Reducing enteric methane emissions from dairy cattle

Francisco Peñagaricano, Ph.D.

CDCB Industry Meeting
October 4, 2023

WISCONSIN
UNIVERSITY OF WISCONSIN-MADISON

Methane emissions

- **methane represents 11% of total U.S. greenhouse gas emissions**
  - 2nd most important greenhouse gas after CO_2
- **enteric fermentation accounts for 27% of total U.S. methane emissions**
  - 2nd most important source after natural gas & petroleum systems
- **enteric CH_4 represents a loss of energy, 6-12% of gross energy intake**
  - energy that could otherwise be available for growth or production
- **reducing enteric CH_4 would benefit the environment and improve efficiency**

Integrating genomic, milk spectrometry, and microbial manipulations to mitigate enteric methane emissions from dairy cattle

overall goal: reduce enteric CH_4 emissions from dairy cattle by combining

- **selective breeding**
- **milk mid-infrared spectra**
- **rumen microbiome interventions**

Francisco Peñagaricano, quantitative genomics
Hilario C Mantovani, rumen microbiology
Heather M White, nutritional physiology
Kent A Weigel, breeding & genetics

Michael J VandeHaar, sustainable food systems
Robert J Tempelman, statistical genetics

James E Koltes, genomics & bioinformatics
Ranga Appuhamy, nutrition/sustainable agriculture

José EP Santos, nutrition, health & fertility
Kwang C Jeong, microbiology & food safety

Ransom L Baldwin, nutritional genomics
Paul M VanRaden, sustainable breeding goals
Asha Miles, genomics & microbiology
Elizabeth A French, precision feeding
Kenneth F Kalscheur, sustainable production


GREENER
CATTLE
INITIATIVE


CDCB
COUNCIL ON DAIRY CATTLE BREEDING


FOUNDATION FOR
FOOD & AGRICULTURE
RESEARCH


INNOVATION
CENTER FOR U.S. DAIRY
HEALTHY PEOPLE • HEALTHY PRODUCTS • HEALTHY PLANET


ADM


CDCB
COUNCIL ON DAIRY CATTLE BREEDING


Elanco


Genus


NATIONAL
DHIA


JBS


Nestlé


NEW ZEALAND
AGRICULTURAL GREENHOUSE GAS
Research Centre

Our plan

phenotyping
4,000 lactating cows
(6 research farms over 3 years)

measure CH_4 production, feed intake, milk energy, body weight, and milk spectra for 6-8 weeks in mid-lactation

selective breeding

develop genomic evaluations for methane emission traits

milk spectrometry

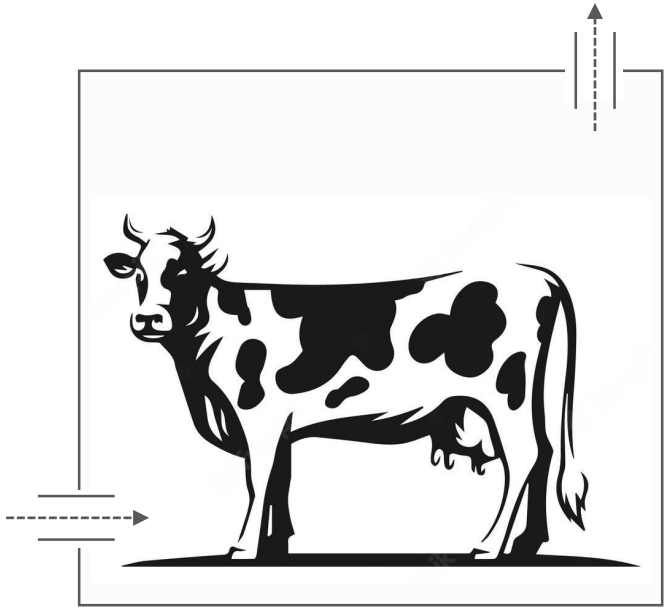
evaluate the use of milk spectra to predict CH_4 emissions

rumen microbiome

reveal the composition/activity of the rumen microbiome of cows with low & high CH_4 emissions
using metagenomics and metabolomics

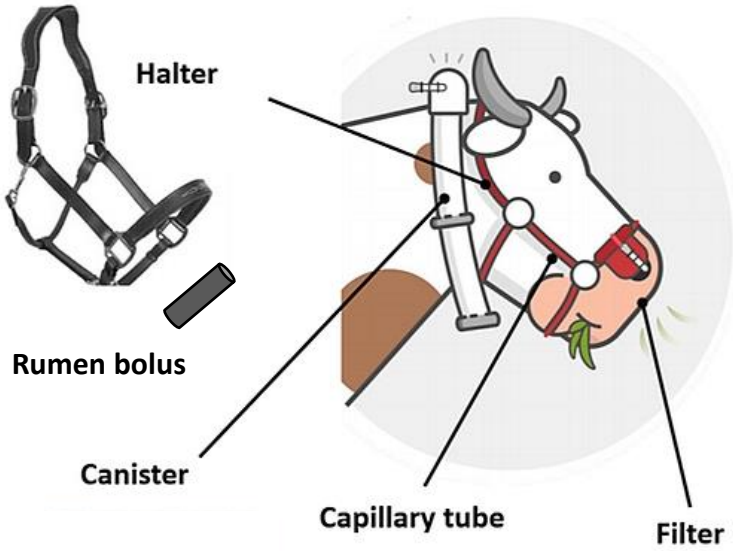
exchange ruminal contents of low and high methane-emitting cows
decipher the relative contributions of hosts and microbes to CH_4 production

Phenotyping



respiration chamber

(gold standard)



Sulphur Hexafluoride (SF6) tracer technique

GreenFeed system

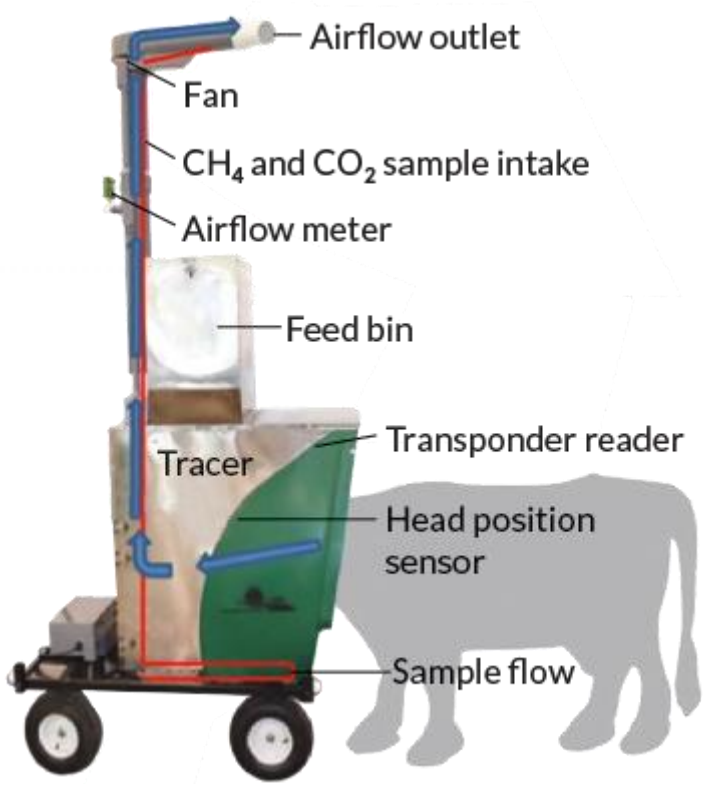
sniffers

(automatic milking systems)

Laser detector

GreenFeed system

This system delivers reliable estimates of enteric methane emissions

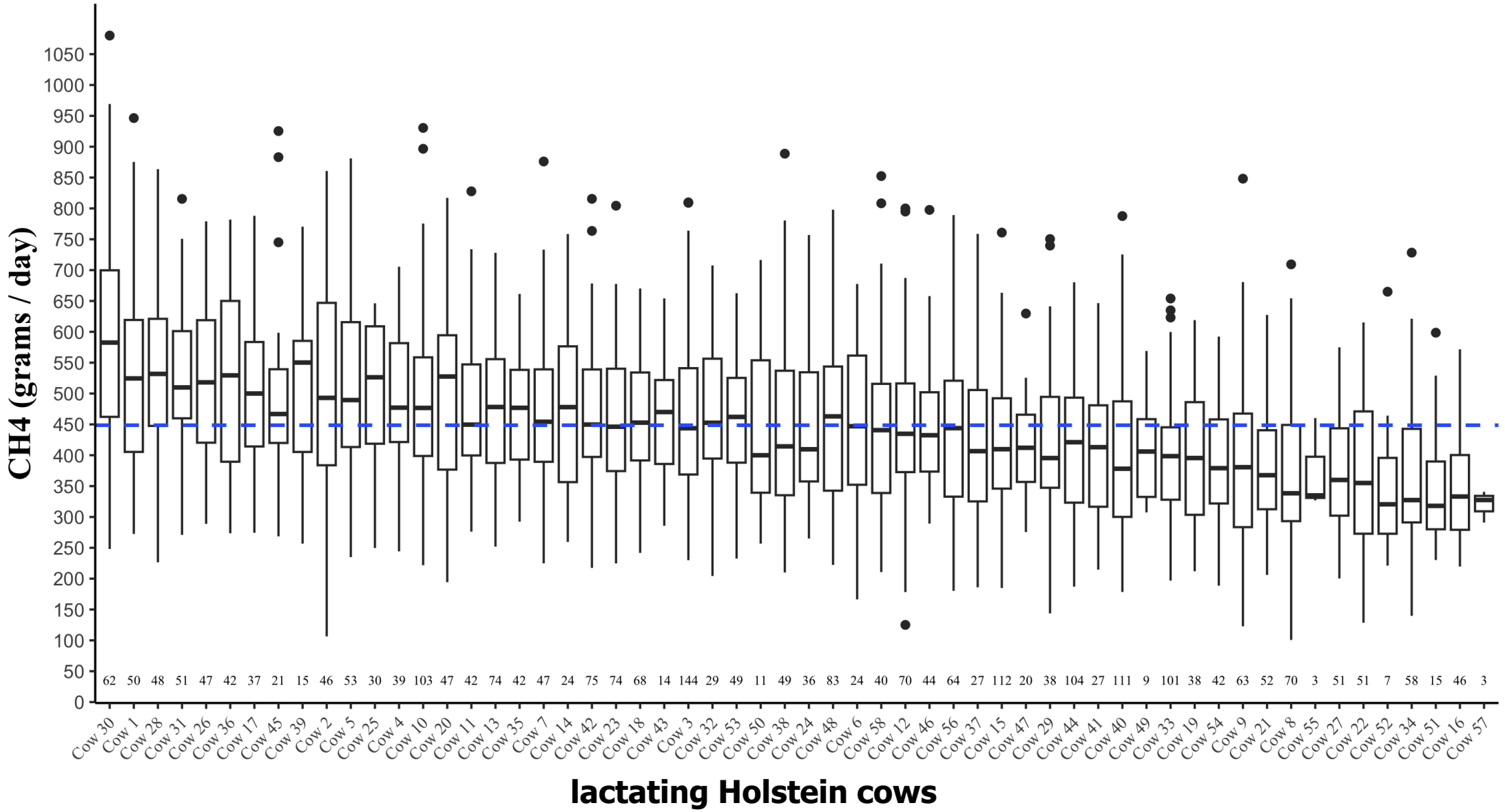


key: obtain numerous short-term records measured at different times of the day for multiple days

GreenFeed system

Pen 30 at UW Emmons Blaine Arlington Dairy Research Center

Variability in CH_4 emissions



lactating Holstein cows

Selective breeding

- **selection is a promising tool to mitigate enteric methane emissions**
  - recent studies have shown that methane emission traits are heritable

- **genomics has facilitated selection for traits like methane emissions**
  - phenotyping can be performed on a few genotyped cows,
  - and this population can be used to predict gPTAs for the entire population

our goal:

- develop a reference population for methane emissions
- develop genomic evaluations for methane emission traits, and
- facilitate their incorporation into selection indices

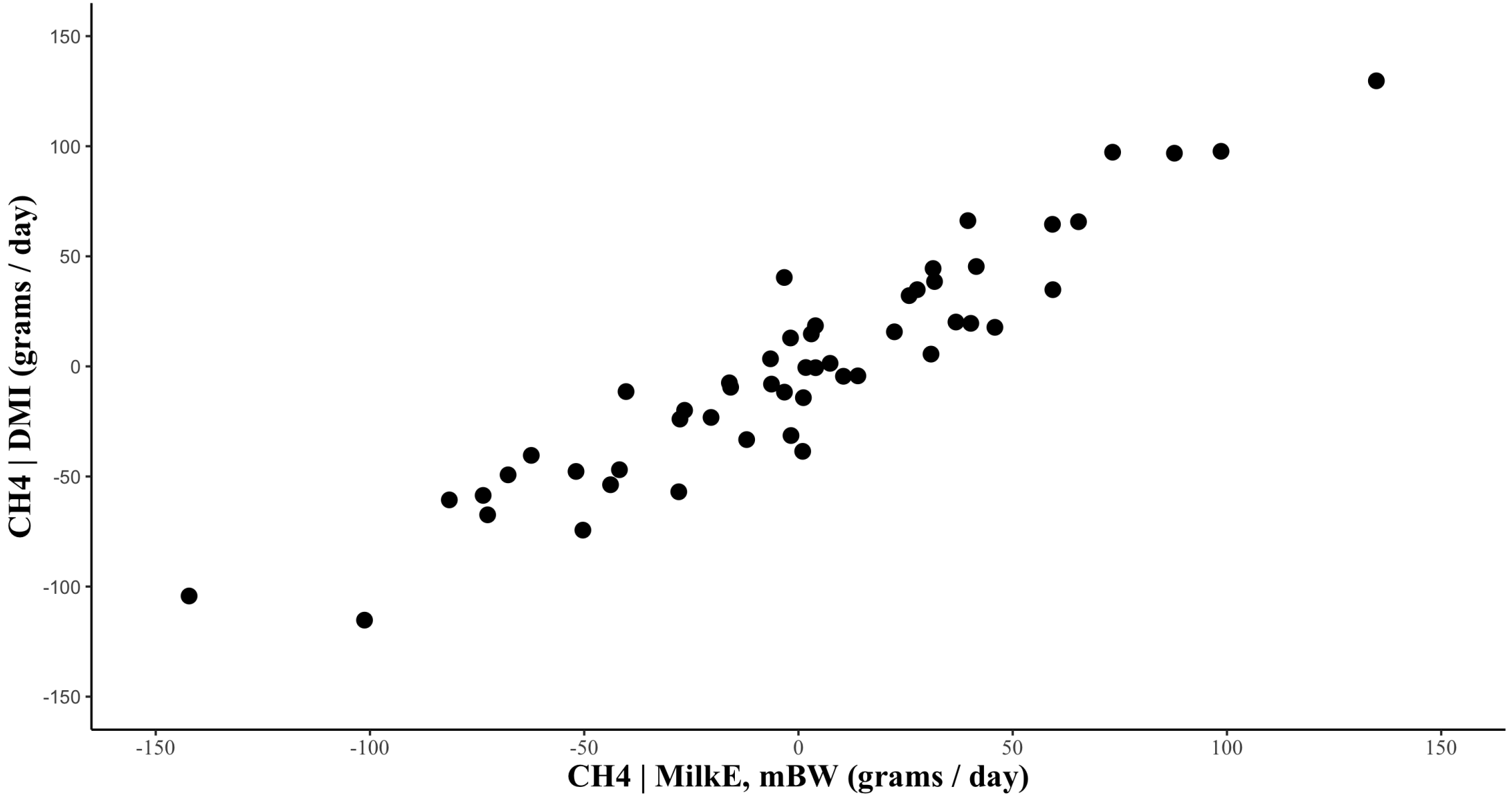
Trait definition

Alternative methane emission traits

- **methane production** (grams CH_4 per day)
- **methane yield** (grams CH_4 per kg of dry matter intake)
- **methane intensity** (grams CH_4 per kg of energy-corrected milk)
- **residual methane** (grams CH_4 regressed on DMI, BW, and MilkE)

Residual CH_4 production

CH_4 production regressed on (MilkE + mBW) or (DMI)



Milk spectrometry

- **Fourier transform infrared spectroscopy is a powerful phenotyping tool**
  - high-throughput, low-cost, non-invasive, real-time predictions
- **milk mid-infrared spectra data has been used to predict complex traits**
  - energy status, metabolic profiles, health status, and fertility, among others

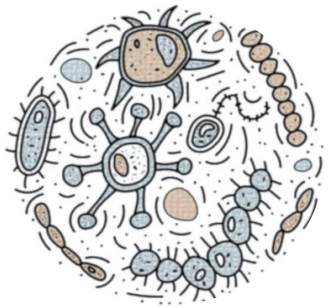
our goal:

- determine the value of using milk spectra to predict CH_4 emissions

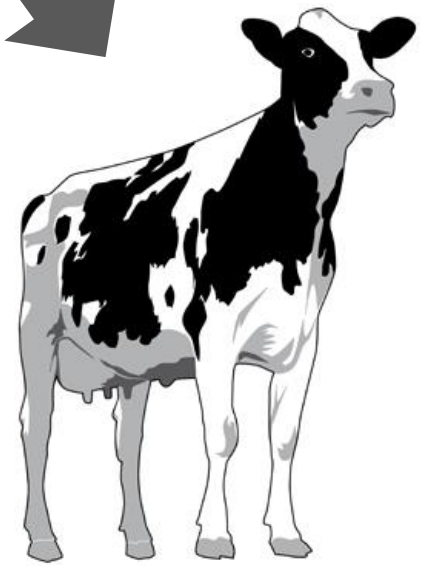
Rumen microbiome

enteric CH_4 is formed exclusively by methanogens in the rumen

Host Genome



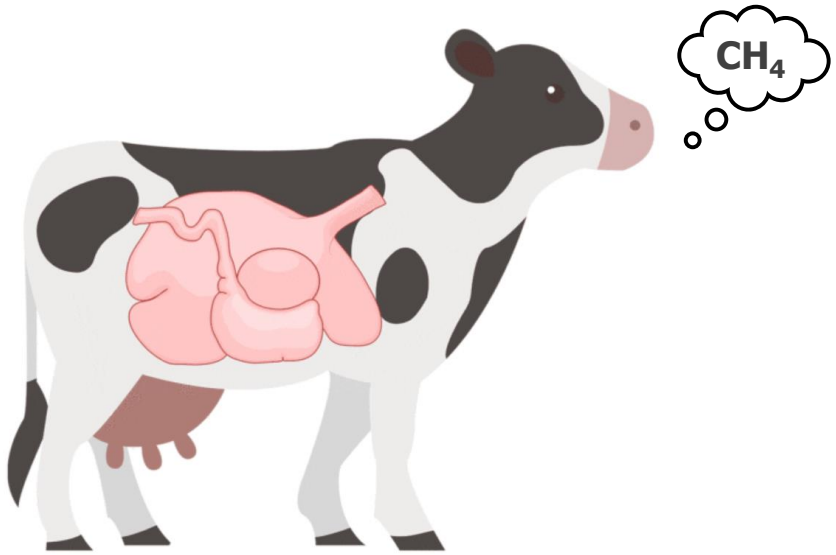
Microbiome

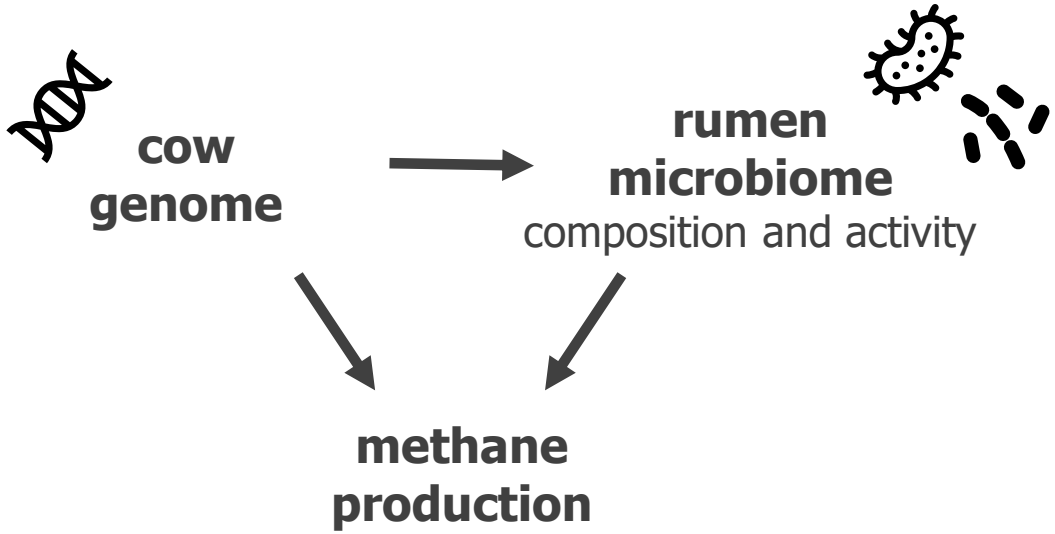


Phenotype

Rumen microbiome

enteric CH_4 is formed exclusively by methanogens in the rumen



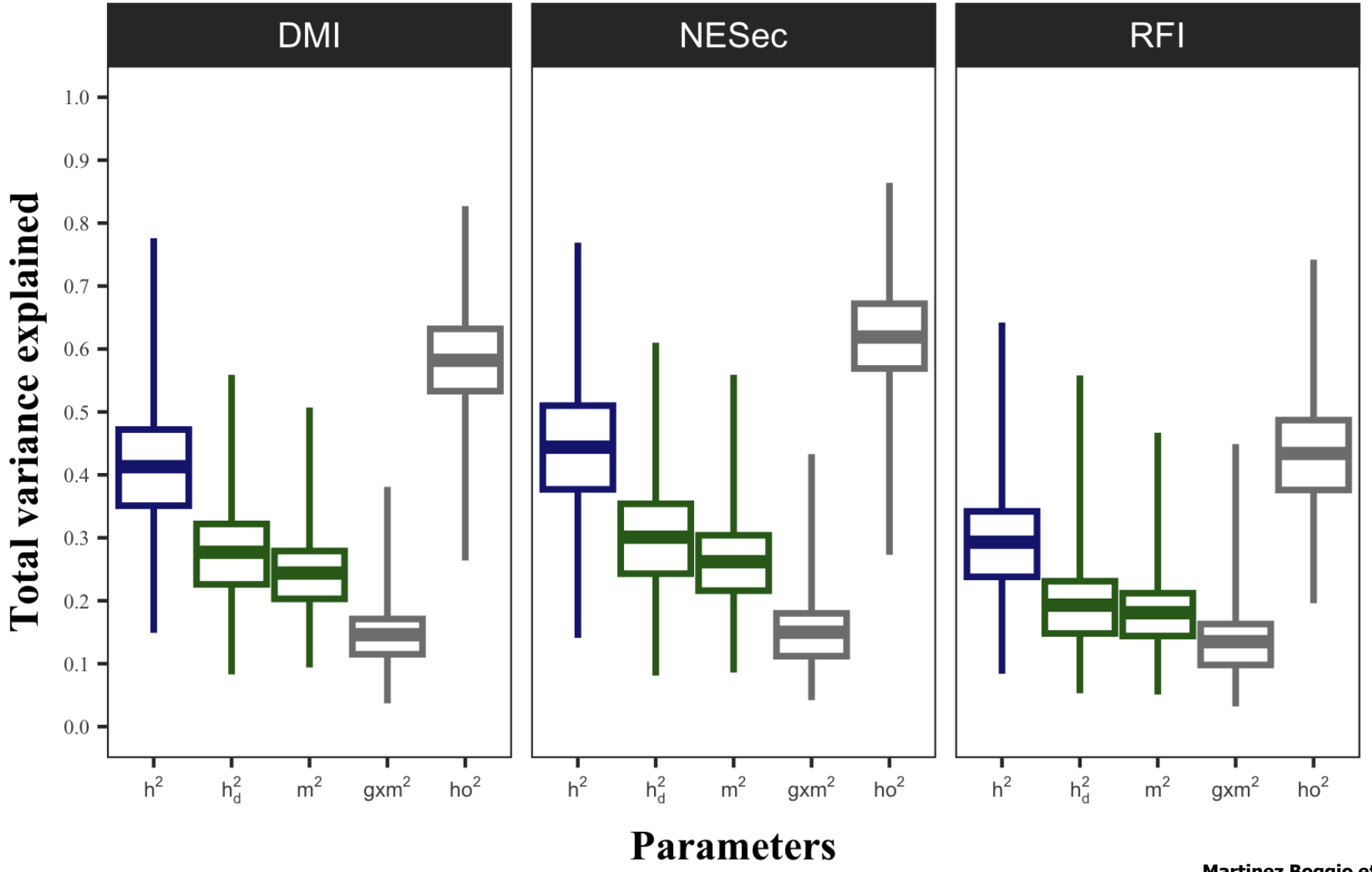


our goal:

- reveal how the microbiome composition/activity affects CH_4 formation
- assess the relative contribution of host and microbes to CH_4 formation

Rumen microbiome

Rumen microbiome mediates part of the cow genetic effects

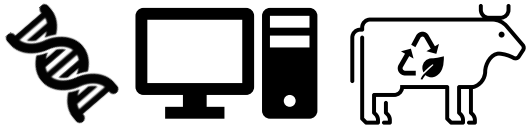


Martinez Boggio et al. (2023) JDS (under review)

Outcomes/Solutions

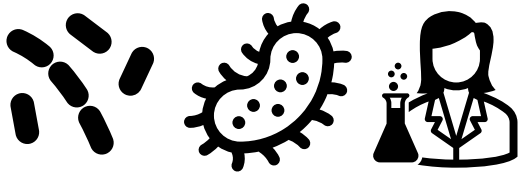
routine genomic evaluations for CH_4 emission traits in U.S. dairy cattle

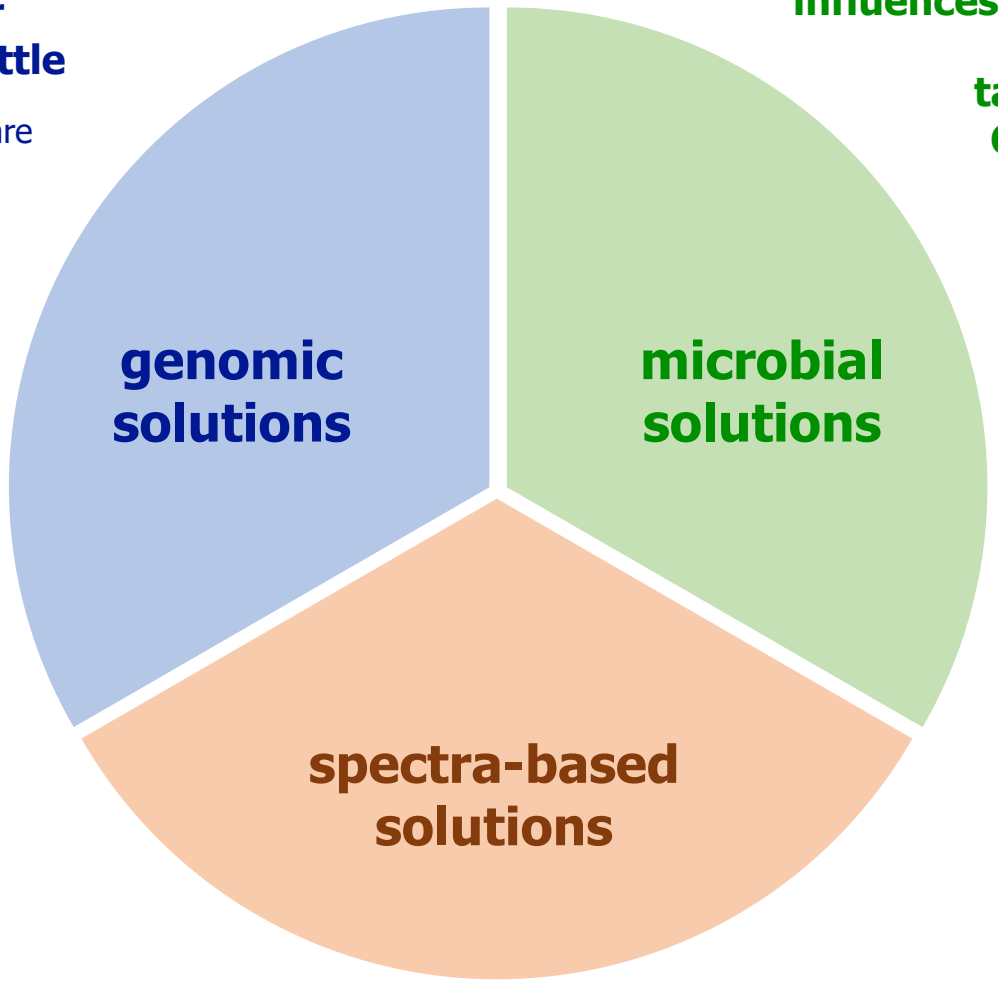
changes achieved through genetic selection are incremental, cumulative and permanent
(very cost-effective strategy)



deeper understanding of how the host influences diversity/activity of methanogens

targeted strategies to reduce CH_4 formation in the rumen





reveal if milk spectra is a good predictor of CH_4 emissions

milk spectra could be used to increase the accuracy of genomic evaluations of CH_4 traits

milk spectra could be used to optimize cow management in the dairy farm
(assign high methane-emitting cows to specific diets)

Acknowledgments

GREENER CATTLE INITIATIVE

CDCB
COUNCIL ON DAIRY CATTLE BREEDING

Francisco Peñagaricano, quantitative genomics
Hilario C Mantovani, rumen microbiology
Heather M White, nutritional physiology
Kent A Weigel, breeding & genetics

MICHIGAN STATE

Michael J VandeHaar, sustainable food systems
Robert J Tempelman, statistical genetics

STATE

James E Koltes, genomics & bioinformatics
Ranga Appuhamy, nutrition/sustainable agriculture

UF
UNIVERSITY of FLORIDA

José EP Santos, nutrition, health & fertility
Kwang C Jeong, microbiology & food safety

USDA

Ransom L Baldwin, nutritional genomics
Paul M VanRaden, sustainable breeding goals
Asha Miles, genomics & microbiology
Elizabeth A French, precision feeding
Kenneth F Kalscheur, sustainable production

Thanks for your attention!

Department of
Animal & Dairy Sciences
UNIVERSITY OF WISCONSIN–MADISON

Dr. Francisco Peñagaricano

fpenagarican@wisc.edu

http://fpenagaricano-lab.org