STATE OF SCIENCE

Breeding low-emitting cattle

Dr Lorna McNaughton, LIC
Dr Suzanne Rowe, AgResearch

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NEW ZEALAND
AGRICULTURAL GREENHOUSE GAS
Research Centre

The Presenters

Dr Lorna McNaughton (Livestock Improvement Corporation)
Lorna is a senior scientist at Livestock Improvement Corporation (LIC) where she leads the LIC/CRV Low Methane Bulls project. Her areas of expertise are phenotype development for genetic selection, dairy cattle reproduction, once-a-day milking and heifer live weight targets and the impact of reaching targets on reproduction and milk production.

Dr Suzanne Rowe (AgResearch)
Suzanne is a senior scientist at AgResearch and a co-leader of the NZAGRC-PGgRc programme to breed low methane ruminants. Her research expertise is in breeding low methane ruminants, development of genomic tools for the deer industry and genetic mapping of genes associated with disease and production traits in sheep.

Presentation

YouTube video link is: https://youtu.be/L__ng1sG57c

Question & Answers

Thank you all for your participation. Over the page are the answers to questions which were asked post presentation and were not answered live.

Please note: these answers are provided by the presenters and do not represent the particular views of the NZAGRC or MPI.

Why do you think you will not make a significance difference in cattle by 2030?

Because it will take us until 2025 to gather sufficient data and determine the genetic correlations and ensure that the lactating daughters are also low in methane.

How many animals can a single GreenFeed hood measure during a given measurement study?

Around 20 - we are targeting up to 13 animals (depending on how big the animals are) and aiming to get up to 6 measurements a day from the animals in our pens

Have you looked at Zeddy as a data capture system?

It's something that is being looked at by us and others – once it is commercially released it could be a useful way to measure methane at pasture

Was it found that all animals in each pen would use the hoods?

We had one bull in the LIC trial that didn't use the GreenFeed hood, but all the bulls at CRV used it. We think that making sure the bulls have had access to the pellets that we offer in the GreenFeed hood before we expose them to it helps encourage the bulls to visit, but we do expect to have a small proportion of bulls that won't use it.

How many records in a GreenFeed do you need to get an accurate indication/measurement of the methane emissions (in grams/day) of that animal?

Initially we were aiming for 100 measurements per animal. Our analysis of the pilot trial data suggests this is about right. We are targeting 28 days of measurements with 5 - 6 GreenFeed visits per day.

Is there a set amount of variation you hope to see in a particular animal before selecting his genes for propagation, or is it just going to be a matter of selecting the lowest methane/Dry Matter ratio and running with it?

It will be a balance between methane production and other traits that are important to dairy farmers. We will not want to go down the single trait selection path as you could end up selecting for bulls with low methane production, but with undesirable other traits. The more variation we find between animals the easier it will be to make selection progress. However, we need to understand the genetic relationship between methane and other traits such as milk production and fertility before we start any selection.

In past work at AgResearch, the repeatability of methane measurements made over longer intervals (months) on individual animals (sheep and cows) was quite low. Has this changed?

No, the repeatability value has not changed. This question actually has two parts in the answer. The first addresses the variability of the measurement technique, and the second is the variability of the animal's emissions over its life. The low repeatability over longer intervals is largely due to the variability of the animal and suggests a benefit of multiple measures over an extended period. Regarding the second aspect, our research has shown that the component of an animal's methane emission that is consistent over time is largely genetic. This means you can measure at a young age confident that genetic selection will change emissions throughout the animal's life.

Genomics leads to a decrease of progeny testing (because you can select your best bulls for production etc already at young age). How will this affect your setup for selection for low methane?

Our measurements will be taken on bulls before they would be used - so we would have the potential to combine our methane measurements with the genomic prediction to make our selection decisions. It would mean that we would be measuring less bulls per year.

You took microbiome samples from the gut, or are they taken from the rumen? How easy is that to do on commercial farms (sheep or cattle)?

The sample is taken from the rumen by using vacuum to draw a small amount of fluid through a soft plastic feeding tube. The sampling only takes 1-2 minutes per animal and is straight forward on-farm as long as you have trained operators following well designed protocols.

Thanks Lorna and Suzanne, this is really exciting and great work you are doing. Hopefully we can get some options for beef cattle too!

It would be great to expand this work to beef animals once we have got some robust measurement processes in place.

Any changes in lamb growth or health that are weaned on low-methane vs high-methane milk profiles?

We tend to see slightly higher weaning weights in the low methane sheep line. As we measure more flocks, we will re-evaluate this.

The GreenFeed system does not measure methane emissions when the animal is not at the GreenFeed device. The pattern of methane emissions is known to be related to the pattern of feed intake. Taking this into account, could the GreenFeed system provide a misleading measure of daily methane output if animals have different patterns of feed intake throughout the day?

This is possible. We are trying to mitigate this by programming the visits to the GreenFeed machine across the day. This means that when an animal visits the GreenFeed, they cannot return again for 2.5 hours, so the 6 daily visits are spread across the day. We will have a lot more data to look at the timing of feeding bouts and visits to the GreenFeed when we have completed the current trial work.

If 11% after three generations, where do you think the limit is, and when?

We don't know this. It is likely that given the small flock size and that we breed our own replacements that we will stop due to inbreeding, rather than a limitation of the trait. There is currently no evidence that the rate of genetic gain is slowing down.

Have you estimated genetic correlation between the microbiota and methane? Could you comment on the value of this?

Yes, we have, and it varies greatly but it appears to be moderately genetically correlated with estimates ranging from 0.3-0.8.

How much of the methane burped is related to what is growing in the pasture, or what and how much chemical fertiliser has been used on it? I understand you can breed for low emissions, but I

am still concerned that I have heard very little about cattle diet and soil life, where no urea has been used but soil is alive with mycorrhizae and bacteria?

I am not aware of any studies of the impact of fertiliser on the methane emissions of pasture. To understand the genetic variation, we want to minimise the impact of the environment and standardise the diet that we feed. Work on the impact of diet on methane production is an ongoing area of research – but does not fit into this particular research programme.

Have you started publishing reports or article on your work as yet that I could have a look at?

If you go to https://www.researchgate.net/project/Breeding-low-methane-ruminants there are links to published papers and under the "project log" tab to a variety of presentations. The new NZAGRC website will also have related publications.

In the Q+A after the presentations, Dr Rowe mentioned higher somatic cell counts in low methane group sheep. Could Dr Rowe explain a bit more about somatic cell counts in those sheep? Somatic cell counts are particular important for dairy cows.

These are preliminary results. The somatic cell counts in the low line were significantly higher than the high line, but not of clinical significance and not associated with infection. Please also note these ewes were suckling lambs, not being milked, and this may have also affected results.

Can you please tell the audience if you have been able to value the lowered methane production based on the current studies in animals? What is the financial impact, greenhouse gas impact and long-term benefit to New Zealand and the world?

The economic impact is entirely dependent on the price set for carbon, the Global Warming Potential (GWP) and how the Government chooses to account for methane emissions. The physical impact based on current studies could be a cumulative reduction in farmed livestock of around 1% per year.

Do you consider that through your work of genetically selecting more specific bacterial species, we would be able to further reduce methanogenesis in the ruminal universe?

We hypothesise that the microbial community that we select for is creating less hydrogen during fermentation and therefore less substrate for the methanogens, but this is a complex and little understood system.