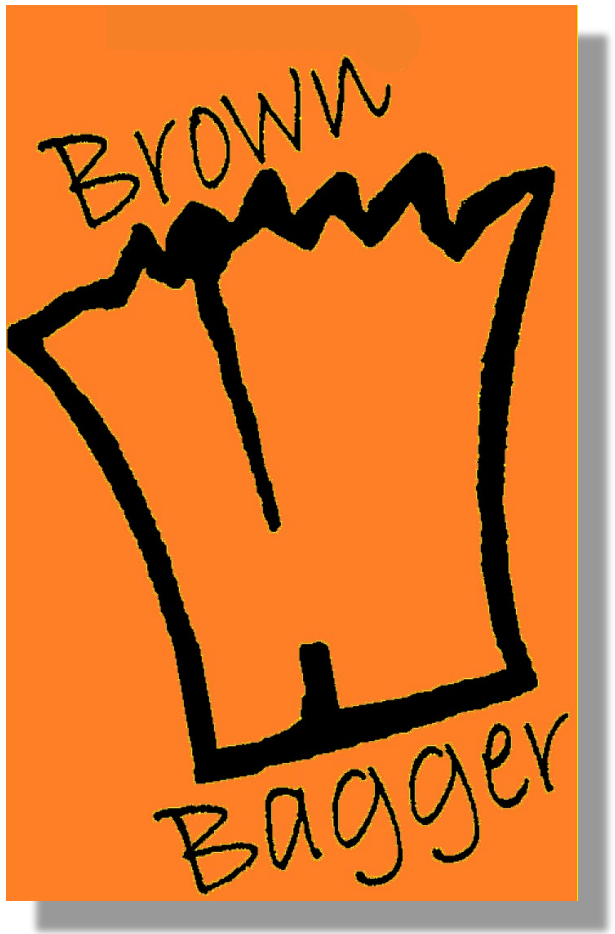
Welcome to Session 3



2024 Future-proofing Beef Selection Decisions

eBEEF.ORG

Session 3-Part 2
Understanding Methane: From Phenotyping to Selection Opportunities

Selecting for Methane Emissions: Global examples and opportunities in the US beef industry

Dr. Troy Rowan
University of Tennessee

Selecting for Methane Emissions: Global examples and opportunities in the US beef industry

INSTITUTE OF AGRICULTURE
THE UNIVERSITY OF TENNESSEE

Troy Rowan

2024 Brown Bagger Webinar Series
October 16, 2024

Rowan Lab
beef cattle genomics

Genetics and the Methane Conversation

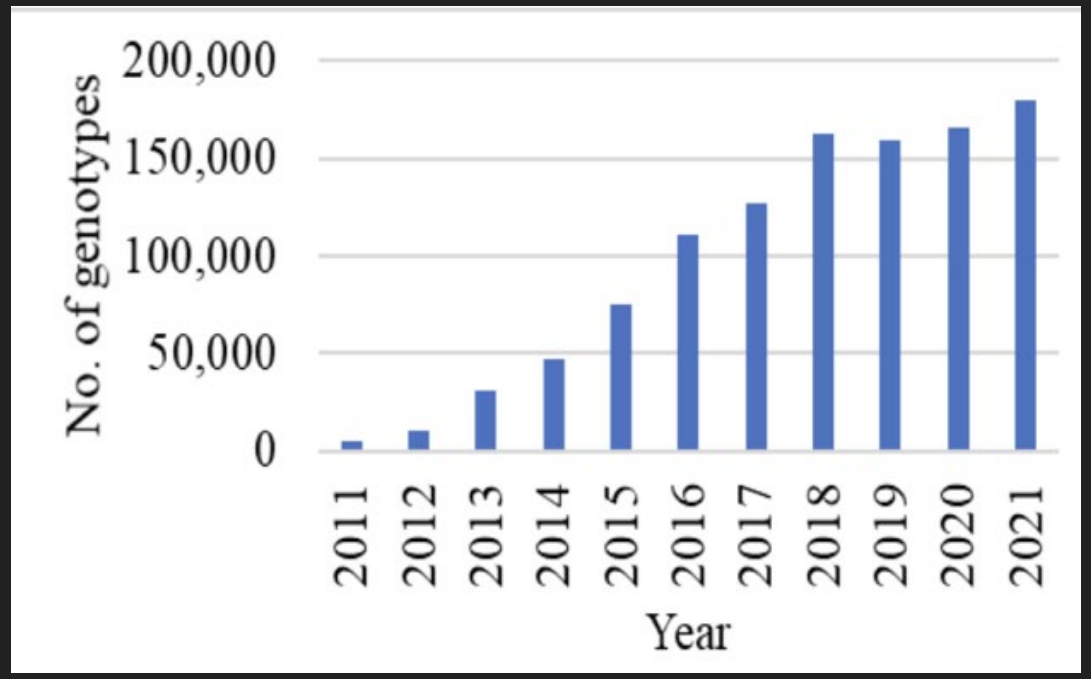
If we can measure a trait…

We can make genetic predictions

With predictions…

We can accelerate genetic progress

“In the age of genotyping, Phenotype is king!” – Prof. Mike Coffey



AAA genotypes added per year (Retallick et al. 2022)

Some Good News

- Methane production is heritable
  - h^2 = ~0.2 - 0.3 (similar to weaning weight) [Dressler et al. 2024]

- Continued genetic progress across efficiency traits is reducing emission intensity
  - Growth & productivity
  - Cow-centric traits

Some big questions:

- Genetic correlations with other ERTs unclear
  - DMI favorably correlated
  - Larger animals make more methane (generally)
  - r_G with feed efficiency is unclear [Lakamp et al. 2024]

- Market signals are unclear
- Insets vs offsets (i.e., is increasing productivity enough)
- Concentrate vs. forage (different traits?)

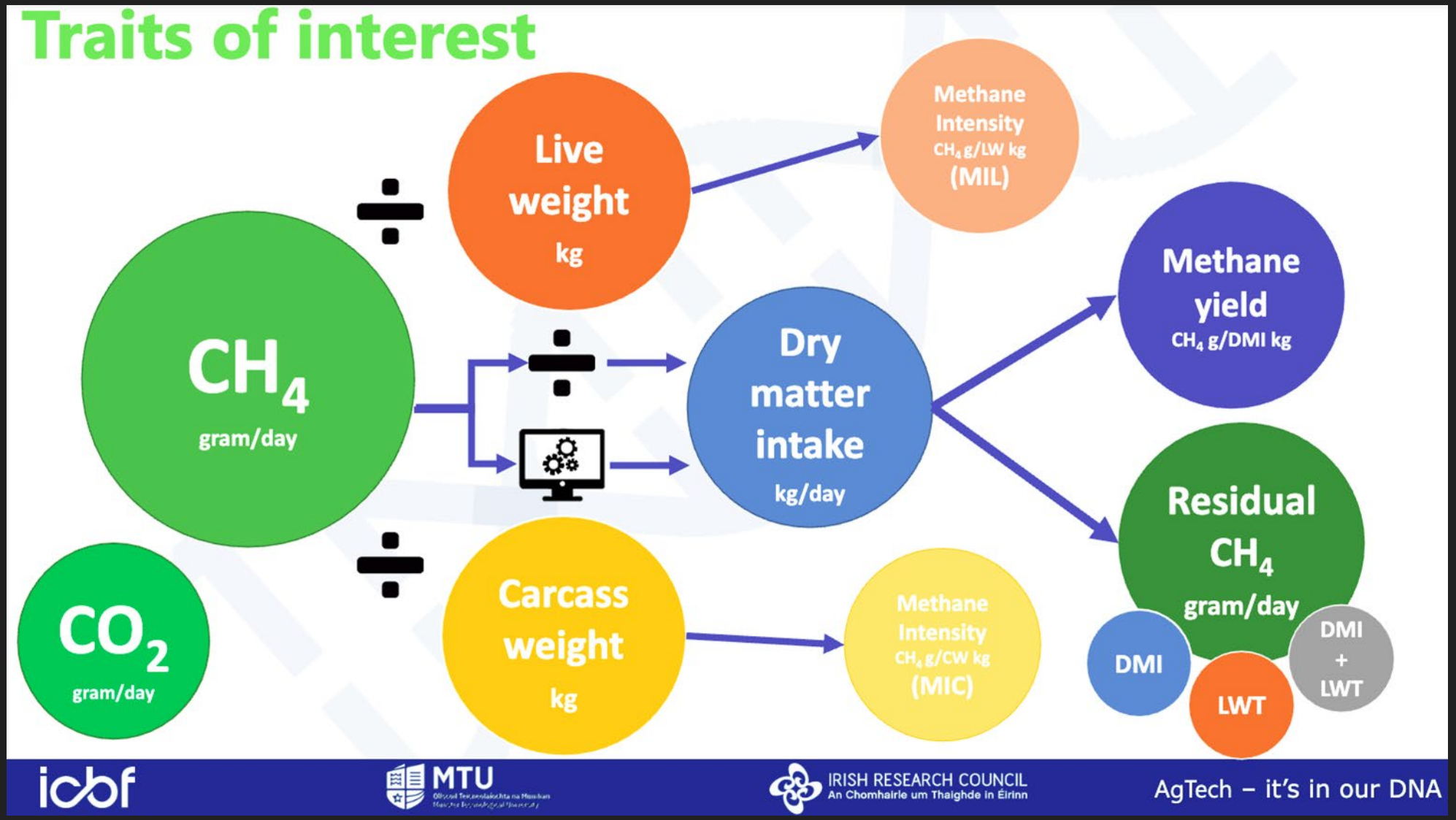
Our Challenge

- **How do we capture a phenotypes?**
  - Cost prohibitive to producers
  - Infrequent interactions in extensive systems
  - Data sharing of limited phenotypes

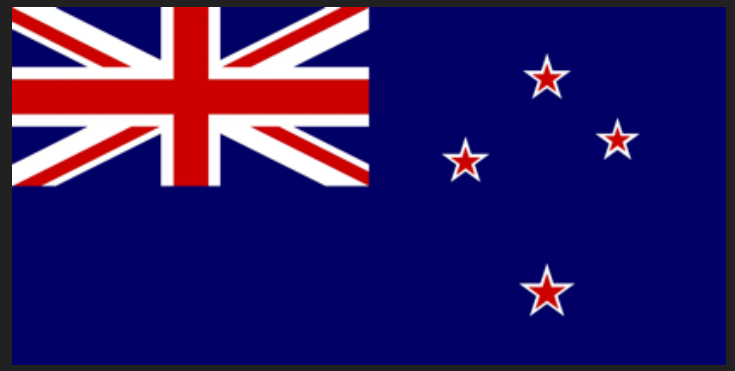
What is the cost of a single CH_4 phenotype with a GreenFeed?

Conservatively: $75-$100

What do we measure??



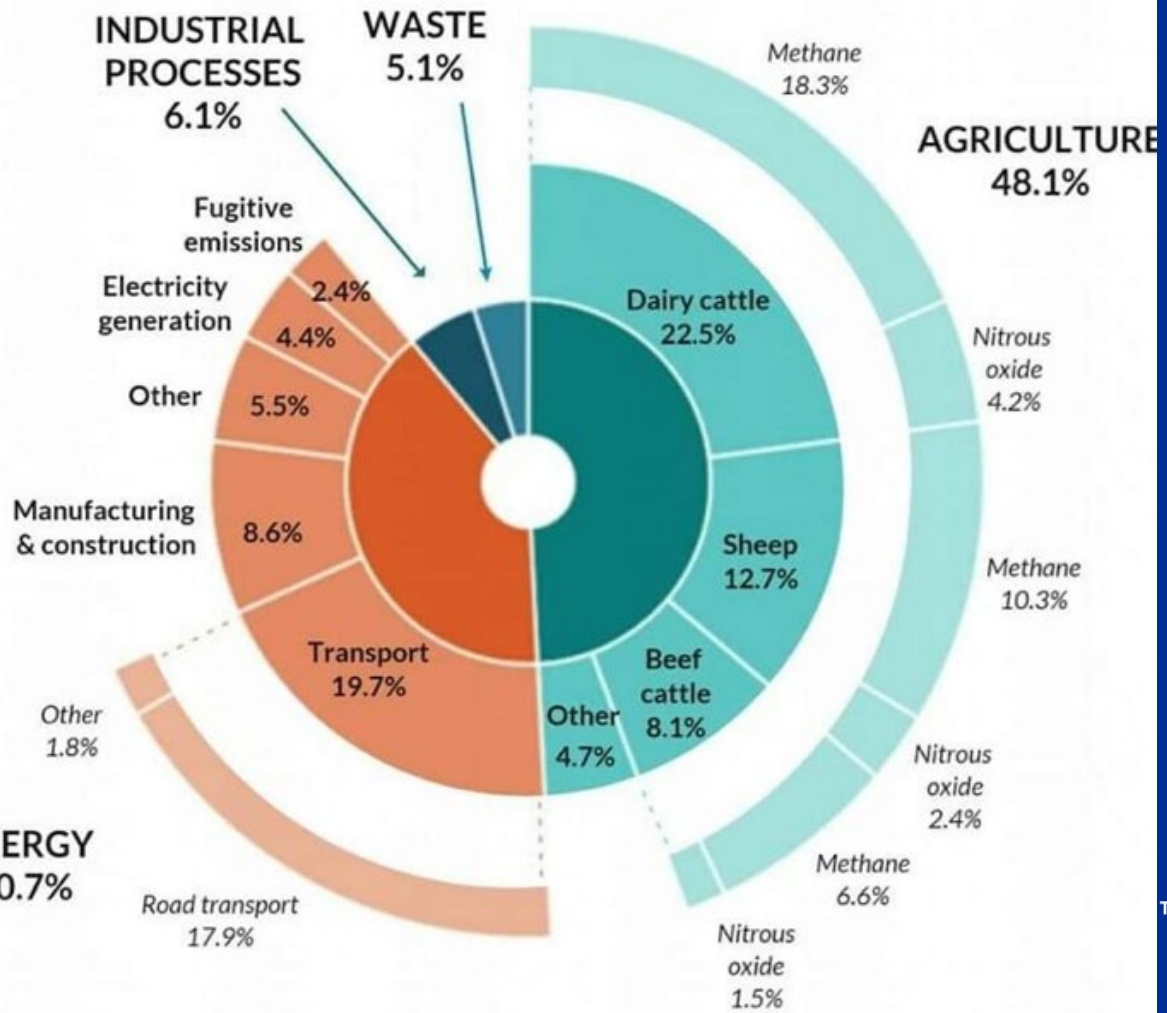
C.V. Ryan et al. 2022 – WCGALP

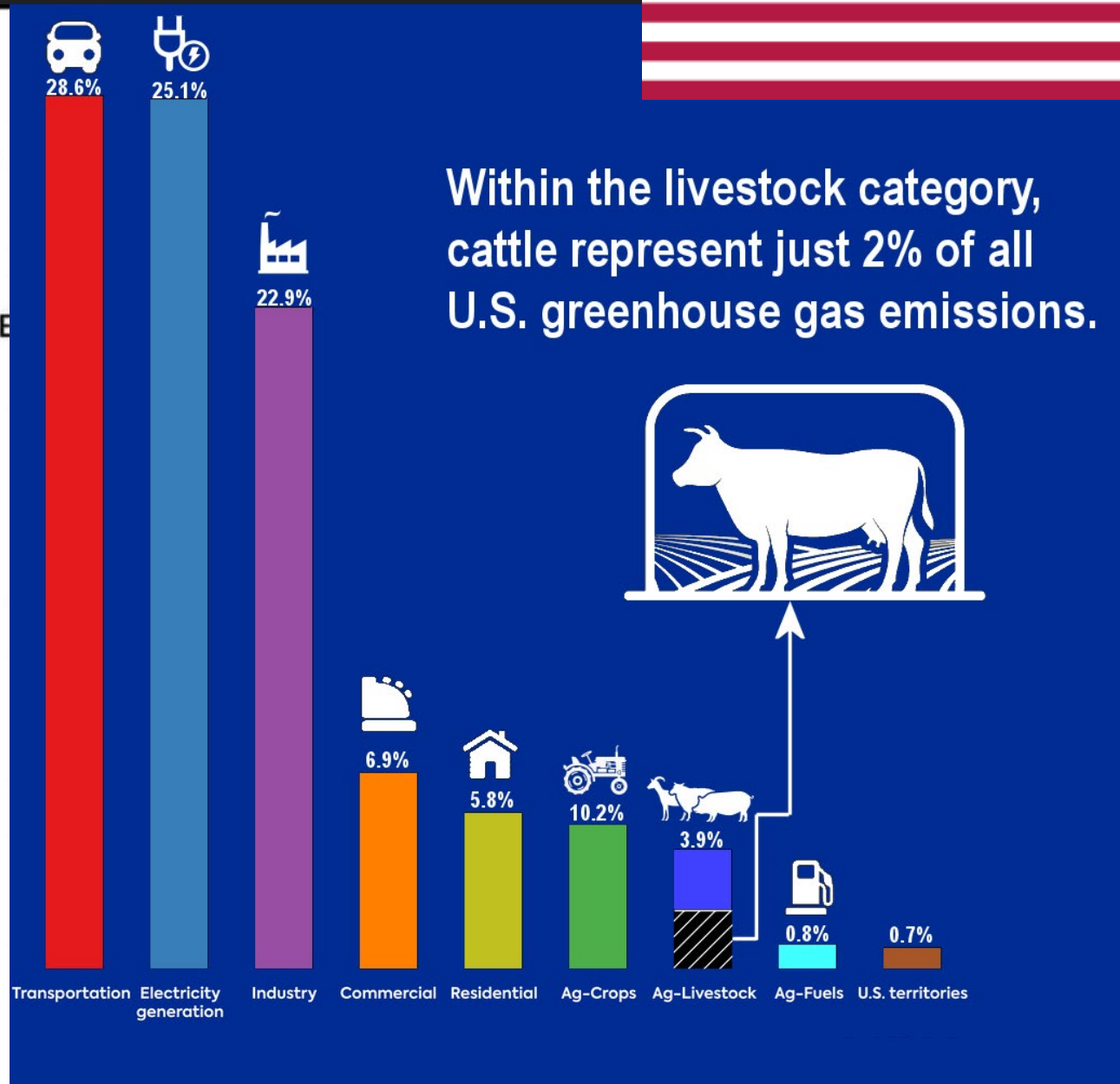


Why have other countries been leading efforts in enteric GHG emission research?

Greenhouse Gas Emissions

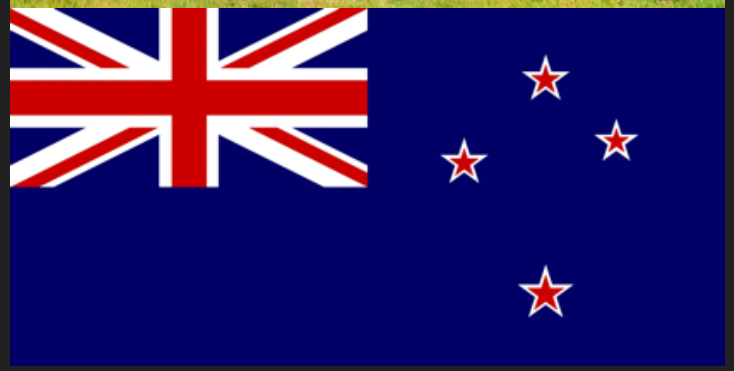
Source: New Zealand's Greenhouse Gas Inventory 1990-2017, published April 2019





Within the livestock category, cattle represent just 2% of all U.S. greenhouse gas emissions.

How are other species & countries performing genetic evaluations for methane emissions?



New Zealand Sheep Genetic Evaluations

- Brute force phenotyping using portable accumulation chambers
- Targeted phenotyping initiative
- Phenotyping is a “one-and-done” endeavor for producers

What will methane selection do to other traits?

- Long-term selection experiment in NZ sheep population
- Lamb and ewe CH_4 emission is highly correlated [Jonker et al. 2018]
- Methane emission phenotypes are most important in pasture settings
  - Not correlated with fertility traits in sheep [Hickey et al. 2022]
- No negative impacts on feed efficiency or productivity [Rowe et al. 2022]
- No negative impacts on meat quality or carcass traits

UTAgRESEARCH
INSTITUTE OF AGRICULTURE
THE UNIVERSITY OF TENNESSEE

Breeding values for methane emission

What do we do when methane phenotypes remain too expensive/ difficult to measure at scale?

Canadian dairy cows among first in world bred to belch less methane

New genetics could help reduce one of the biggest sources of potent greenhouse gas

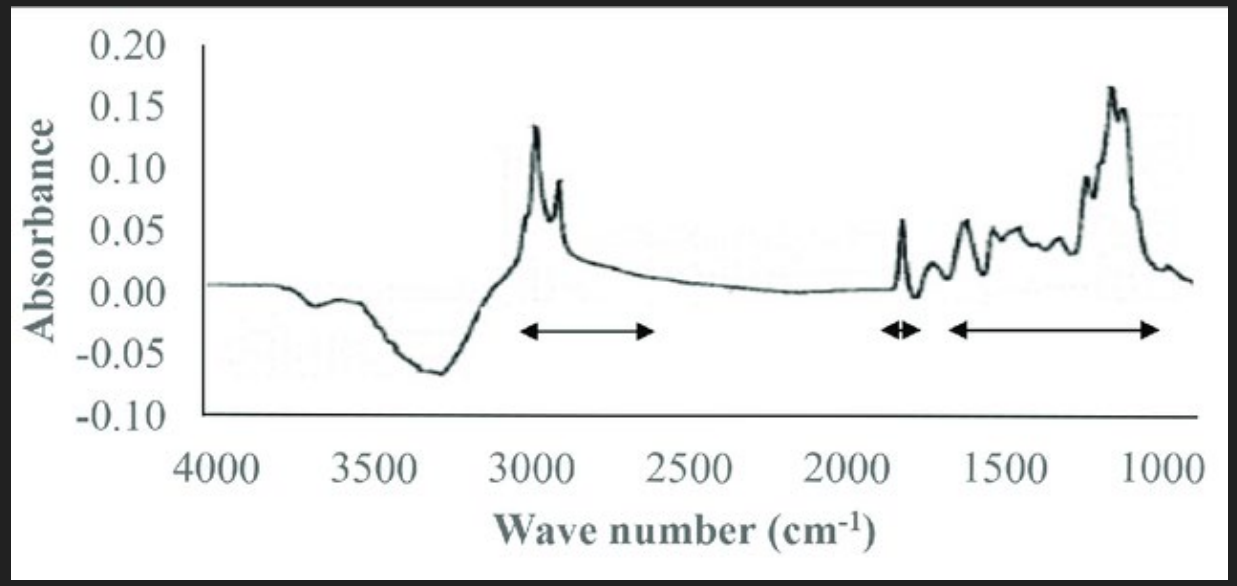
Rod Nickel · Thomson Reuters · Posted: Aug 08, 2023 1:30 PM EDT | Last Updated: August 8

A Holstein cow stands in a pasture at a dairy farm near Calgary in this file photograph. Livestock account for 14.5 per cent of the world's greenhouse gas emissions. (Jeff McIntosh/The Canadian Press)

Measure an indicator phenotype!

Genetic Evaluations – Canadian Dairy

GreenFeed records on 1000+ animals



Milk spectral data models trained for measured methane

UTAgRESEARCH INSTITUTE OF AGRICULTURE THE UNIVERSITY OF TENNESSEE

THE Resilient Dairy GENOME PROJECT

UTCVM INSTITUTE OF AGRICULTURE THE UNIVERSITY OF TENNESSEE

Canadian Dairy Methane Efficiency Evaluation

- MIR predicted CH_4 on first lactation Holsteins between 120 and 185 days in milk
  - 700,000 MIR records being used for predicted CH_4
- ssGBLUP implementation with other Lactanet traits
- Delivered as a relative breeding value (higher value = less CH_4)
  - 5 point increase in RBV = 3 kg/year reduction in CH_4
  - Modelling suggests this could drive a 20-30% reduction in CH_4 is possible by 2050

Ongoing Developments

Widespread “sniffer” deployment in automatic milking systems (AMS)

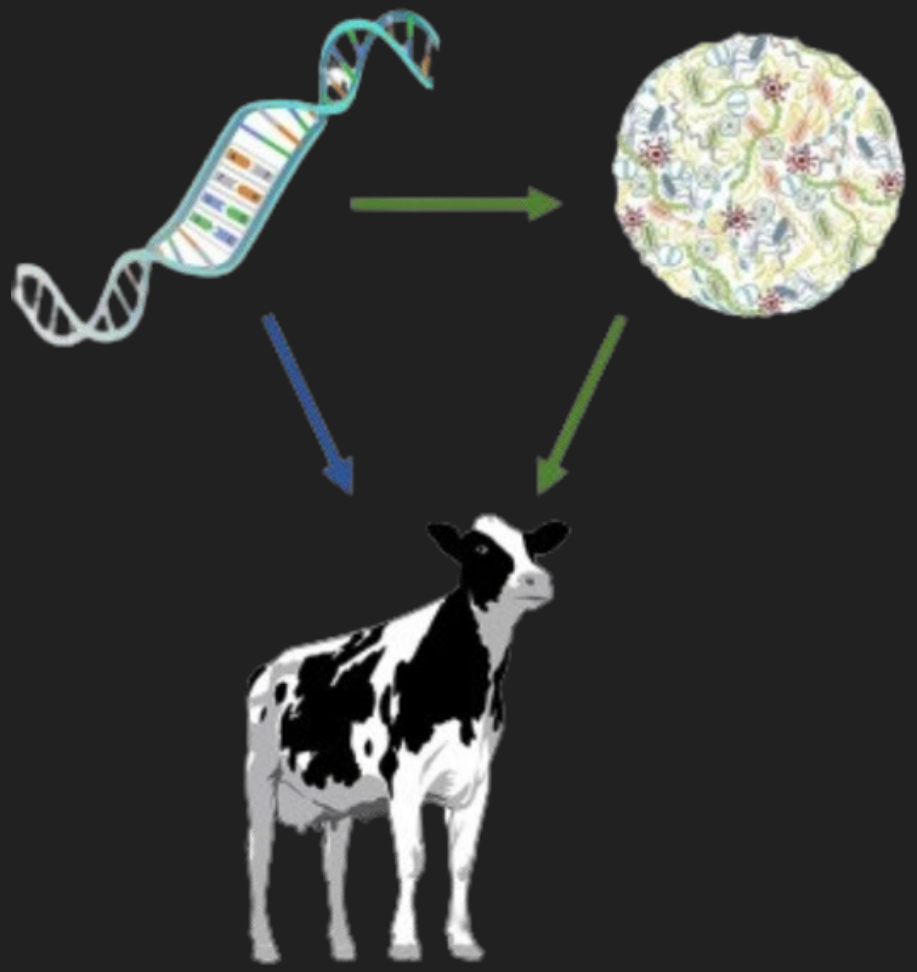
Multi-trait modelling with various measurement technologies

Identifying how we handle “incomplete” records?

Challenges for the US Beef Industry

- **<u>Phenotyping challenges:</u>**
  - Cost prohibitive to producers
  - Collection in extensive systems
  - Data sharing of limited phenotypes
  - Data heterogeneity/quality
  - Which correlated traits do we fit together?
- Market signals are unclear (how to we fit into an index)

Other Opportunities & Ongoing Research

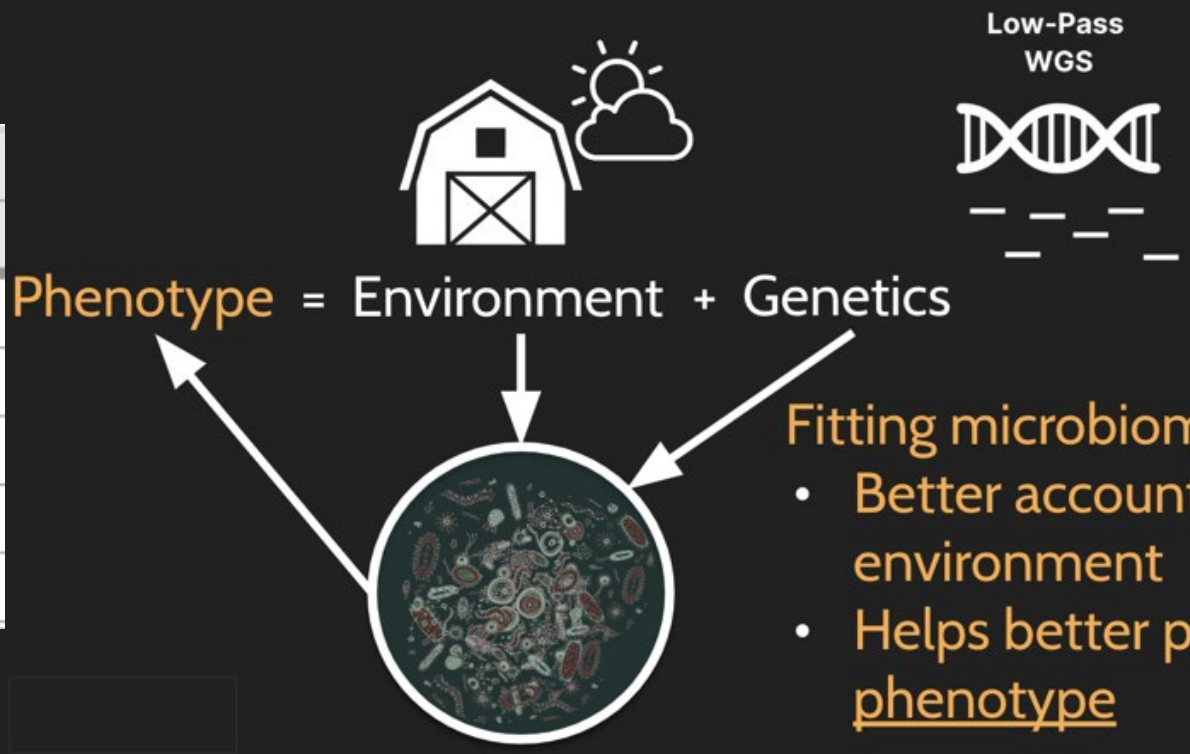


Can we keep ignoring the rumen microbiome?

Modelling the Microbiome

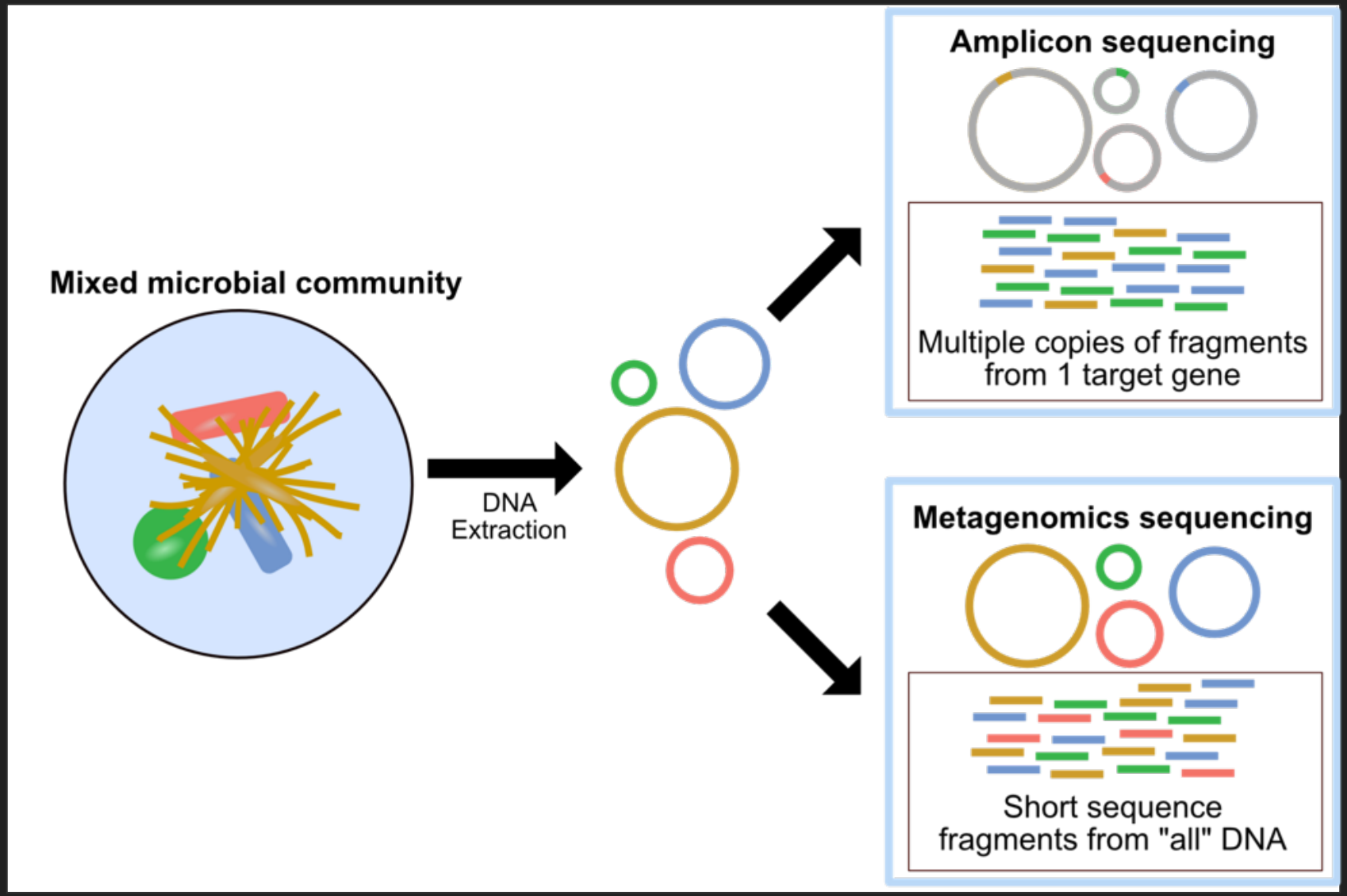
Model[a]	Component[b]	Grass adult	
		PropVar[c]	Accuracy[d]
G	G_G	0.33 ± 0.07	0.18 ± 0.08
M	M_M	0.95 ± 0.20	0.31 ± 0.14
G + M	G_{G+M}	0.25 ± 0.11[f]	0.17 ± 0.08[f]
	M_{G+M}	0.75 ± 0.11[f]	0.31 ± 0.14[f]
	$G + M_{G+M}$	1.00 ± 0.00[f]	0.35 ± 0.12[f]

Hess et al. 2023



How do we make rumen microbiome characterization easier, cheaper, and less invasive?

Microbiome Sequencing Approaches

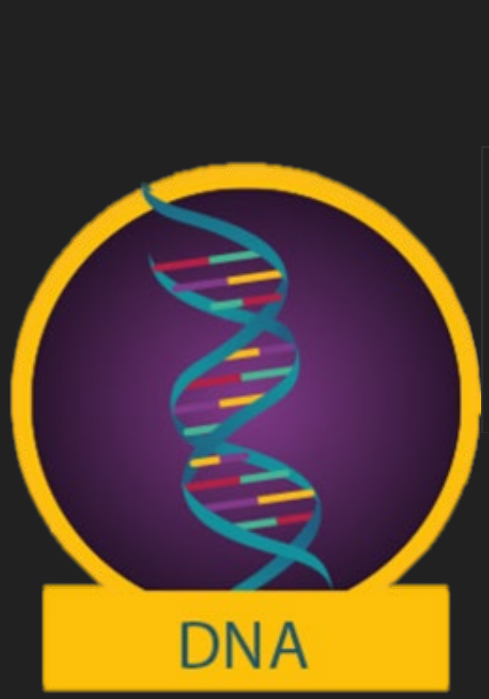


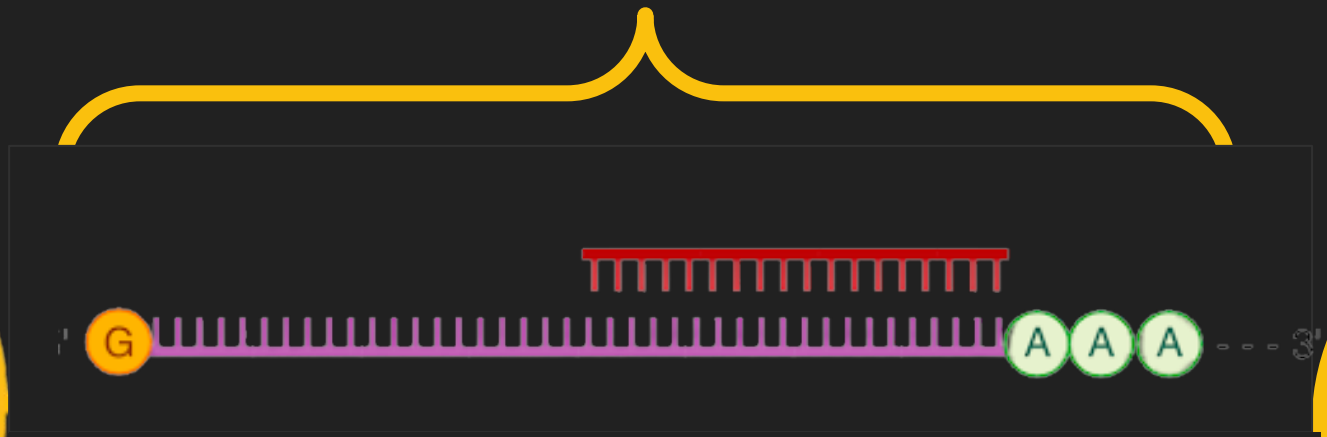
Buccal Swabs: Collect non-invasive microbiome proxy while generating a DNA sample

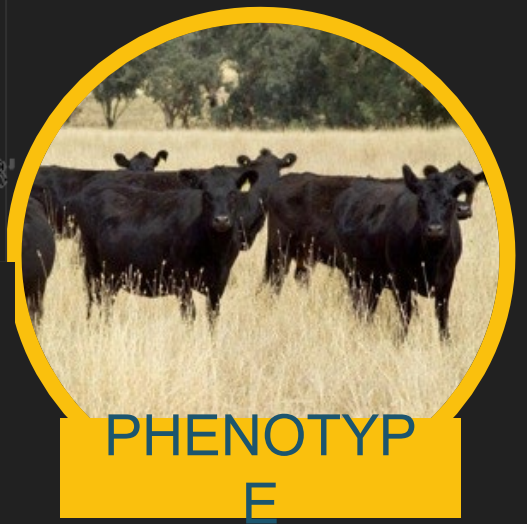
Sequencing doesn’t distinguish between host/microbe DNA!

Do proxies for CH_4 emission exist (like MIR for dairy cows) that we could measure in beef animals?

Can we use these as “proxy” phenotypes for hard-to-measure traits?







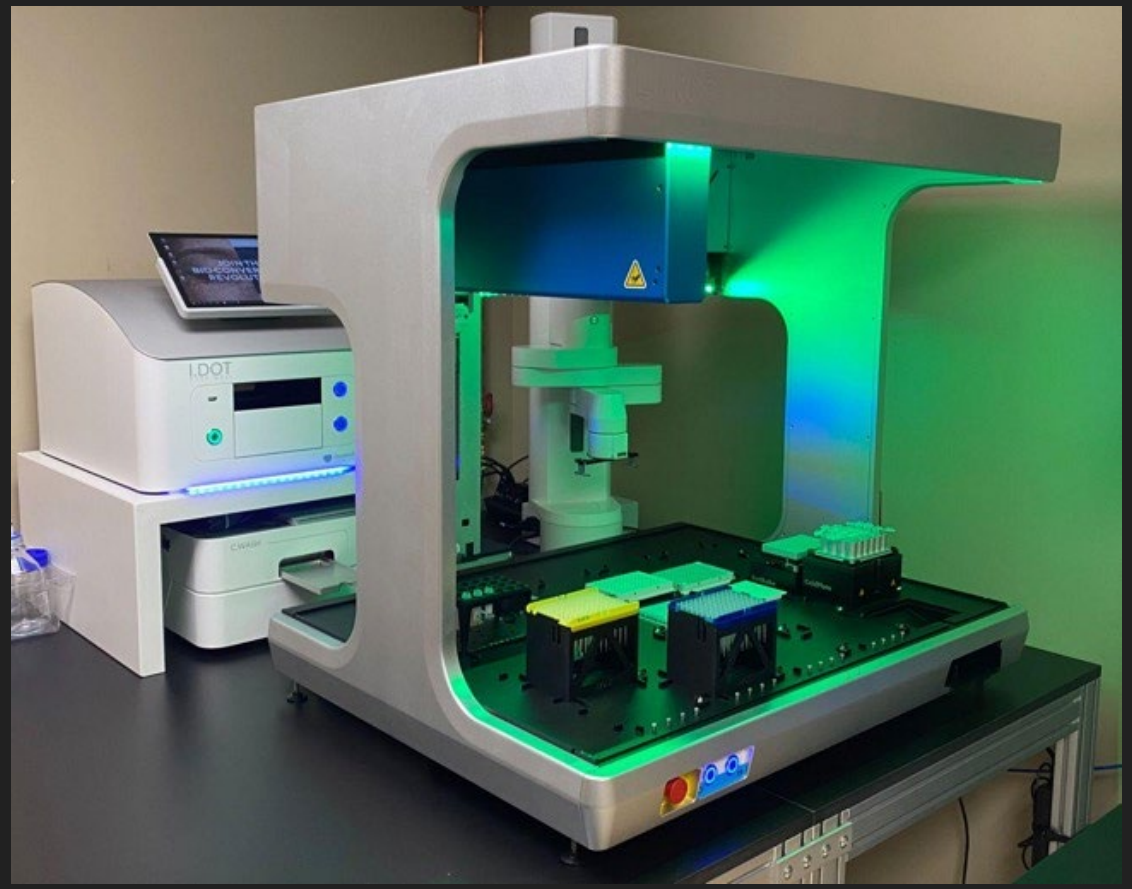
< $10 USD Gene Expression w/ 3’ RNA-Seq

MUST BE COST EFFECTIVE

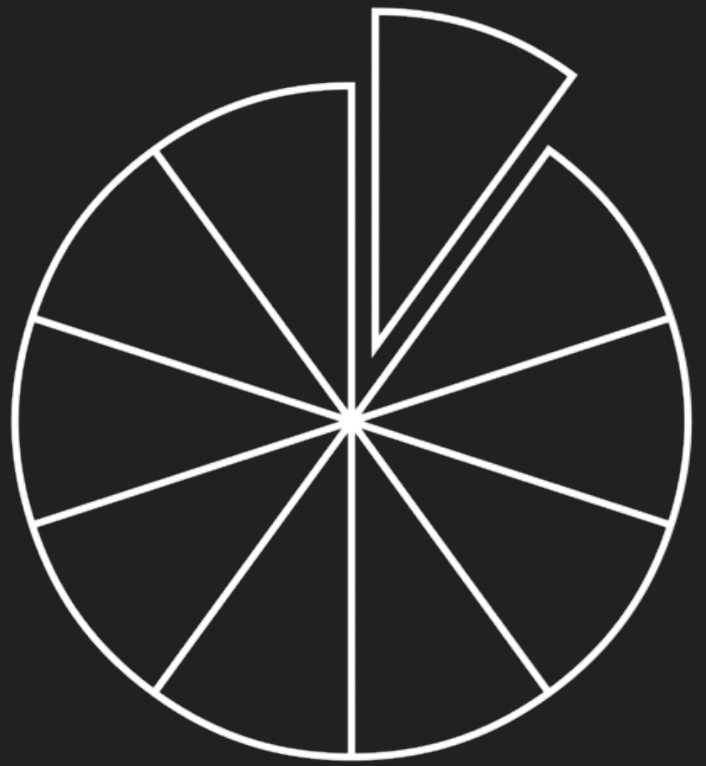
Using gene expression as efficiency indicators

UTAgRESEARCH
INSTITUTE OF AGRICULTURE
THE UNIVERSITY OF TENNESSEE

“Wet Lab” Developments



Robotic preparation



Fractional reactions

Genetics is a tractable approach to reducing methane in ruminant production

Canadian dairy and NZ sheep industries have active genetic evaluations for CH_4

Assembling genetic evaluation-sized datasets is a major challenge

Strategies exist for integrating rumen microbiome profiles into predictions

Research presented in this presentation was funded by Foundation for Food and Agricultural Research (FFAR) Grant No. 22-000087

Rowan Lab
beef cattle genomics

Reach out with questions!

trowan@utk.edu
(865) 974-3190

UTAgRESEARCH INSTITUTE OF AGRICULTURE THE UNIVERSITY OF TENNESSEE

UTCVM INSTITUTE OF AGRICULTURE THE UNIVERSITY OF TENNESSEE