

Weighted single-step genome-wide association studies for methane intensity in Chinese Holstein cattle

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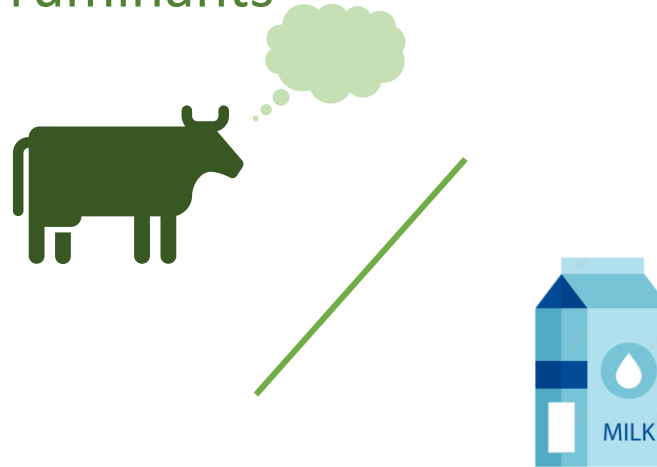
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Introduction

A non-ignorable source of greenhouse emissions in the agricultural field is methane emission from **ruminants**



Methane intensity (MeI) refers to the CH_4 per kilogram of output product (e.g. milk, g/kg). It strongly dependent on milk production and the energy requirements

Introduction

Two measurement methods used in our study are as follows:

Directly

Sniffer

convenient,
sufficient reliable

- Sniffers measure the **concentration of gas**
- Usually installed in the **feed bin** of automatic milking system (AMS)



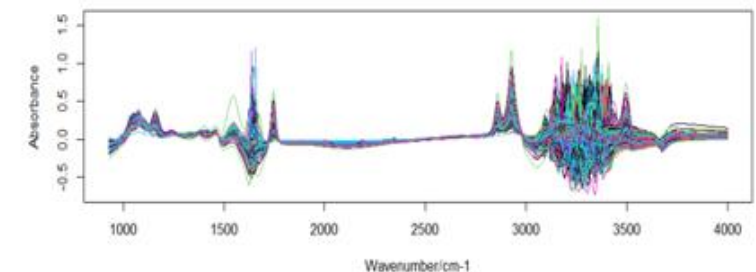
collector

Indirectly (prediction)

Mid-infrared spectra (MIRS)

Simple to collect,
high through-put

- Widely reported to **have potential for predicting methane emission traits**

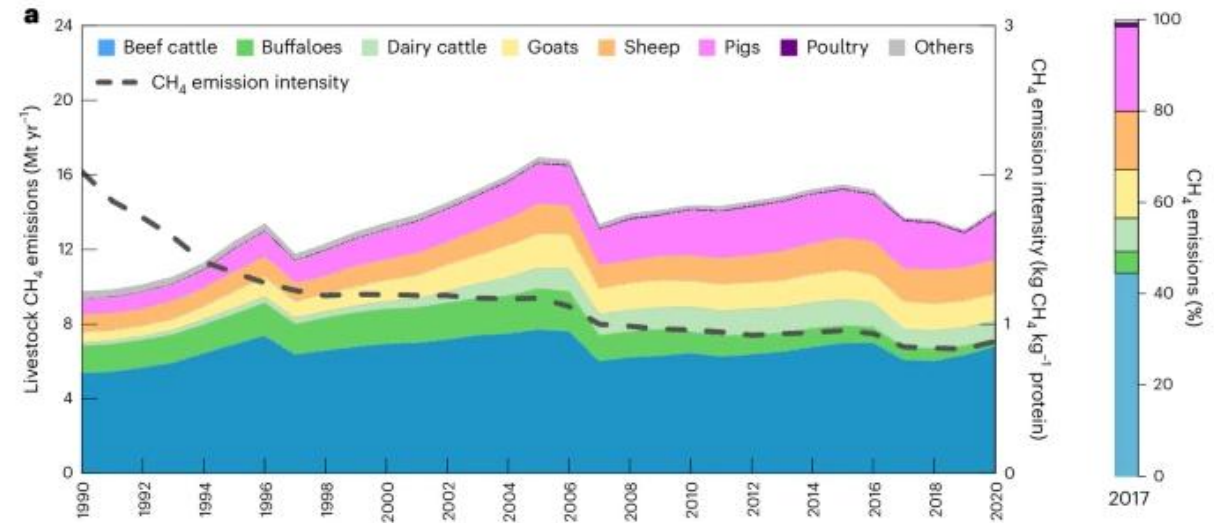


Introduction

In China, Livestock production accounts for 24% of CH₄ emissions

Over the past 30 years, CH₄ emissions from China's livestock sector ranged from 9.7 ± 2.2 Mt to 16.9 ± 2.3 Mt

Among all the animals, contribution of dairy cattle's emission increased from 1.9% to 7%



Yue Wang et al., 2024; MEE, 2018

AIM!

Methane emission



Breeding

Genetic background

Objectives

- ① To measure **sniffer-based** methane intensity and predict methane intensity based on **MIRS** in Chinese Holstein population
- ② To estimate genetic parameters for methane intensity
- ③ To identify candidate genomic regions for methane intensity

Materials & Methods

Gas Collection

Monitoring the gas concentration when milking cows



Sniffer measure gas concentration in real time



Pump the gas to sniffer

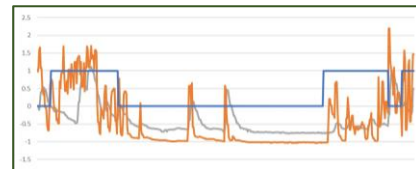


current signal

Record (per 2-4 seconds)



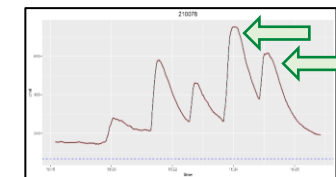
Match:



— CH4 — CO2 — AMS

Find and calibrate environmental gas concentration

Data edit :

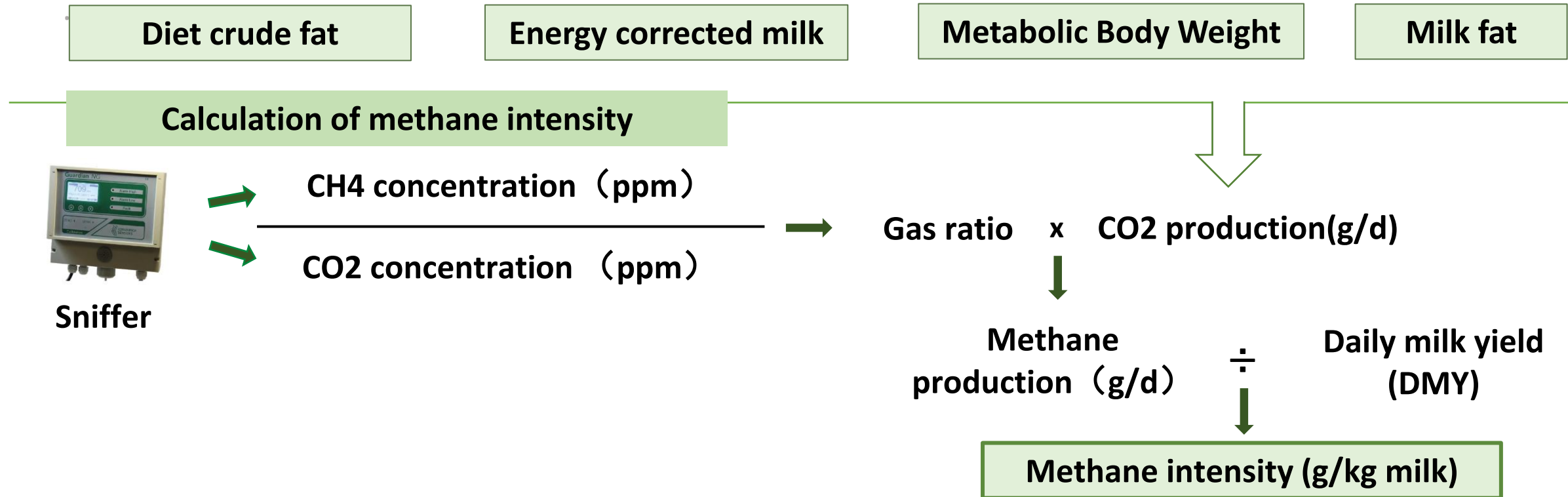


Quality control : Elimination of measurement days on which the machine may broken

Data covered 138 days, 20 weeks, 6 220 tests, 208 cows from 2 farms with 5 sniffers

Materials & Methods

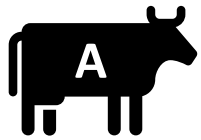
CO₂ production (g/d) was estimated based on the “On-farm model” developed by Kjeldsen et al. 2023. The following information were used:



Weekly average methane intensity was used as phenotype in this study
Finally, **758 weekly averages** were retained for subsequent analyses

Establish prediction model

Dataset



120 cows

227 MIRS records

Have both

methane records

&

MIRS + Individual

information

(Parity+ DIM+ DMY)

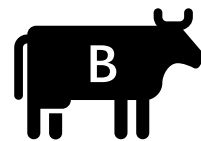
Partial least
squares regression



Phenotype prediction

Prediction formula

Dataset



21 772

MIRS records

Quality control

- 1) DIM, daily milk yield, milk protein and fat
- 2) Excluding samples with Mahalanobis distance outside of **dataset A**
- 3) A cow must have more than 3 records per year



WssGWAS

Predicted methane
intensity (PMel)



Cows with coefficient of variation (in one parity) higher than **25%** were deleted



Genetic analysis

4 995 data from 1 187 cattle (1 120 had genotype information)

$$y = X_1\beta + X_2\phi + Z\alpha + Wpe + e$$

$\alpha \sim N(0, H\sigma_a^2)$

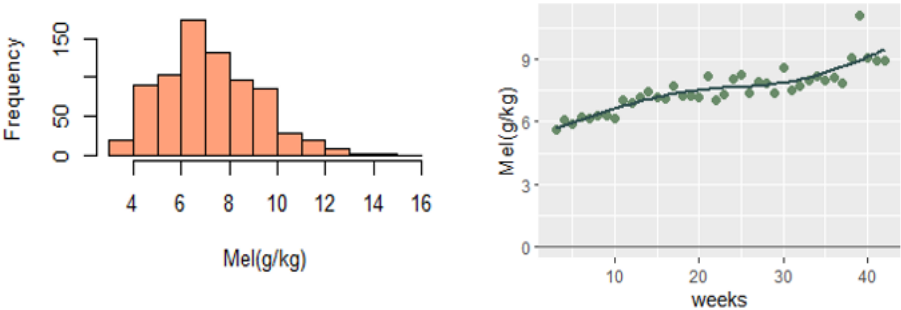


WssGWAS

(10 SNPs window, five iterations)

Results: ① Phenotypes

Trait	Mean	SD	Max	Min
Mel (g/kg)	7.22	1.99	15.04	3.11

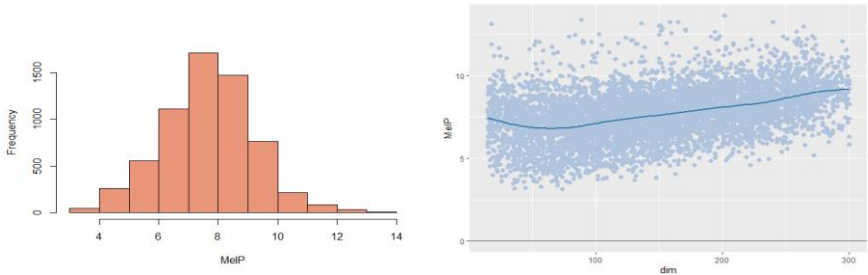


The evaluation for prediction formula via 10-fold cross-validation

Trait	R2	RMSE
Mel	0.66	1.25

Acceptable precise for discriminating high and low group

Trait	Mean	SD	Max	Min
PMel (g/kg)	7.67	1.52	13.62	3.14



Results: ② Genetic parameters of predicted methane intensity



trait	h^2	repeatability	σ_a	σ_{pe}	σ_e
PMel (g/kg)	0.15 ± 0.04	0.42 ± 0.02	0.19 ± 0.05	0.33 ± 0.04	0.71 ± 0.02

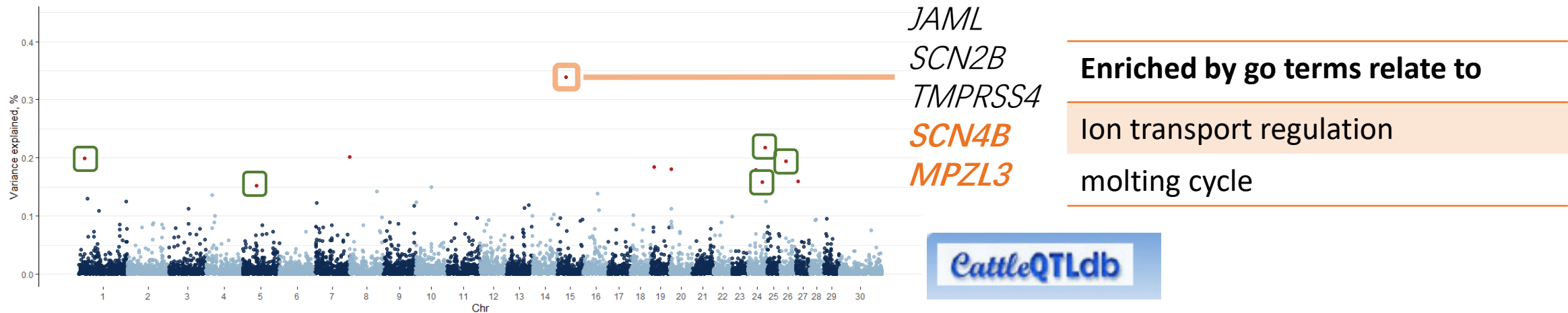
PMel has moderate heritability

PMel has moderate repeatability



Results: ③ WssGWAS

Eleven 10-SNP regions explaining more than 0.15% of the genetic variance were identified on BTA1, 5, 8, 15, 19, 20, 24, 26, and 27, which contained 19 protein-coding genes. These regions explained 2.17% of the genomic variation



Chromosome	Region	Genetic variance explained, %	Trait associated
1	20.03-20.29	0.20	MP
5	44.96-45.20	0.15	MF, MY
24	47.10-47.32	0.16	MF
24	56.77-56.93	0.22	MP, BW
26	19.74-20.23	0.19	MF, MP

MP: milk protein, MF: milk fat, MY: milk yield, BW: body weight



- ① It is feasible to use sniffers and MIRS to measure and predict large-scale methane intensity traits, but strict data processing is required
- ② Methane intensity has moderate heritability in Chinese Holstein populations

However, these results are **very preliminary** and require further exploration

We will expand the research population and use **transcriptomics** for gene validation

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Thanks for your attention!

Q&A

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