#### Animal Selection Genetics & Genomics Network ASGGN



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#### Genetics to mitigate methane

- Bringing together scientists
- Identification of new collaborations and connections
- Defining traits and breeding objectives
- Establishing the heritability of methane emissions and its genetic associations with other performance traits
- Sharing data, methods & protocols for prediction







#### • Consensus methods for breeding low methane emitting animals

N. K. Pickering, Y. de Haas, J. Basarab, K. Cammack, B. Hayes, R. S. Hegarty, J. Lassen, J. C. McEwan, S. Miller, C. S. Pinares-Patiño, G. Shackell, P. Vercoe and V. H. Oddy

- International committee for animal recording trait definitions and working group
  - Methane production grams/day
  - Methane yield per kg dry matter intake
  - Methane intensity per unit product (e.g., milk, meat, human edible protein)
  - Proxies CO<sub>2</sub>, Volatile fatty acids, MIRS
  - Meta data





#### Workshops

#### World Congress on Genetics Applied to Livestock Production

Aotea Centre Auckland, New Zealand, 11–16 February 2018

- WCGALP Vancouver 2014 Methane measures and feed efficiency
- GGAA Melbourne 2016 Proxies and adaptation
- WCGALP 2018 Feed Efficiency, Methane, Microbiomes
- EAAP August 2018 ?





## Contacts

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## The ASGGN environment.

- Ability to debate and reach agreement on a variety of topics including: common protocols for measurement of CH4 emissions(and associated traits) or at least calibrations of measurement differences between countries
- co-measurement of appropriate correlated and productive traits
- formalised protocols for collection and storage of DNA from all animals measured and also protocols for collection and storage of rumen samples from all animals measured
- criteria for data sharing and analysis (including meta analysis) among all contributing parties

#### **Enteric Fermentation Flagship Project: Rumen** microbiomes to predict methane

- Methane is heritable but expensive to measure directly
- Need measures that are high throughput, low cost and accessible lacksquareto all.

Bacteria

fungi

protozoa

sermentati

Acetate

CH₄

- Microbial community profiles from rumen samples
- Use as predictors
- Genomics & host control



# Methane from Microbes – Genotyping by Sequencing

- Generic hurdle optimise sequence information for processing time and cost
- New method to sequence a few percent of the genome.
  - Reference free
- Used for genotyping over 50 species
  - Genomic prediction & discovery
  - ~80,000 markers for NZ\$30
- Adapt for microbial sequencing
  - Fill the void between marker genes 16s and full sequencing



**GBS** library construction



Elshire et al. 2011 PLOS On





GLOBAL RESEARCH ALLIANCE on agricultural greenhouse gases

#### Methane from Microbes

- Sequencing < 30 euros
- Optimise Sample handling/DNA extraction
- Optimise sequencing methods
- Functional grouping information bioinformatics
- Develop agnostic predictors





**GBS** library construction

(Elshire et al., 2011 PLOS One)







#### **Sheep Microbiomes**

- Global Production Livestock Emissions research (GPLER)
- Currently a large library of sheep samples collected ~7,000NZ plus 500 merino (DPI New South Wales)
- Known methane status, known feed intake
- Variation in individual, breed, diet
- Detect low methane signatures across systems/environments





### Expand to Cattle.....GRA Flagship

- LEARN Post-Doc Quantitative Genetics
- Starting with sequencing 280 NZ HF and Jersey animals
- Expand to additional systems and partners
- Make new sequencing methods available to all partners
- Protocols and agreement to share samples and phenotypes
- 1,000 samples fully funded
- Developing microbial and genomic predictors for differences in methane





#### Cattle - collaboration

- Beef Cattle Canada, Australia, UK, Ireland
- Dairy Cattle NZ, Australia, UK, Denmark, Netherlands
- Bos Indicus Australia, Brasil, Africa
- Other Networks and programs
- Post Doc visit to other institutions





#### **Global Outcomes**

- Trained LEARN Post-doctoral fellow
- Low cost microbial predictor to compare and evaluate systems, feeds, individuals
- Pan species characterisation of rumen microbial communities
- Greater understanding of the rumen microbiome and biological differences between high and low emitters
- Potential for low cost accessible global breeding solutions
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