Genetic correlations between daily dry matter intake, body weight and enteric methane in Norwegian Red dairy cows

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Background

o Geno has equipment for phenotyping individual feed intake,

   methane & body weight

o Commercial dairy herds (**14**) + 1 research herd

o Farms with AMS

o Norwegian Red dairy cows

o All cows are genotyped (~ **1.000** / year)

Project aim

Select for improved feed efficiency and reduced enteric methane emissions in NR cows

Sub aim

Estimate heritabilities and genetic correlations between daily dry matter intake, methane production and body weight of Norwegian Red cows
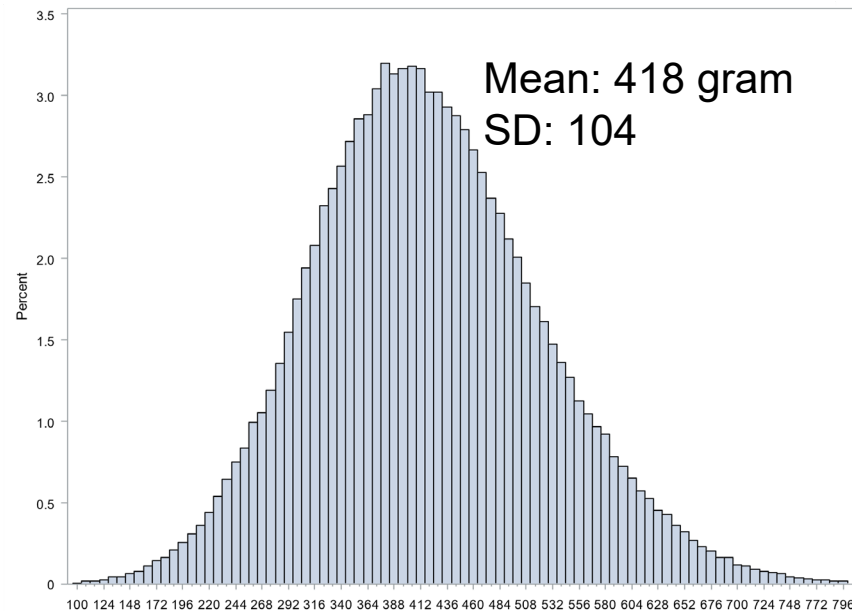
Data

o CH4 from 25 commercial herds

o Feed intake and body weight from 8 of these herds

o Data on 2 074 cows

o Data from 2020 to 2024
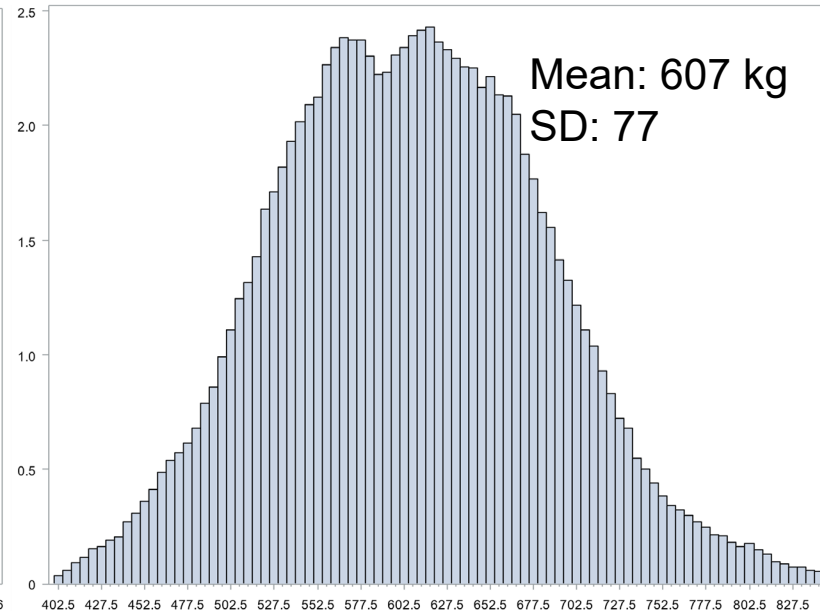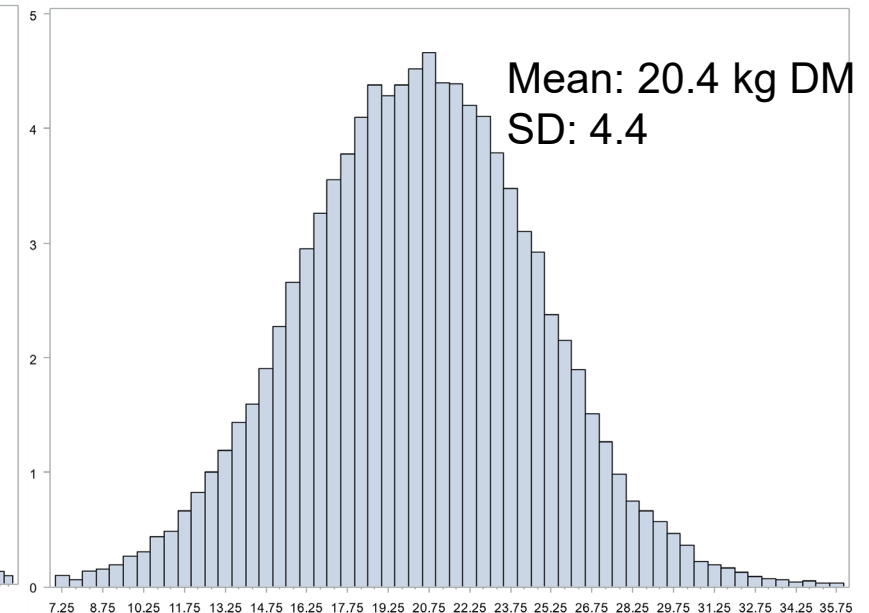
o A total of 452 055 daily observations

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Phenotypic distributions

CH4

Mean: 418 gram
SD: 104

Body Weight

Mean: 607 kg
SD: 77

Dry matter intake

Mean: 20.4 kg DM
SD: 4.4

Models

Linear animal repeatability models (bivariate)

Y = Herd + Week + Pa_CaAge + htd + a + pe + e

Traits (Y)

CH4: avg daily methane (gram)

BW: avg daily body weight (kg)

dDMI: sum daily dry matter intake (kg)

Models

Linear animal repeatability models (bivariate)

$$Y = Herd + Week + Pa\_CaAge + htd + a + pe + e$$

> **Herd**
> **Week:** *lactation stage as weeks in milk*
> **Pa_CaAge:** *calving age for first parity, or parity (>1)*

FIXED EFFECTS

Traits (**Y**)

CH4: avg daily methane (gram)

BW: avg daily body weight (kg)

dDMI: sum daily dry matter intake (kg)

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Models

Linear animal repeatability models (bivariate)

Y = Herd + Week + Pa_CaAge + htd + a + pe + e

htd: testday within herd
a: animal genetic
pe: permanent environment animal
e: residual

RANDOM EFFECTS

Traits (**Y**)

CH4: avg daily methane (gram)

BW: avg daily body weight (kg)

dDMI: sum daily dry matter intake (kg)

Results

- **dDMI:** sum daily dry matter intake (kg)

- **BW:** avg daily body weight (kg)

- **CH4:** avg daily methane (gram)

Heritabilities (h^2) and genetic correlations

Trait	dDMI	BW	CH4
dDMI	**0.29** (0.05)		
BW	0.59 (0.11)	**0.57** (0.05)	
CH4	0.65 (0.10)	0.50 (0.09)	**0.39** (0.04)

h^2 calculated as: $(\sigma^2_a / (\sigma^2_a + \sigma^2_{htd} + \sigma^2_{pe} + \sigma^2_e))$

Conclusion

o Estimated heritabilites were relatively high (0.29 - 0.57)

o Heritability of dDMI increased when a bivariate model with CH4 was used (0.18 to 0.29)

o Logical results and expected direction of genetic correlations

o Heavier cows, increased dry matter intake and more methane

o Further research is needed to better understand effects of selecting for improved feed efficiency and methane emission

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