Wednesday, March 6, 2024

# Abstract Submission Form

**Title (Mr./Mrs/Dr./Prof.)** Dr.

**Presenting author** Michael Aldridge

**Institute**

Institute/company: Animal Genetics & Breeding Unit

Adress: University of New England

ZIP/Postal code: 2351 City: Armidale

Country: Australia

**Insert all authors and institutions**

Aldridge M.N. (1), Brown D.J. (1), Fitzgerald P.T. (2), Clayton E.H. (3), Donaldson A. (3), Paganoni B. (4), Thompson A. (5) and van der Werf J.H. (2)
(1) Animal Genetics and Breeding Unit, A Joint Venture of NSW Department of Primary Industries and University of New England, Armidale, Australia; (2) School of Environmental and Rural Science, University of New England, Armidale, Australia; (3) NSW Department of Primary Industries, Armidale Australia; (4) Department of Primary Industries and Regional Development, Bunbury, Australia; (5) Centre for Animal Production and Health, Murdoch University, Murdoch, Australia

**Preferred presentation** Poster

**Preferred session** Session 8: Global challenges in measuring methane in ruminants

**Email of corresponding author** michael.aldridge@une.edu.au

**Title of your paper** Phenotyping more animals for methane is more important than precise measures of methane

**Insert ABSTRACT text**

Across countries and ruminant species, animal breeding was identified as a desirable method of reducing methane (CH4) emissions. The high cost and slow throughput of phenotyping, are key reasons for the delay in publishing sheep CH4 breeding values. We hypothesised that by reducing measurement duration, the accuracy of measurements would decrease, but the reliability of prediction would increase, as more animals could be phenotyped.

The most common method of measuring CH4 on sheep, is with portable accumulation chambers (PAC). Over the past two decades, projects in Australia measured CH4, carbon dioxide (CO2) and oxygen (O2) at 20-min and 40-min durations on over 6,000 sheep with PACs, using two measurement devices referred to as FID (CH4) and FoxBox (CO2 and O2). Current projects aim to measure CH4, CO2, and O2, on 10,000 additional sheep, with 4,500 already phenotyped. To date, sheep in the current project have been measured using FID and FoxBox, additionally a device referred to as Eagle was used to measure CH4, CO2,



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and O2. The Eagle device has become common practice for use with PACs, as it is both cheaper and easier to use. However, there are concerns about the lower sensitivity and precision of the Eagle compared to FID and FoxBox. The current project has been measuring with each of the three devices at 20-min and 40-min. Before the historic data on 6,000 sheep is included in current analyses, or the FID and FoxBox are replaced by the Eagle, evidence that the devices are measuring the same trait is needed.

Preliminary analyses with 987 merino ewes and 984 merino lambs (lambs measured at 25-min and 50-min), fitted bivariate animal models for methane rate (mL/min), with fixed effects: time of measurement, contemporary group (flock, year, management group), dam age, birth and rearing type, run, pen, chamber, sex (lambs only), and live weight as a covariate.

The heritability of CH4 (0.12 to 0.17, with high standard errors) were not significantly different regardless of CH4 measurement device, measurement duration, and ewe or lamb traits. The genetic correlation for CH4 measured using FID or Eagle was equal to one, and the phenotypic correlation ranged between 0.92 and 0.97. The genetic correlation for CH4 measured at 20-min and 40-min with the Eagle was equal to one, with a phenotypic correlation of 0.86 ± 0.01. In comparison, when CH4 was measured with FID, it had a lower genetic correlation between measurement durations (0.89 ± 0.07) but a slightly higher phenotypic correlation (0.89 ± 0.01) compared to the Eagle (0.86 ± 0.01).

Assuming only the Eagle device is used, reliability of prediction was estimated with different simulated recording strategies. With the current recording strategy (40-min) for 10,000 animals, a reliability of prediction of 0.19 was achieved. The FID and Eagle results showed the historic data on 6,000 sheep should be included (16,000 animals total), which increased reliability of prediction to 0.27. If only 20-min duration is used (previously 40-min) and the historic data is combined, a reliability of prediction of 0.27 is achieved. An additional 3,000 sheep would be needed to achieve a reliability of over 0.30.

The PAC methodology, can sacrifice some precision, by reducing measurement duration, the time saved can be used to phenotype more animals. The overall benefit is a lower cost per animal and an increase in reliability of prediction. Before the current project implements shorter measuring periods, the analysis will be repeated using all 4,500 animals already phenotyped for both CH4 and CO2. This can be applied to other projects using PACs and potentially has application for automated CH4 devices which require weeks of repeated measuring, such as GreenFeed.

**Enter keywords** methane, sheep, small ruminant, phenotyping, protocol



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