Selecting for more methane efficient sheep: progress towards publishing EBVs

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Selecting for more methane efficient sheep
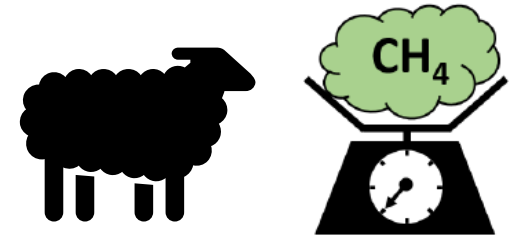
Julius van der Werf
Pete Fitzgerald
Mette Madsen

Daniel Brown
Sam Walkom
Andrew Swan

Sue Mortimer
Edward Clayton
Alistair Donaldson
Hutton Oddy

All of the technicians
and sheep breeders.

Beth Paganoni

Andrew Thompson

Project No. P.PSH.2011

Aim

Provide the Australian sheep industry with methane breeding values.

Background

- 76.5 million sheep in Australia (x3 more sheep than cattle)

- ~18 $MtCO_2eq$ of CH_4 or 4% of Australia's GHG emissions in 2023

- Accurate breeding values can reduce methane by at least 1% p/a
  - ~20% (3.5 $MtCO_2eq$) reduction by 2050
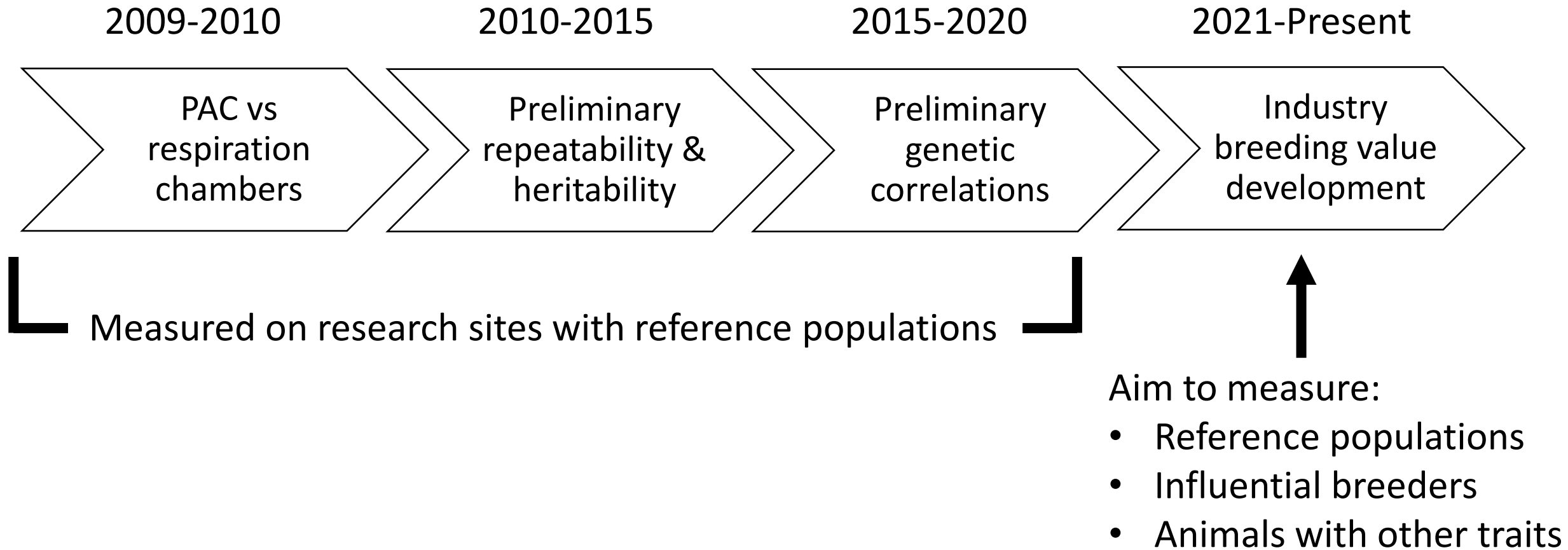
Portable Accumulation Chamber (PAC)
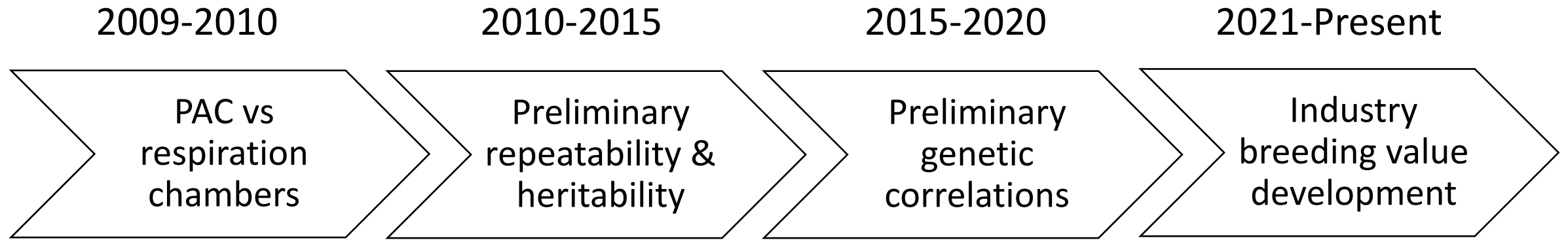

If you know the:
- Volume of the chamber
- Volume of the sheep
- Duration in chamber
- CH_4 concentration in chamber

You can calculate the rate of methane production

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Timeline of PACs in sheep breeding

2009-2010	2010-2015	2015-2020	2021-Present
PAC vs respiration chambers	Preliminary repeatability & heritability	Preliminary genetic correlations	Industry breeding value development

Measured on research sites with reference populations

Aim to measure:
- Reference populations
- Influential breeders
- Animals with other traits

Goopy *et al.* (2011), Goopy *et al.* (2015), Robinson *et al.* (2014), Paganoni *et al.* (2017), Robinson *et al.* (2020), Wahinya *et al.* (2022), Rose *et al.* (2023)

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Phenotyping animals for genomic prediction

Pre 2020 most
measures were
with FID + FoxBox

Post 2020 there
has been a
move to Eagle

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The bottleneck is phenotyping

FID + FoxBox

Eagle

a) 24 hours random 72 animals selected

b) 1 hour 12 sheep taken off feed

c) 2 devices per time point

- Future only Eagle will be used

d) 2 time points per animal

- Mid and end-point (40 or 50min)

e) Rumen sample after each run

f) 6 runs per day (Repeat b to f)

- Now up to 7 runs

g) 7 days per visit (Repeat a to g)

h) 504 sheep per site

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Currently available data

| Data	Pre 2020	Post 2020	Used in analysis
Sites	8 Research sites	13 Sites	**17 Sites**
Number of animals	5,680	8,988	**14,668**
Records	12,069	11,159	**14,668**
Animals	Lambs, Ewes or Rams	Lambs or Ewes	
Devices	FID-FoxBox and Eagle	FID-FoxBox and Eagle	
Max time in PAC	30, 40, 50, 60min	40min or 50 min	

Number of animals and records are after quality control

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Heterogeneous variance
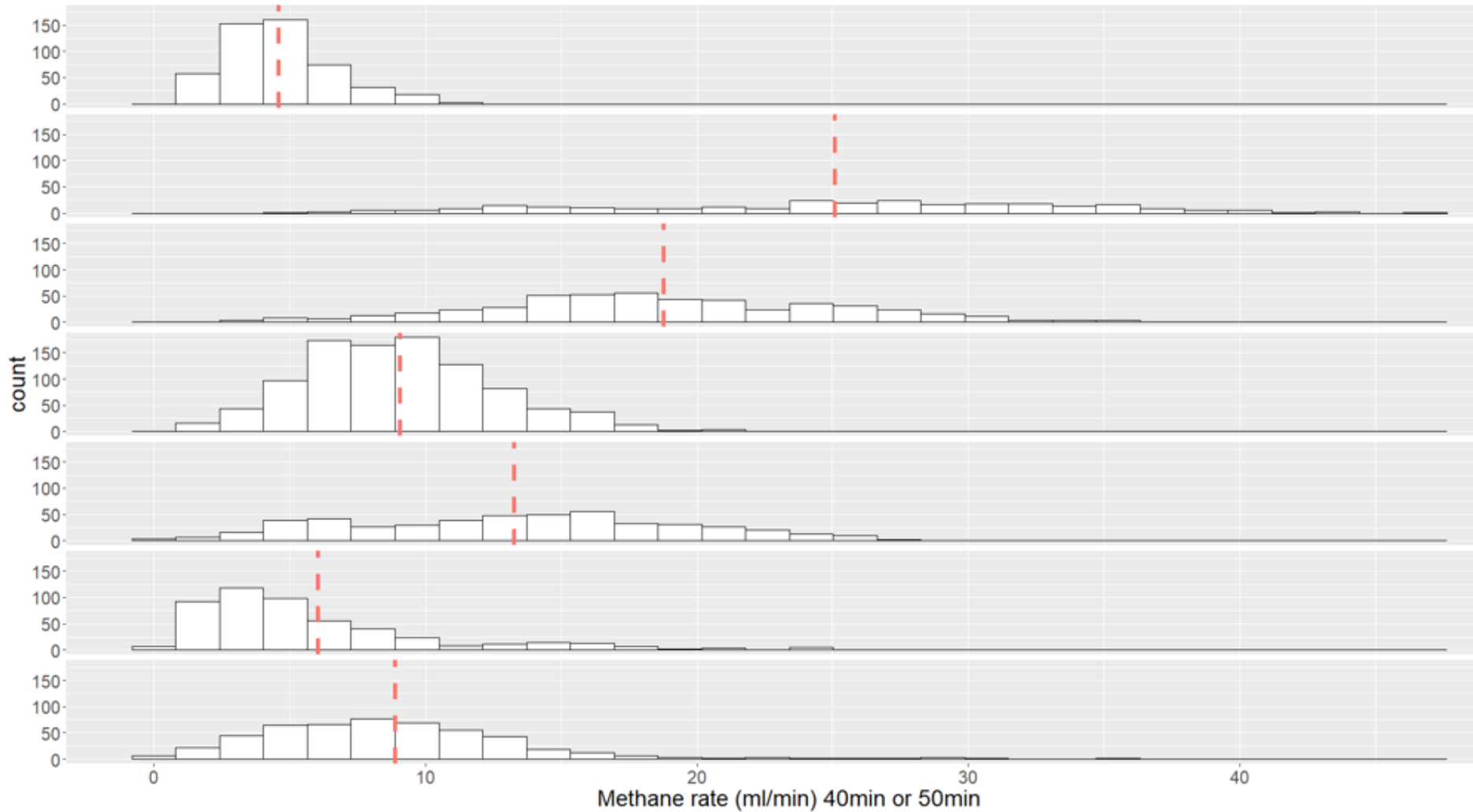
This is only a subset of sites

After standardisation
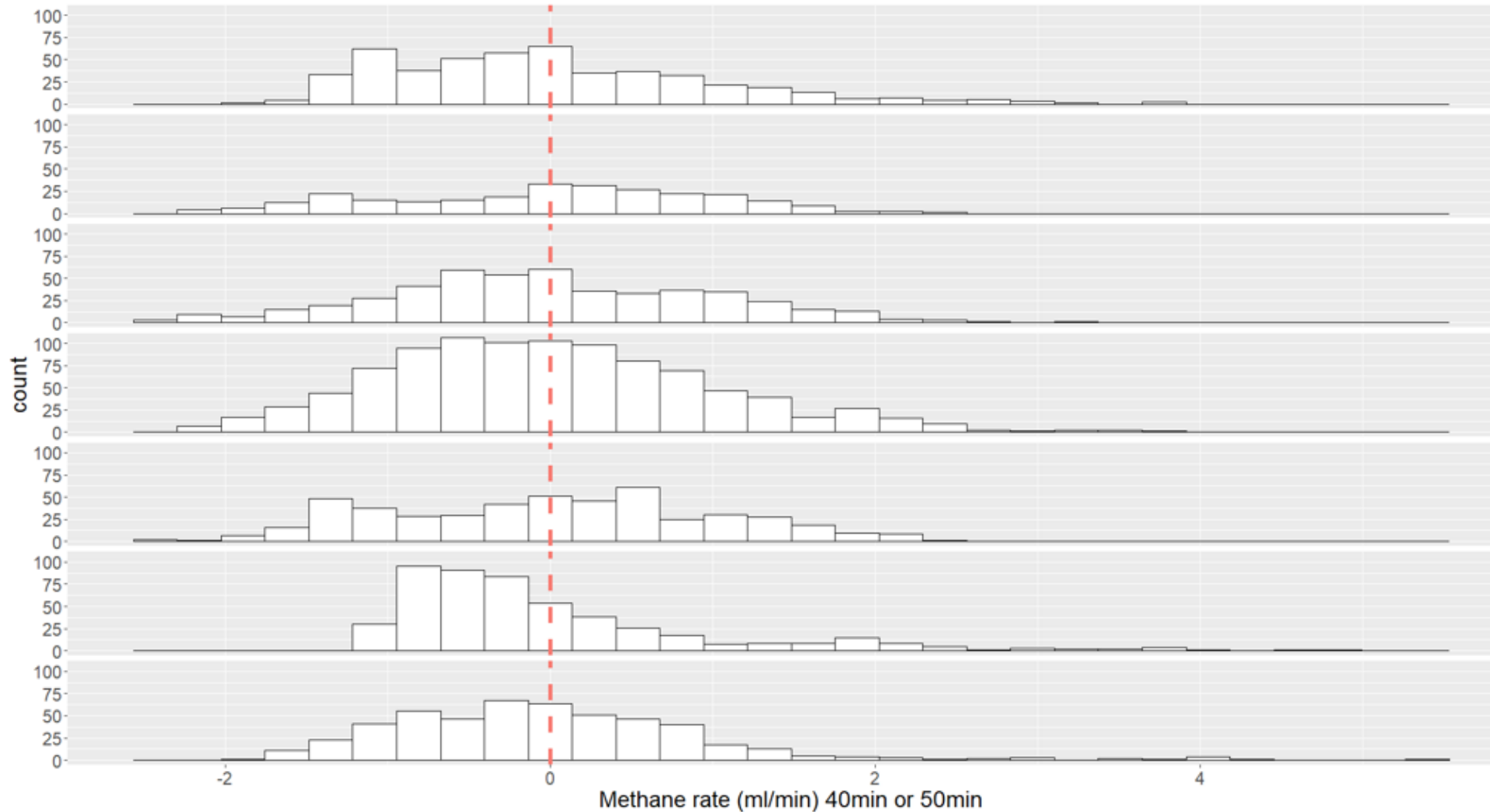
Hypothesis: Differences in feed on offer and feeding behaviour leading up to methane measure.

Both long and short term.

Some assumptions

- Methane rate (ml/min)
  - Some historic data was converted

- Results presented focus on Sheep methane trait (lamb and ewe)
  - Lamb and Ewe traits have also been treated as separate traits

- Max time in PAC used
  - Mid-points and different max times have been ignored

- Different devices across experiments
  - Eagle and FID-FoxBox rank animals the same

- Repeated records (Across lifetime)
  - For this analysis only the first observation was used

- Experimental method
  - Date.Run.Location but needs further investigation

$y = 2.57 + 0.842\ x \quad R^2 = 0.91$

$y = -0.376 + 0.815\ x \quad R^2 = 0.94$
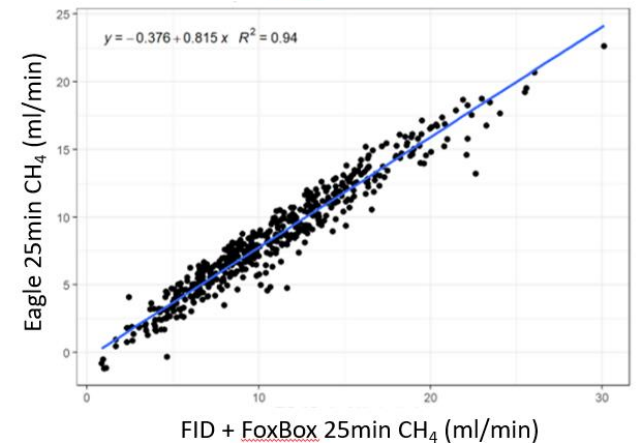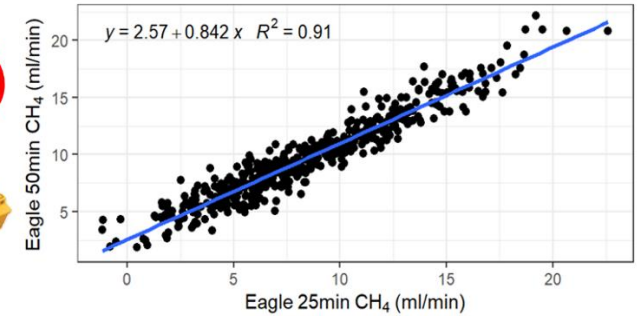
Animal model

$$y = X\beta + ZQg + Za + e$$

β **= Vector of fixed effects**
- Date.Run.Location
- BT.RT
- Sex
- Age

a = Vector of additive genetic effects
- Within genetic groups

g = Vector of random genetic group effects
- Due to multiple breeds and crossbreds
- Flock and breed based

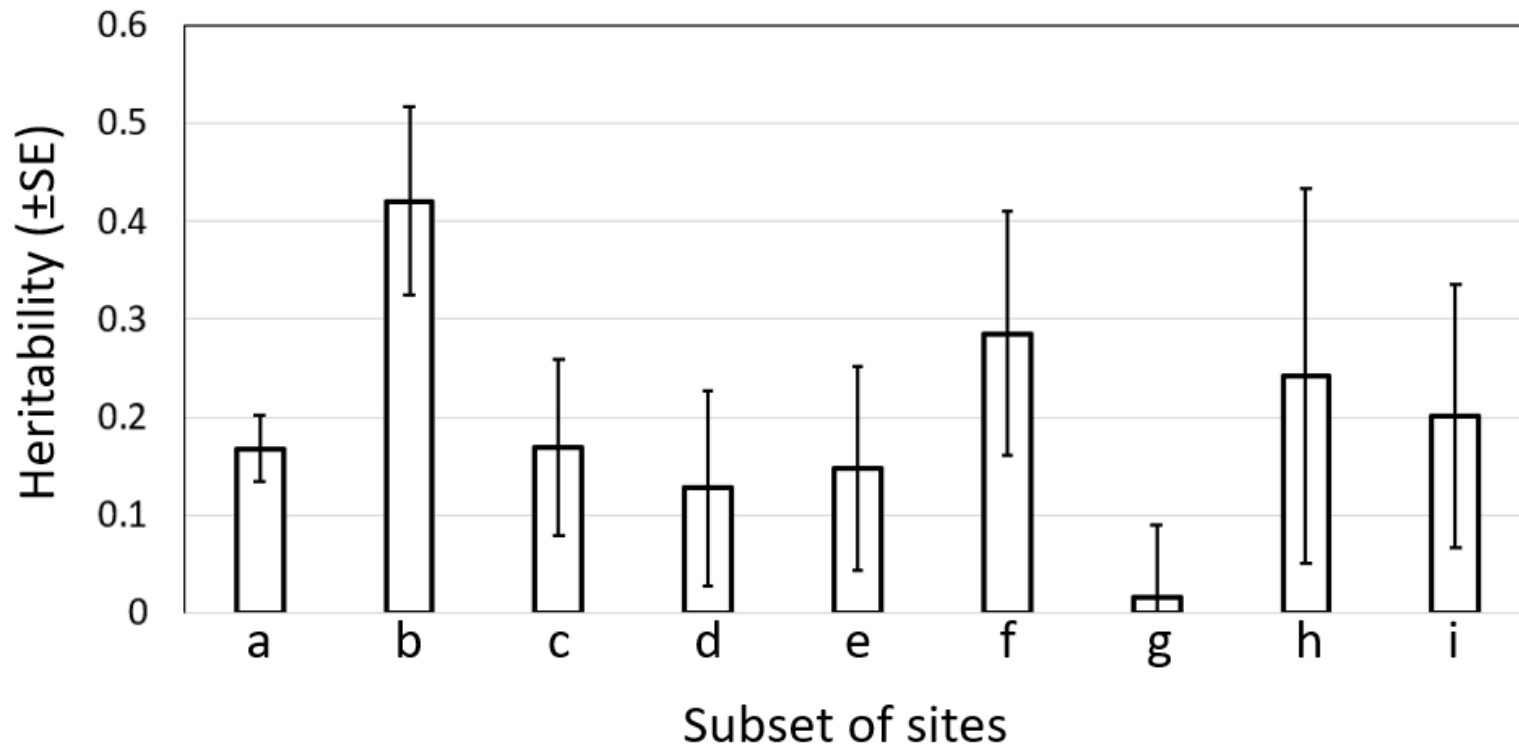Aim is to "Provide the Australian sheep industry with methane breeding values."

Genotyped animals
- Every animal post 2020
- Majority of animals pre 2020

For future integration with national evaluations
- Single-Step
- WOMBAT

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Results – Heritability by site

- Australia has a lot of variable production systems

- Variation is needed

- Feed -> Fermentation = CH_4

- Limited feed = Limited CH_4

- Limited CH_4 = Limited variation

- Future protocols will avoid this

Results

Data used	σ_P^2	σ_e^2	σ_a^2	h^2
All data (2009-2024)	0.49	0.42	0.07	0.14
Lambs only (2009-2024)	0.50	0.42	0.08	0.16
Ewes only (2009-2024)	0.48	0.41	0.08	0.17
Recent data (2021-2024)	0.47	0.40	0.08	0.16
Recent data (Remove feed issues)	0.46	0.38	0.08	0.18

Genetic correlation between the lamb and ewe trait 0.85 to 0.99

Analysis next steps

Project goals

- Genomic prediction validation

- Genetic correlations
  - Feed intake and other important traits

- **Updating selection indexes**
  - SheepObject currently has a predicted methane trait
  - Per head vs Intensity

- Breeding values for industry

Improving modelling

- Relatedness
  - Historic and recent data
  - Commercial data

- Breed corrected GRM

- Accounting for feeding behaviour

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Phenotyping next steps

- ~2,500 methane records to be measured
- Feed intake ~1,000 pre 2020
- Feed intake ~2,500 post 2020 (~2,500 to be measured)
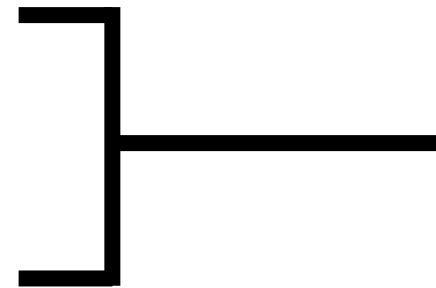- New feed intake facility under construction

- Collaboration is the path forward
- PAC trailer from NZ
- Data sharing

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- Phenotyping nearing required thresholds

- Project breeding values 2024

- Research breeding values 2025

- Australian Sheep Breeding Values ASAP

Producer engagement is paramount

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Australia's genetics institute for agriculture