IMPROVING THE ACCURACY OF SELECTING ANIMALS FOR REDUCED METHANE EMISSIONS

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SUMMARY

Enteric methane emissions of livestock represent 10.3% of Australia's greenhouse gas emissions, so it is important to identify low-emitting animals in order to study the mechanisms that lead to low emissions relative to production. This will require field testing of large numbers of animals to identify those with the lowest emissions, and at the same time generate useful data from which heritabilities, and also genetic and phenotypic correlations with production traits, can be estimated.

The repeatability of methane emissions from a 1-2 hour field test are expected to be much lower than for daily methane production measured in a respiration chamber. Use of multi-stage selection procedures is therefore recommended to increase the accuracy of identifying animals with low methane emissions. For example, if field tests have a repeatability of 0.25 and resources are available for 1,000 tests, the lowest 50 emitters will have a mean of -1.03 standard deviations below the population average if 1,000 animals are tested once, compared to -1.31 using a multi-stage selection system testing 725 animals, re-testing the best 180 and then the best 95. Other multi-stage schemes to select individuals, as well as sires or families, are evaluated and discussed.

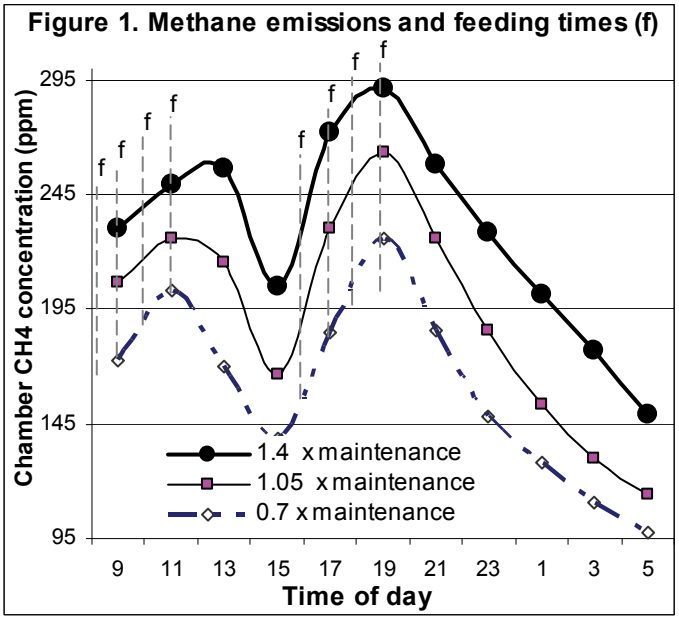
INTRODUCTION

Greenhouse gas emissions from Australian livestock in 2006 amounted to 62.8 million tonnes of CO_2-equivalent. This represents 69.7% of the agricultural sector's emissions and 10.9% of net national emissions (DCC 2008). The vast majority of this (59.3 million tonnes) was enteric methane emissions. It is therefore important to find ways of reducing methane emissions from livestock. A promising research strategy is to identify the lowest emitting individuals, in order to study the mechanisms and identify physiological indicators associated with their low level of emissions relative to their production value. This will require large numbers of animals to be tested in the field, with the data being used to identify extreme animals, as well as provide useful information on phenotypic and genetic correlations between methane emissions and production traits, needed in order to include methane emissions in future breeding objectives.

A review of between- and within- animal variation in daily methane production from respiration chamber measurements suggests that the trait is moderately repeatable for some groups of animals (Robinson, in preparation). However, field measurements of emissions taken over 1 or 2 hours will be much less repeatable (Goopy *et al.* 2009). This paper evaluates the potential increase in accuracy from using sequential selection systems to screen large numbers of animals for traits with low repeatability, using repeat tests on promising individuals to achieve the best possible accuracy of selection.

REPEATABILITY OF FIELD MEASUREMENTS

For methane emissions, a respiration chamber experiment (Goopy *et al.* 2009) with sheep on 3 feeding levels (0.7, 1.05 and 1.4 x maintenance) showed that, as long as animals have been synchronised to the same feeding pattern, 2-hour measurements provide useful estimates of daily methane production. Emissions were strongly dependent on feeding level, with a daily pattern related to time of feeding; in this case four morning (8, 9, 10, 11 am) and four afternoon feeds (4, 5, 6, 7 pm) of equal size (Fig 1).



The results demonstrate the need for an effective protocol to synchronise or adjust for feeding patterns and/or time of day. If this effect is ignored, an animal measured at 7 pm on the lowest feeding level would appear to have higher emissions than when on the highest feeding level, if measured at 3 pm, implying that repeatability of field measurements could be very low.

A range of possible field measurement protocols are currently under consideration, from simple schemes to measure animals in batches of 10-20 and statistically adjust for batch (which will include time of day and feeding effects) to more complicated schemes controlling feeding times. For example, animals could fast overnight until 2 hours before testing the following day, then graze for 1 hour, fast for a second hour, with methane emissions then measured for 1-2 hours in a transportable chamber. It is hoped that the chosen protocol will allow adjustment for feeding and time of day effects, and so achieve repeatabilities between 0.25 and 0.5.

As well as estimating the heritability of methane emissions and genetic correlations with production traits, the aim is to identify animals (and perhaps also sire groups) with low emissions relative to their level of production. Once identified, the extreme animals will be transported to the research facilities to confirm their level of emissions in respiration chambers, and study the mechanisms responsible for favourably low emissions.

Because of the expense and difficulty of identifying these animals, and the expectation that 1-2 hour field measurements will have low repeatability, use of multi-stage selection procedures was considered to improve the accuracy of selecting extreme animals and provide an estimate of the repeatability of field measurements. An additional benefit is that increased accuracy of identifying low methane emitters should also improve knowledge about the phenotypic and genetic relationships between low methane emissions and production traits.

STATISTICAL METHODS

Repeatability is defined as the correlation between one measurement and another recorded under the same conditions. In statistical terms, if **x** is the vector of true measurement (CH_4 emissions of each animal) and **e** the error, observed measurements, **m**, can be expressed as:

m = **x** + **e**, with repeatability, r = Var(**x**)/(Var(**x**)+Var(**e**)) where Var = variance.

In multi-stage selection procedures (Robinson 1984) the best estimate of an animal's phenotypic performance is calculated from all available measurements. In the case of a simple trait with constant Var(**e**), this is the mean of all prior measurements (including the current one). If more extreme than a specified value, the animal is either re-tested or, at the final stage, selected.

The methods of Robinson (1984) were used to evaluate various one, two and three-stage selection strategies for repeatabilities of 0.5, 0.33 and 0.25, assuming that errors, **e**, and true methane measurements, **x**, are both normally distributed.

RESULTS

Table 1 presents results of four strategies to select the lowest emitting 50 animals using 1,000 individual test results. The first strategy is to measure 1,000 animals once. The second is to test half as many animals twice, increasing the accuracy of assessing each individual animal, at the expense of being able to test fewer animals. The first strategy is more accurate for repeatability of 0.5, resulting in a mean of the selected animals of -1.46 s.d. from the population mean (Table 1). In contrast, for less accurate tests (repeatabilities of 0.33 and 0.25) taking repeat measurements on a random sample of 500 animals results in more accurate selection and a lower mean of the selected animals. This, in fact, is the better strategy whenever repeatability is less than 0.45.

An even better strategy is to use multi-stage selection, carrying out a first test, then a second (and if desired a third) test on animals that perform well in previous tests. The improvement from use of multi-stage selection can be substantial. For example, the mean of selecting the lowest 50 from 1,000 animals using a three-stage strategy for a test with a repeatability of 0.33 is -1.45, almost as good as the mean of -1.46 from a single stage selection strategy from a test with only a half the error variance (repeatability of 0.5, Table 1).

Table 1. Mean of 50 selected animals (expressed in standard deviations of the true values, x, from the population mean), based on 1,000 individual test results

	Mean of the 50 selected animals		
Repeatability	0.5	0.33	0.25
1,000 animals tested once	-1.46	-1.19	-1.03
500 animals tested twice	-1.43	-1.24	-1.11
Test 850, then lowest 150	-1.61	-1.38	-1.23
Test 725, then lowest 180, then lowest 95	-1.65	-1. 45	-1.31

Results from strategies to select 100 animals using 1,000 tests (Table 2) show a similar pattern, although the mean of selected animals is not as negative, because more animals are selected. In this scenario, there is little or no benefit from repeat testing all animals, even for low repeatabilities. For repeatability of 0.25, repeat testing 500 animals produces a gain of -0.89, only marginally better than the gain of -0.88 from testing 1,000 animals once. At repeatabilities of 0.33 and 0.5, testing all animals once is better than repeat testing 500 animals. However, there are still gains from multi-stage selection. For repeatabilities of 0.33 and 0.25, the mean of the 100 lowest emitters from a two-stage strategy testing 800 then 200 animals (Table 2) are 12% to 14% lower than for the one-stage strategy. In fact, the means (-1.13 and -1.00 for repeatabilities of 0.33 and 0.25) of the lowest 100 from the two-stage strategy (Table 2) are almost as low as those for the lowest 50 (-1.19 and -1.03) testing 1,000 animals only once (Table 1).

Table 2. Mean of 100 selected animals (expressed in standard deviations of the true values, x, from the population mean), based on 1,000 individual test results

	Mean of the 100 selected animals		
Repeatability	0.5	0.33	0.25
1,000 animals tested once	-1.24	-1.01	-0.88
500 animals tested twice	-1.14	-0.99	-0.89
Test 800, then lowest 200	-1.32	-1.13	-1.00

For breeding purposes, there is also a need to identify families as well as individuals. This could be done as part of the multi-stage selection procedure, by using genetic analyses to rank sire groups prior to each stage of testing. However, even when the main focus is to select individuals, the increased accuracy of selection should also mean that superior families will have a higher proportion of individuals tested at subsequent stages, leading to increased accuracy of selecting families as well as individuals.

Tables 1 and 2 show than even simple strategies, such as re-testing the most extreme 15% or 20% of animals based on the initial test results, are substantially better than one-stage testing. Such strategies also provide information on repeatability and assist with the selection of both genetically and phenotypically extreme individuals.

DISCUSSION

Identifying low emitting animals for further study is an important part of the strategy to reduce methane emissions from livestock. Although the technology to measure field emissions based on a 1 or 2 hour test looks promising, its accuracy will be limited by the ability to synchronise animals or statistically adjust for time of day effects, the latter perhaps being more practical for field tests with non-research flocks.

Given the difficulties and expense of field testing, other methods (such as testing for the presence or absence of indicator organisms in the rumen) might in the long run become the preferred strategy. Critical to the development of effective, new strategies is our ability to identify and study exceptional animals, either extremely low emitters, or high and low extremes, so that we identify and understand what causes the differences. As well as facilitating the development of alternative tests, understanding the mechanisms that lead to high or low emissions could aid the development of other possible ways of reducing emissions (e.g. dietary additives).

If atmospheric greenhouse gases are to stabilise, it may be necessary to reduce global emissions by 50% by 2020, a very ambitious target that is unlikely to be achieved for livestock solely by breeding strategies. Nonetheless, breeding from the most extreme animals (or extreme families) will provide useful information about the trait and whether responses at the extremes are linear.

Strategies to identify low or extreme emitting animals are therefore seen as at least as important to the research program as estimating genetic parameters. Multi-stage selection strategies are practical only if the results of the first test are available in time to select animals for the next stage of testing, which might be scheduled immediately after the end of the first stage. As long as this is feasible, multi-stage testing is recommended to improve the accuracy of selecting the most extreme animals, as well as provide an estimate of repeatability, without re-testing substantial numbers of animals, allowing the bulk of effort to be concentrated on testing animals at least once to maximise the amount of useful information collected on phenotypic and genetic variability.

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