Genome-wide association study of nitrogen use efficiency and methane production and intensity on Swiss Holstein cows

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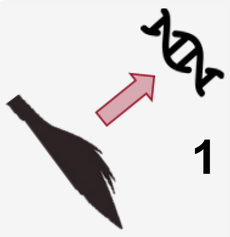
Background

Meat and dairy production is responsible for a large proportion of the annual **global nitrogen surplus**. Moreover, methane (CH_4) production and intensity from cows contributes significantly towards **greenhouse gas emissions**. Genetic selection on nitrogen use efficiency (NUE, milk N yield / N intake) and CH_4 traits offers a **permanent and cumulative solution towards reducing emissions from cattle**. The main goal of this project is to identify genomic variation linked to NUE and CH_4 with regards to diets.

Material and Methods

Feed analysis
1 × / farm and measuring period



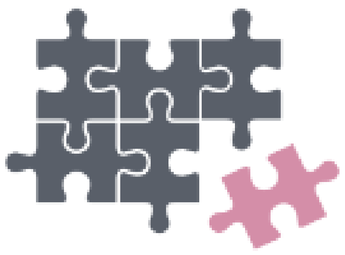
1 × / cow
Hair (for DNA)

★ ***Genotyping***

Whole-genome Sequencing
low-pass (Ø 1x coverage)

Ongoing

Imputation = "filling the gaps"
Predict missing pieces of genome with information based on surrounding DNA fragments ("loimpute" pipeline by Gencove)



VCF file with ~10 Millions of **SNPs** expected

Genotype

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##contig=<ID=2,length=51304566>
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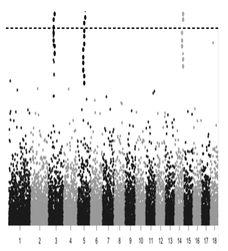
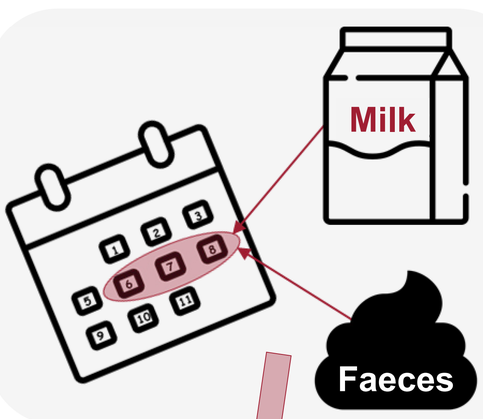
##FORMAT=<ID=DP,Number=1,Type=Integer,Description="Read Depth">
##FORMAT=<ID=GQ,Number=1,Type=Integer,Description="Genotype Quality">
#CHROM  POS ID  REF ALT QUAL FILTER  INFO FORMAT     SAMPLE1     SAMPLE2     SAMPLE3     SAMPLE4
2  81170  .  C  T   .  .    AC=9;AN=7424  GT:DP:GQ  0/0:4:12    0/0:3:9     0/1:1:3     0/1:9:24
2  81171  .  G  A   .  .    AC=6;AN=7446  GT:DP:GQ  0/1:4:12    0/0:3:9     0/0:1:3     0/0:9:24
2  81182  .  A  G   .  .    AC=5;AN=7506  GT:DP:GQ  0/0:5:15    0/0:4:12    0/0:5:15    0/0:9:24
2  81204  .  T  G   .  .    AC=2;AN=7542  GT:DP:GQ  1/0:5:15    0/0:9:27    0/0:10:30   0/0:15:39
```

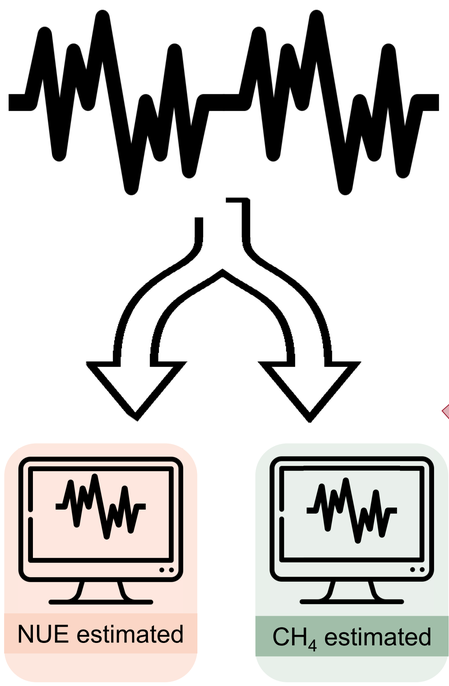


Genome wide association study



Ongoing

★ ***Infrared spectroscopy***



Phenotype

Low-pass sequencing

Benefits		Limitations	
• Low-cost	++	• Computational expenses (vs arrays)	- -
• Information (vs microarrays)	++	• Stricter Bonferroni threshold → power decrease	- -
• genomics variants	++	• Structural variant detection	- -

Status as of Mai 01, 2024

- **33 farms** in cantons Fribourg and Bern – only Posieux experimental farm equipped with feed weigh troughs
- **1,425 cows** sampled between 90 and 250 days in milk (164 ± 44 DIM)

- **Average milk yield** = 27.7 ± 6.9 L (28.7 ± 6.6 kg energy corrected milk)
- **Estimated average dry matter intake (DMI)** = 22.3 ± 3.6 kg DM (Posieux = 20.8 ± 3.3 kg DM)
- **Estimated average proportion of concentrate** = 12.2 ± 8.4 % DMI (Posieux = 6.4 ± 5.7 % DMI) *Except mixed ration*
- **Estimated average N intake** = 550 ± 109 g/kg DM (Posieux = 533 ± 121 g/kg DM)
- **Average milk urea N** (MIRS) = 10.6 ± 3.4 mg/dl

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