy detection was done 12 weeks after the start of mating. Ewe live weight and body condition score was recorded at pregnancy scanning, pre lambing (1-2 weeks prior to expected start of lambing) at lamb marking and weaning.

Calculations and Statistical Analysis

We analysed the 2013 and 2014 groups of ewes separately. Residual feed intake was estimated from the regression of average feed intake over the feeding period against mean metabolic mid weight (predictor of maintenance requirements) and average daily livewight gain over the feeding period.

Reproductive rate was analysed using a General Linear Model with a multinomial distribution and logit link function with fitted effects of RFI, birth type and joining weight, where appropriate. Restricted maximum likelihood method (REML) was used to fit the various methane analyses with RFI as a fixed effect. Methane measurement date and run within measurement date along with animal were fitted as random effects. Variance accounted for was calculated from the estimated variance components derived using REML analysis. All statistical analyses were done using GenStat (VSN International 2012). Pearson correlation was used to examine the association between age groups.

Results

Activity #1: Feed efficiency and methane production post weaning in relation to reproductive performance of ewe lambs and activity #2: of adult ewes

Intake (kg DM/day) and weight increased as sheep aged in both 2013 and 2014 group ewes (Table 19). Methane emissions were similar at post weaning and hogget ages but increased for adults in the 2013 group. Post weaning ewes (mated as ewe lambs) had lower pregnancy rates (lambs/ewe) than ewes at hogget and adult ages.

Status	MMWT	Growth Rate	Intake	Methane	Pregnancy
	(kg)	(g/day)	Kg DM/day	(g/day)	Scan
Post Weaning					
2013 Drop	46.6 ± 5.6	272 ± 52	1.31 ± 0.19	33.1 ± 9.71	0.69 ± 0.63
2014 Drop	42.9 ± 4.2	167 ± 54	1.38 ± 0.26	21.4 ± 7.05	0.96 ± 0.62
Hogget					
2013 Drop	54.3 ± 6.2	119 ± 49	2.06 ± 0.29	33.8 ± 8.28	1.41 ± 0.57
2014 Drop	59.7 ± 6.6	155 ± 55	2.15 ± 0.37	39.9 ± 7.93	1.62 ± 0.59
Adult					
2013 Drop	67.2 ± 7.1	239 ± 72	2.68 ± 0.42	47.3 ± 8.62	1.34 ± 0.63

Table 19. Summary of Animal performance parameters measured during feed efficiency testing.

Variance in RFI explained by live weight, intake and live weight change

Variance in residual feed intake explained by mean midpoint weight and growth rate is in Table 20. Live weight and live weight change explained more variance in residual feed intake in 2013 than 2014 groups. The proportion of residual feed intake explained decreased as sheep aged.

Status/ Group	Year	Cohort	Number	% var	F Prob
Post Weaning					
2013 Drop	2014	1	94	55.8	<0.001
2014 Drop	2015	2	208	37.6	<0.001
Hogget					
2013 Drop	2015	1	209	43.0	<0.001
2014 Drop	2016	2	210	27.7	<0.001
Adult					
2013 Drop	2016	1	232	17.5	<0.001

Table 20. Variance in RFI explained by MMWT and live weight changes and significance (F-Probability) of relationships.

Range in Residual Feed intake, Dry Matter Intake, Growth Rate and Methane Emissions

Residual feed intake measured in the 2013 group ewes ranged from -0.339 to 0.324 at the post weaning age, -0.690 to 0.803 at the hogget age and -1.088 to 1.043 at the adult age (Table 21). Dry matter intake varied lots at each age group, although intakes increased from post weaning to adult ages. The most efficient post weaners consumed 0.66 kg DM less than the least efficient (for the same level of growth), hoggets 1.49 kg DM and adults 2.13 kg DM.

Table 21. Range in RFI, DMI, Growth Rate and Methane Emissions for 2013 drop Maternal Composite Ewes measured at three ages.

	Post Weaning		Hogget		Adult	
	2013 Drop		2013 Drop		2013 Drop	
	Min	Max	Min	Max	Min	Max
RFI (kg DM)	-0.339	0.324	-0.690	0.803	-1.088	1.043
DMI (kg DM)	0.84	1.79	1.41	2.95	1.66	3.91
Growth Rate (g/day)	149	427	18	264	57	469
Methane (g/day)	11.6	64.8	9.2	52.6	20.0	71.5

RFI measured in the 2014 group of ewes varied more at both post weaning and hogget ages (Table 22) that the 2013 group of ewes (Table). There was also greater variation in DMI and growth rates. For a given level of growth, the most efficient post weaner consumed 1.2 kg DM less than the least efficient post weaner. There was 1.74 kg DM difference between the most and least efficient hoggets in the 2014 drop.

 Table 22. Range in RFI, DMI, Growth Rate and Methane Emissions for 2014 drop Maternal

 Composite Ewes measured at two ages.

	Post Weaning 2014 Drop		Hog 2014	iget Drop
	Min	Max	Min	Max
RFI (kg DM)	-0.62	0.58	-0.72	1.02
DMI (kg DM)	0.53	2.16	0.67	3.34
Growth Rate (g/day)	30	327	-24	359
Methane (g/day)	5.5	48.2	15.8	63.3

Feed intake, growth rate, RFI and methane - within age group correlations

In 2013 group at the post weaning age there was no correlation between RFI and methane, intake and methane or growth rate and methane. At the hogget age, there was a significant negative correlation between methane and RFI (P<0.05, r = -0.326). However the relationships between intake and methane and between growth rate and methane were not significant. In adult ewes there was a

significant relationship between RFI and methane emissions (P<0.05, r = 0.31), intake and methane (P<0.01, r = 0.45) but not between growth and methane emissions.

In 2014 group post weaner ewes there were significantly positive correlation between RFI and methane (P<0.001, r = 0.27), between intake and methane (P<0.001, r = 0.41) and between growth rate and methane (P<0.01, r = 0.22). At the hogget age, the correlation between RFI and methane was not significant. However there were significant positive correlations between intake and methane (P<0.05, r = 0.20) and between growth rate and methane (P<0.001, r = 0.31).

Feed intake, growth rate, RFI and methane - between age group correlations

There were 43 of the 2013 group ewes that were measured at post weaning, hogget and adult ages and 183 were measured at hogget and adult ages. When animals were measured at three ages (n = 43), adult intake were correlated both with intake in hoggets (P<0.001, r = 0.45) and intake post weaning (P<0.01, r = 0.47). Adult methane emissions were also correlated with post weaning methane (P<0.05, r = 0.32). For animals measured as hoggets and adults (n = 183), Hogget intake was positively correlated with adult intake (P<0.001, r = 0.43) as was hogget methane emissions and adult methane emissions (P<0.01, r = 0.24). There was a positive correlation between RFI as a hogget and RFI as an adult (P<0.05, r = 0.17).

There was 195 2014 group ewes measured at post weaning and hogget ages. Intake at post weaning was significantly correlated with intake as a hogget (P<0.001, r = 0.40) as was methane (P<0.01, r = 0.20) and RFI (P<0.01, r = 0.19).

Residual Feed Intake and Methane

Residual feed intake was significantly (P<0.001) associated with methane emissions for only the 2014 drop ewes when measured as hoggets, however % variation explained was low (7.6%). For all other groups measured there was no relationship between residual feed intake and methane emissions.

RFI and Reproduction

Lambs scanned (ultrasound scanned 80 days after the start of joining) was used as a measure of reproductive performance. RFI had a significant (P<0.001) effect on reproduction in only the 2014 group measured as post weaners. Predictions of reproductive rate (lambs scanned/100 ewes) indicate low RFI (more efficient) ewes in this group had higher numbers of lambs scanned than those with high RFI (less efficient). Expected numbers of lambs scanned from ewes with an efficiency of - 0.3 was 134.2, 108.6 for RFI -0.1, 84.0 for RFI 0.1 and 58.0 for RFI 0.3.

Discussion

For non-Merinos there were big differences in how the much most and least feed efficient animals ate, particularly in adults. Also, high variation in daily dry matter intake, growth rates and residual feed intake were found for maternal composite ewes measured at different ages. This implies that we should be able to select individuals for divergent RFI.

Residual feed intake at post weaning and hogget ages (for 2014 drop ewes) and hogget and adult ages (for 2013 drop ewes) was positively correlated, however correlations were low. This suggests that while some animals continue to be more efficient as they grow, there is likely to be a substantial amount of re-ranking of low and high efficiency animals occurring between growth stages. Despite this, there are still large gains in lower feed required even with re-ranking of animals, since there was a different in 2.13 kg DM between the most and least efficient animal.

We found a positive correlation between methane emissions and RFI for only 1 of the 5 measurement periods (P<0.001). The level of variance, however, in methane emissions accounted for by RFI was very low (7.6%). Methane emissions were also associated with growth rate and intake during some feed intake test periods. Furthermore, despite some association with reproductive performance in the post weaning age group (for a single measured group) there was not a repeatable relationship between RFI and reproductive performance.

Combined discussion for Merinos and non-Merinos

There were differences in results between Merinos and non-Merinos. It is difficult to compare them because the Merinos have more measurements across more years and the genetic analysis of the non-Merino data has not been completed. One common theme includes resilience being repeatable across years. Also, there were some positive correlations between methane and intake in non-Merinos which is consistent with Merinos.

Significance for Australian Agriculture and specific industries/ Impact and application for policy makers, industry groups and individual farmers

Everyone wins from our project

- 1. Farmers farmers and breeders can breed sheep that eat less. This breeding can be done using carbon dioxide as a proxy for feed intake given the strong genetic correlation. Carbon dioxide is easier and cheaper to measure than feed intake. Therefore farmers and breeders can start breeding for feed intake something that has not been possible before.
- 2. Policy makers and industry groups Government and industry now know how to convince farmers to breed for more efficient sheep. They will be able to market Australian product as being better for the environment and know how to convince farmers to change the way they breed their sheep.
- 3. Society Lower greenhouse gas emission, more efficient sheep and less feed required may also improve the welfare of the sheep. For society that is becoming more concerned with how sheep are managed in Australia, these results are significant.

Contribution to reducing greenhouse gas emissions and/or adapting to climate change/Contribution to Carbon Farming Initiative/Emissions Reduction Fund methodology development

Decreasing feed intake decreases the methane produced by sheep but also the carbon produced when growing feed for sheep. If we investigate the full reduction in carbon from more efficient sheep eating less, then it is not just related to the sheep and farm that they are managed but to the whole carbon cycle.

Contribution to increasing productivity/ Contribution to sustainable land use

Farmers can now increase production without feeling conscious about increased feed costs and effects on the environment. Farmers can reduce methane production and intake per kg of product produced by just breeding for more lambs and more wool. Also, sheep may be selected to grow fast whilst still being feed efficient. In relation to sustainable land use, the amount of product per ha can be increased whilst decreasing the methane emission per ha. Therefore, farmers will have more productive animals and land whilst being more sustainable.

Contribution to the aim and expected outcome of the project.

Huge contribution – we know how to make animals efficient and reduce their environmental footprint whilst making them productive.

3. Future research needs

Low correlations between intake, gas and wool and reproduction traits may be because the intake measurements took up a small part of the feed intake. Also, they did not coincide with the reproduction period. Therefore, these feed intake measurements may not represent how much they ate during other periods of the year. We may need to look at feed intake at different times of the reproduction cycle.

We used a high quality pellet in our experiments but most Merino sheep in Australia are managed outdoors in warm to hot-summer Mediterranean climatic zones. These areas have high variation in pasture quality and quantity during the year. Therefore, we need to understand if these relationships between wool and reproduction with intake, residual feed intake, methane and other gas traits are consistent on different types of feed. The genotype by environmental interactions, however, between these traits on different types of feed would have to be quite high to change these correlations.

4. Publications

Scientific papers and short communications

- J. Young, B. Paganoni, G. Rose, M Ferguson and A.N. Thompson (2016) Relative economic values for feed intake, methane and production traits for Merino sheep. *Animal Production Science* (see Abstract in Appendix)
- B.L. Paganoni, G. Rose, C.M. Macleay, C.E. Jones, D. Brown, G Kearney, M Ferguson and A.N. Thompson (2016). More feed efficient sheep eating high quality pellets produce less methane and carbon dioxide. *Animal Production Science* (ready to be submitted see Abstract in Appendix)
- B.L. Paganoni, G. Rose, C.M. Macleay, C.E. Jones, D. Brown, G Kearney, M Ferguson and A.N. Thompson (2016). Merino sheep can be bred for feed efficiency, methane, reproduction and wool simultaneously but not growth. *Animal Production Science* (ready to be submitted see Abstract in Appendix)
- S.K. Muir, N. Linden, A. Kennedy, R. Behrendt, B. Paganoni, A.N.Thompson and G. Kearney (2016). Correlations between feed intake, RFI, methane emissions and reproductive performance of maternal composite ewes at post weaning, hogget and adult ages. *Animal Production Science* (ready to be submitted – see Abstract in Appendix)
- Macleay, C., Blumer, S. Hancock, Inglis, L. Paganoni, B.L. and Thompson, A.N. (2016). Feed intake can be measured precisely in less than 35 days. *Proceedings of the Australian Society of Animal Production.* Brief communications Ref# 1250.
- Paganoni, B.L., Blumer, S. Hancock, Inglis, L. Macleay, C.M. and Thompson, A.N. (2016). *Maximum* survival of lambs to weaning is achieved when ewes are condition score three prior to lambing. *Proceedings of the Australian Society of Animal Production.* Brief communications Ref# 1252.
- Jones, C.E., Ferguson, M.B., Paganoni, B.L., Vercoe, P.H. and Thompson, A.N. (2014). Improving feed efficiency has a negative impact on the fertility of Merino ewe lambs mated at 7-10 months of age. *Proceedings of the Australian Society of Animal Production*. One page paper submission.

Presentations

Gus Rose, Beth Paganoni, Claire Macleay and Andrew Thompson (2016). Merino sheep can be bred to eat less, be more feed efficient and produce less methane quickly and cheaply. 67th Annual Meeting of the European Federation of Animal Science Belfast UK, 29 Aug – 2 Sept 2016

- Paganoni, B.L., Muir, S., Rose. G. and Thompson, A. N. (2016). Mass, gas and the efficiency Impasse. Presentation for the Rumen Pangenome Program Technical Workshop, UWA Club, 1-2 June, 2016.
- Paganoni, B.L. (2015). Getting more from your maidens. Money Making Mums, AgInnovate Webinar Series, Winter Sessions.
- Paganoni, B.L. (2015). Maternal Efficiency and early reproductive success. Ovis 21 Patagonia, Australian Industry Tour, MPM.
- Paganoni, B.L. (2015). The Five Starts of Efficiency. Mt Ronan Farmer Field Day, York.
- Paganoni, B.L. (2014). Successful joining of Merino ewe lambs. DAFWA 100% Club Dinner Presentation, UWA Club, Perth.
- Paganoni, B.L. (2014). Successful joining of Merino ewe lambs. DAFWA Sheep Updates Plenary Presentation, UWA Club, Perth.

Web publications

https://www.agric.wa.gov.au/livestock-research-development/maternal-efficiency-project

https://www.agric.wa.gov.au/carbon-farming/sheep-reproduction-and-reduced-methane-emissions

Other communications

Paganoni, B. L. (2016). Breeding from Merino ewe lambs can work. Article, Farming Ahead, Feb 2016.

Paganoni, B., Macleay, C. Wainewright, S. and Thompson A. (2015). Marking more from Merinos. Article, Ovine Observer, Spring edition 2015.

Paganoni, B. L. (2014). Joining ewe lambs. Article, Feedback © MLA.

Project 2020 Extension and Outreach workshops - A brief description of this project has been provided at most of the 165 workshops for Project 2020 (Extension and Outreach) throughout NSW, VIC, SA, Tas and WA involving more than 2000 participants over the last 24 months. Workshop material also includes key contacts for this and other FRG projects.

5. Appendix

Paper abstracts

More feed efficient sheep eating high quality pellets produce less methane and carbon dioxide

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Abstract

The Australian sheep industry aims to increase the efficiency of sheep production by decreasing the amount of feed eaten by sheep. Also, feed intake is related to methane production, and more efficient (low residual feed intake) animals eat less than expected. So we tested the hypothesis that more efficient sheep produce less methane. To test this hypothesis we investigated the genetic correlations between feed intake, residual feed intake, methane, carbon dioxide and oxygen. We measured feed intake, methane, oxygen, carbon dioxide from 2800 Merino sheep. We measured these sheep at post weaning (1816 sheep 223 days old), hogget (1051 sheep 607 days old), and adult ages (444 sheep 1080 days old). Sheep were fed a high energy grower pellet for 35 days ab libitum. Individual feed intake was measured using automated feeders. Methane was measured using portable accumulation chambers up to 3 times during the feed intake period. We used ASRemI to estimate heritabilities and phenotypic and genotypic correlations between traits. Oxygen (range 0.10 to 0.20) and carbon dioxide (range 0.08 to 0.28) were more heritable than methane (range 0.11 to 0.14). Selecting to decrease feed intake or residual feed intake will decrease methane (rg range 0.76 to 0.90) and carbon dioxide (r_a range 0.65 to 0.96). Selecting to decrease intake (rg range 0.64 to 0.78) and methane (rg range 0.81 to 0.86) in post weaners would decrease intake and methane in hoggets and adults. Furthermore, selecting for lower residual feed intake (rg = 0.75) and carbon dioxide (rg = 0.90) and higher oxygen (rg = 0.69) in hoggets would also decrease and increase these traits in adults. Therefore, we accepted our hypothesis that making sheep more feed efficient will decrease their methane production. Also, carbon dioxide is a good indicator trait for feed intake. It is a good trait because it has the highest heritability of gas traits, is cheaper, faster and easier to measure than feed intake and has strong phenotypic and genetic correlations with feed intake. Furthermore, selection for efficiency, methane and carbon dioxide can be done early in post weaners or hoggets. This early selection reduces the generation interval for breeding, increasing response to selection.

Merino sheep can be bred for feed efficiency, methane, reproduction and wool simultaneously but not growth

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Abstract

The Australian sheep industry aims to increase the efficiency of sheep production by decreasing the amount of feed eaten by sheep. Sheep that eat less and are more feed efficient produce less methane. If sheep are more feed efficient then they eat less based on their size and production. Therefore, we tested the hypothesis that more efficient animals will produce less methane per unit of production. To test this hypothesis we investigated the genetic correlations between feed intake, residual feed intake, methane and production traits. We measured feed intake, methane, growth, fat, muscle reproduction and wool from 2800 Merino sheep. We measured these sheep at post weaning (1816 sheep 223 days old), hogget (1051 sheep 607 days old), and adult ages (444 sheep 1080 days old). Sheep were fed a high energy grower pellet for 35 days ab libitum. Individual feed intake was measured using automated feeders. Methane was measured using portable accumulation chambers up to 3 times during the feed intake period. We used ASRemI to estimate heritabilities and phenotypic and genotypic correlations between traits. Sheep that grow faster and are bigger eat more at all ages (r_a range 0.50 to 0.94), are less feed efficient as hoggets (r_a range 0.42 to 0.48) and produce more methane as post weaners and hoggets (rg range 0.45 to 0.85). Sheep that gain more fat on high quality pellets eat more as hoggets and post weaners (r_a range 0.34 to 0.54), are less efficient as post weaners ($r_{q} = 0.49$) and produce more methane as hoggets ($r_{q} 0.69$). Sheep that gain more muscle on high quality pellets eat more as post weaners and adults (r_a range 0.73 to 0.84) and produce more methane as post weaners (r_a=0.68). All other genetic correlations were not significant. Also, intake, feed efficiency and methane had no significant genetic correlations with wool and reproduction traits. Therefore, it is difficult to select for high growth in sheep and decrease feed intake and methane production. Residual feed intake had lower genetic live weight and growth compared to intake, and were not significantly different to zero for post weaners and adults. Skinnier and less muscular sheep ate more and gained more fat and muscle than fatter and more muscular sheep. They may have been compensating after transferring from a low quality to a high quality diet. Therefore, partically accepted our hypothesis that more efficient animals will produce less methane per unit of production.

Correlations between feed intake, RFI, methane emissions and reproductive performance of maternal composite ewes at post weaning, hogget and adult ages

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Abstract

Residual feed intake (RFI) estimates how feed efficient sheep are. In growing maternal sheep the relationship between RFI and growth is unknown. Also, the repeatability of these traits across ages is unknown. RFI may also be correlated with other reproduction and methane. The southern Australian (South West Victorian) sheep meat production flock is increasingly becoming based on maternal composite ewes. Understanding the variability, ranges and correlations between traits (RFI, intake, growth, methane emissions) within the maternal composite ewe flock is important for selecting sheep that are feed efficient. We measured feed intake, growth rates, reproductive performance and methane emissions from maternal composite ewes (n= 505) at three ages (post weaning, hogget and adult) using an automated feed intake facility. Feed intake was measured for at least 42 days when ewes were fed *ad libitum*. Live weights were recorded 3 times each week. A range in daily dry matter intake, growth rates and residual feed intake were observed for maternal composite ewes measured at different ages. This implies that we should be able to select individuals for divergent RFI. Correlations between traits (intake, growth, RFI, methane, reproduction) were significant, but effects were not consistent between age groups. Further research is required to further evaluate possible implications of selecting for RFI on other productive traits.

Relative economic values for feed intake, methane and production traits for Merino sheep

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Abstract

Feed intake is the largest cost in sheep production enterprises and therefore reducing feed intake is likely to be a valuable trait in an animal breeding programme. Reducing feed intake will be associated with a reduction in methane production because methane and feed intake have positive genetic and phenotypic correlations. Additionally, methane and intake have important genetic correlations with live weight and growth. The relative importance of methane, intake and production traits for Australian merino sheep breeding objectives is unknown. Therefore, we estimated economic values that can be used in a breeding objective for Australian Merino sheep farmers. We estimated economic values for clean fleece weight, fibre diameter, live weight, number of lambs weaned, methane production and feed intake. These economic values were estimated using the MIDAS whole farm optimisation model. The model represented a self-replacing merino flock on a typical farm with a 6 month growing season in the Mediterranean sheep and cropping region of Western Australia. We estimated relative economic values to compare the relative importance of traits. Clean fleece weight (\$12.5/ha/genetic standard deviation) was relatively more important than live weight (\$9.9), number of lambs weaned (\$7.0), feed intake (-\$6.1), methane (-\$2.28) and fibre diameter (-\$2.3). Production traits, particularly live weight, had a high economic value because feed intake was included in the breeding objective and hence changes in energy requirements for increasing the production traits were not included in the calculation of their relative economic value. The main antagonistic relationships were between methane, feed intake and live weight, they have moderate positive genetic correlations (ranging from 0.50 to 0.94) and opposing economic values. Because of the antagonism between these traits it is expected that the optimal breeding objective for merinos will slow the rate of increase in methane and feed intake as was found in other research for meat sheep.