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Single-step genome-wide association for milk urea concentration in Walloon Holstein

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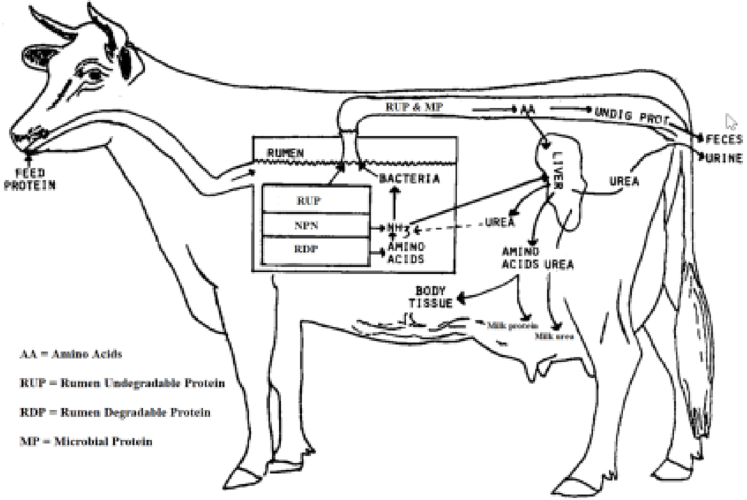
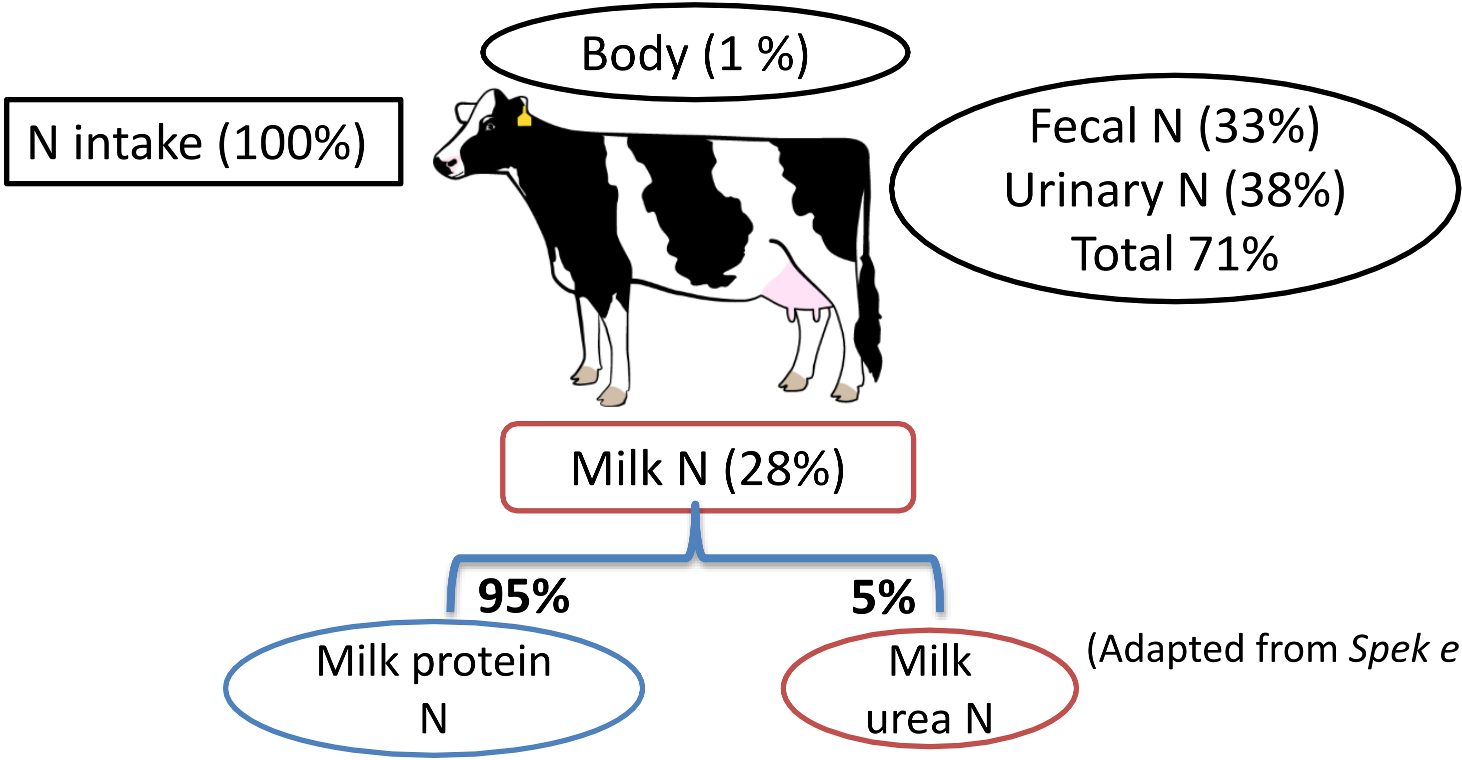
Introduction

- Degradation of RDP results in ammonia (main source of N for MP)
- When ammonia is high or the bacteria can not capture it, the ammonia is absorbed/transferred into the bloodstream



- The liver converts toxic ammonia to urea (blood urea nitrogen)
- BUN is recycled to the rumen via saliva, secreted in milk, or excreted through urine

Introduction



(Adapted from *Spek et al.*, 2013)

Introduction

- ❑ Milk urea (MU) is
  - ✓ a normal NPN component in milk, associated wit NUE
  - ✓ very easy to record ➔ standard MIR based prediction
  - ✓ included as a standard part in most milk recording systems
  - ✓ correlated with MY and composition, reproductive performance, longevity, and health in dairy cows

Introduction

- ❑ Genetic selection for MU?
  - ✓ reducing MU ➔ reducing environmental burden, improving FE and animal health, increasing milk quality and reproductive performance

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  - ✓ reducing MU → reducing environmental burden, improving FE and animal health, increasing milk quality and reproductive performance

- ❑ Genetic background of MU?
  - ✓ genetic parameters for MU and correlations with traditional traits have previously been investigated in Walloon Holstein (Chen et al., 2021, 2022)
  - ✓ genetic relationships between MU and milk technological traits (e.g., CMP)?

Objective

- Genetic correlation between MU and selected cheese-making traits in Walloon Holstein cows

- Identify genomic regions associated with MU concentration

Data

- ❑ Data collected during 2014 to 2020 on 78,073 first-parity and 48,766 second-parity Holstein cows distributed in 671 herds in the Walloon Region of Belgium
- ✓ MY and composition (MIR predicted of calcium content, FP, PP, and casein percentages)
- ✓ cheese-making properties (MIR predicted of coagulation time, curd firmness after 30 min from rennet addition, and titratable acidity)

Data

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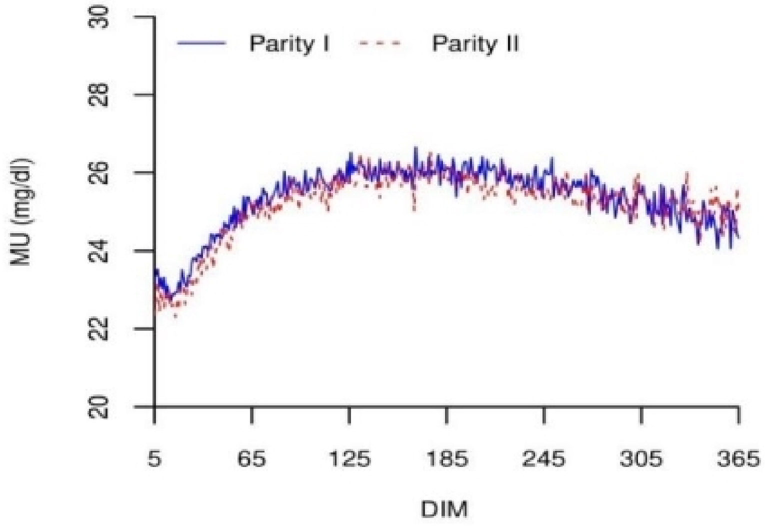
- ❑ Data of 565,533 SNP located on 29 BTA of 6,617 animals (1,712 males)

Statistical Analyses

- ❑ MT multiple-lactation RR-TDM model (BLUPF90)

  - ✓ The proportion of the total additive genetic variance explained by windows of 50 consecutive SNPs (average size of ~ 216 Kb)
  - ✓ Top-three genomic regions explaining the largest rate of the genetic variance were identified

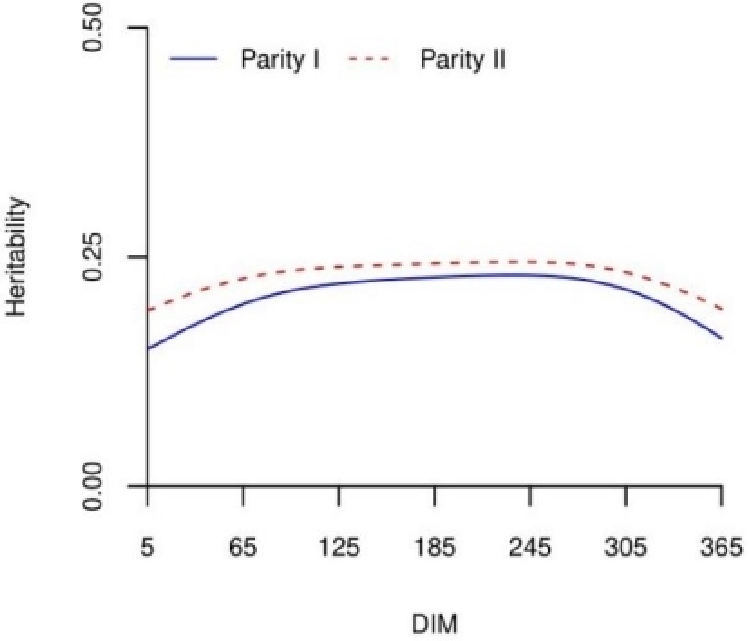
Result



- Mean (SD) MU was 25.38 (8.02) mg/dl and 25.03 (8,06) mg/dl in the first and second lactation, respectively

- In the normal range (15 - 30 mg/dL, Glatz-Hoppe et al., 2020)

Result



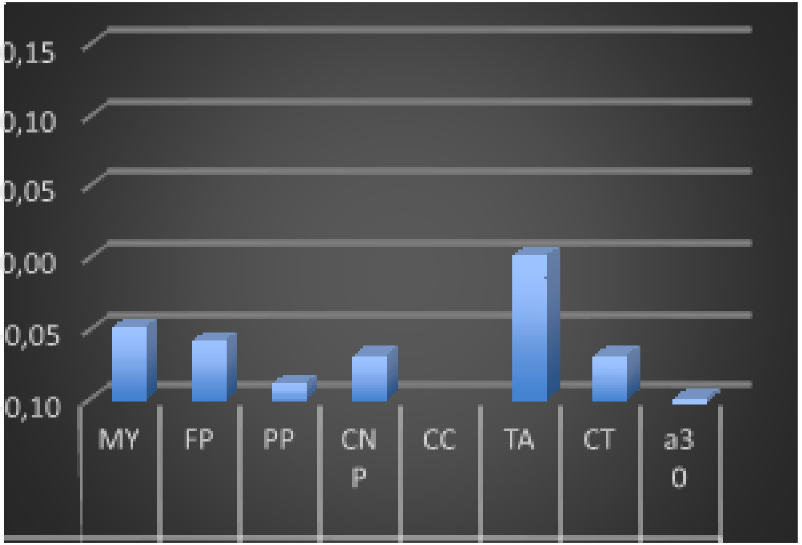
- ❑ Mean heritability estimates for daily MU were 0.21 and 0.23 for the first and second lactation, respectively.

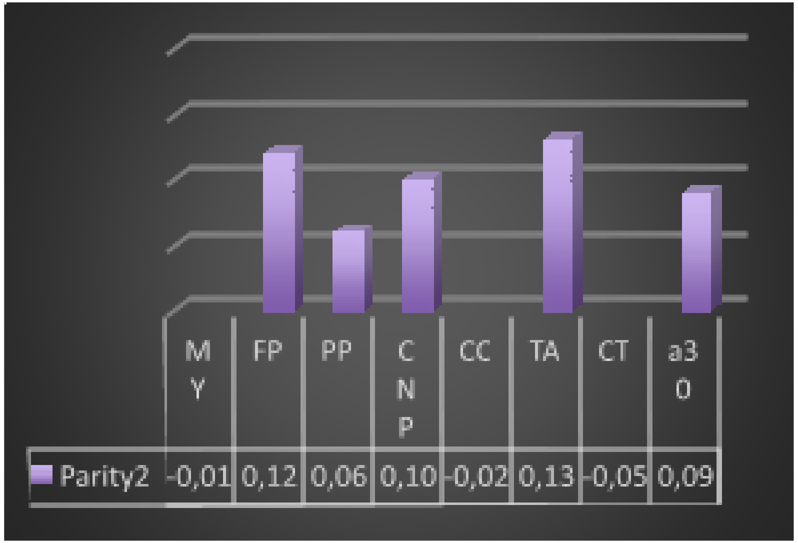
Literature:

- ✓ 0.44 to 0.59 in Canadian Holstein (Wood et al., 2003)
- ✓ 0.17 in Italian Brown Swiss (Samore et al., 2007)
- ✓ 0.22 in Polish Holstein (Rzewuska and Strabel 2013)

Result

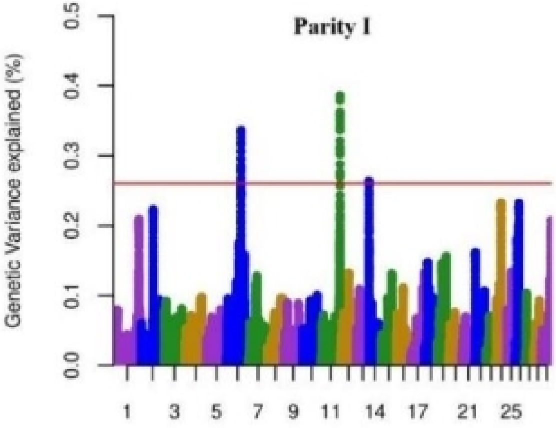
- r_g (MU_1 , MU_2) > 0.95
- r_g between MU and MY, milk composition, and CMP were quite low

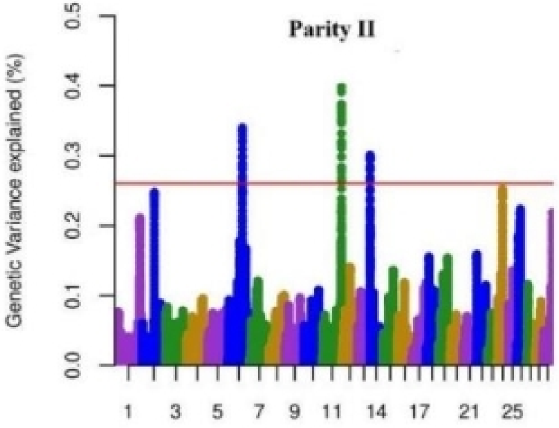




	MY	FP	PP	CNP	CC	TA	CT	a30
🟪 Parity2	-0,01	0,12	0,06	0,10	-0,02	0,13	-0,05	0,09

Result





positional candidate genes for MU: *KCNT1, MROH1, SHARPIN, TSSK5, CPSF1, HSF1, TONSL, DGAT1, SCX, and MAF1*

- ❑ The top-three regions associated with MU were located from:
- ✓ 80.61 to 80.74 Mb on BTA6
- ✓ 103.26 to 103.41 Mb on BTA11,
- ✓ 1.59 to 2.15 Mb on BTA14

Literature:
Conte et al., 2010
Buitenhuis et al., 2016
Pedrosa et al., 2021

Conclusion

- Moderate heritability found for MU
- Weak genetic correlations found with milk yield, milk composition, and cheese-making traits

➔ selection on MU is possible with limited effects on lactation performance

Conclusion

- Moderate heritability found for MU
- Weak genetic correlations found with milk yield, milk composition, and cheese-making traits

→ selection on MU is possible with limited effects on lactation performance

- In general, windows, spread across the genome, explained less than 0.50% of the total additive genetic variance of MU

→ MU is highly polygenic, many regions across the genome contribute

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Thank you for your attention

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