Genetic parameters for the composition of milk fatty acid of Holsteins

Yutaka Masuda

Rakuno Gakuen University, Hokkaido, Japan

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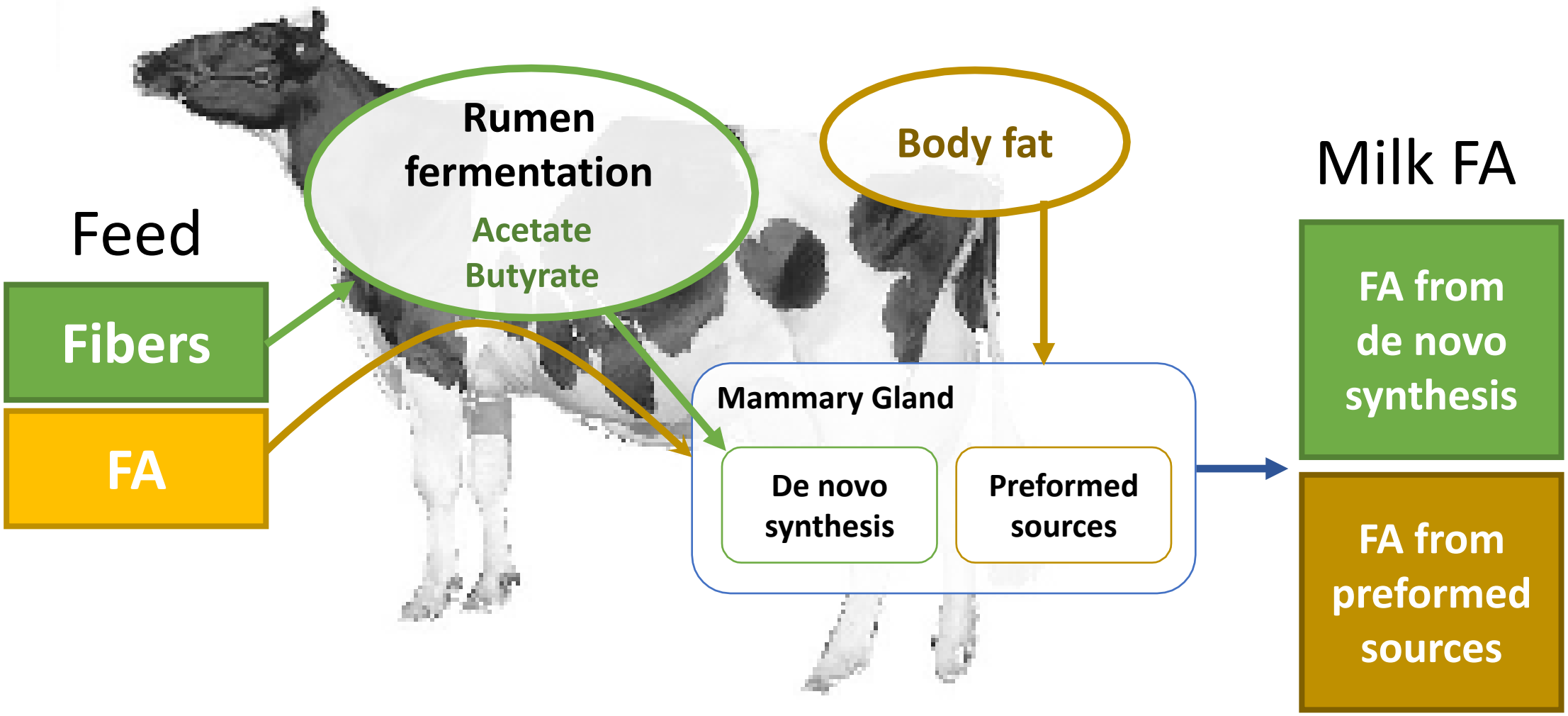
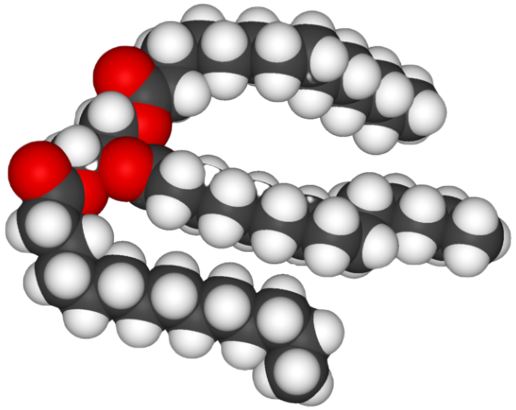
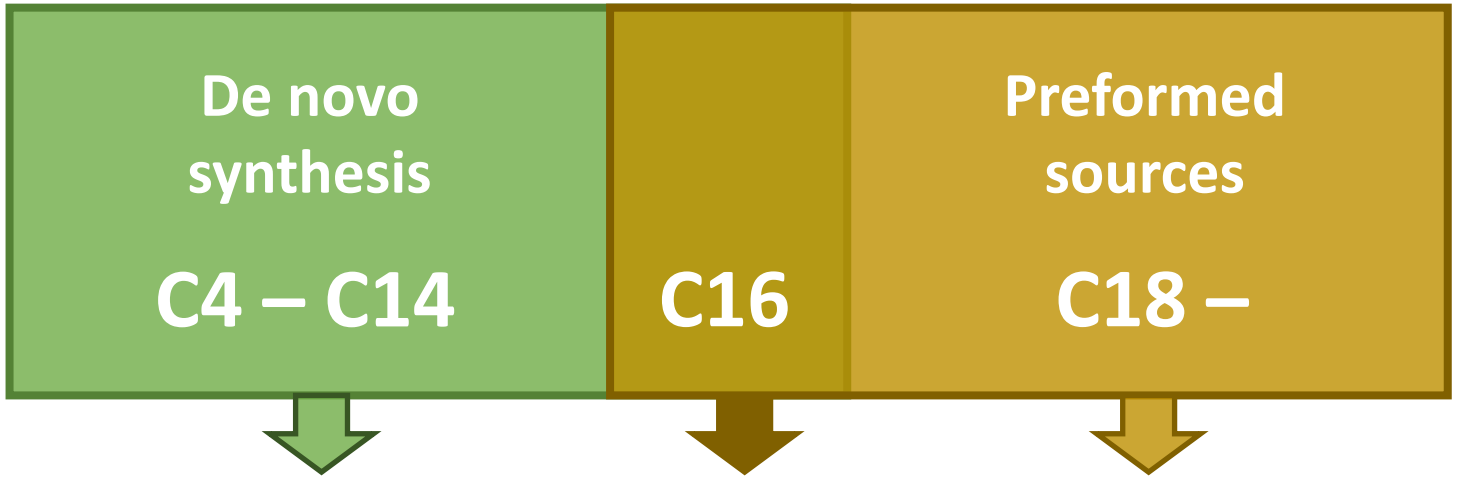
Source of milk fatty acid (FA)



Milk fat and rumen health



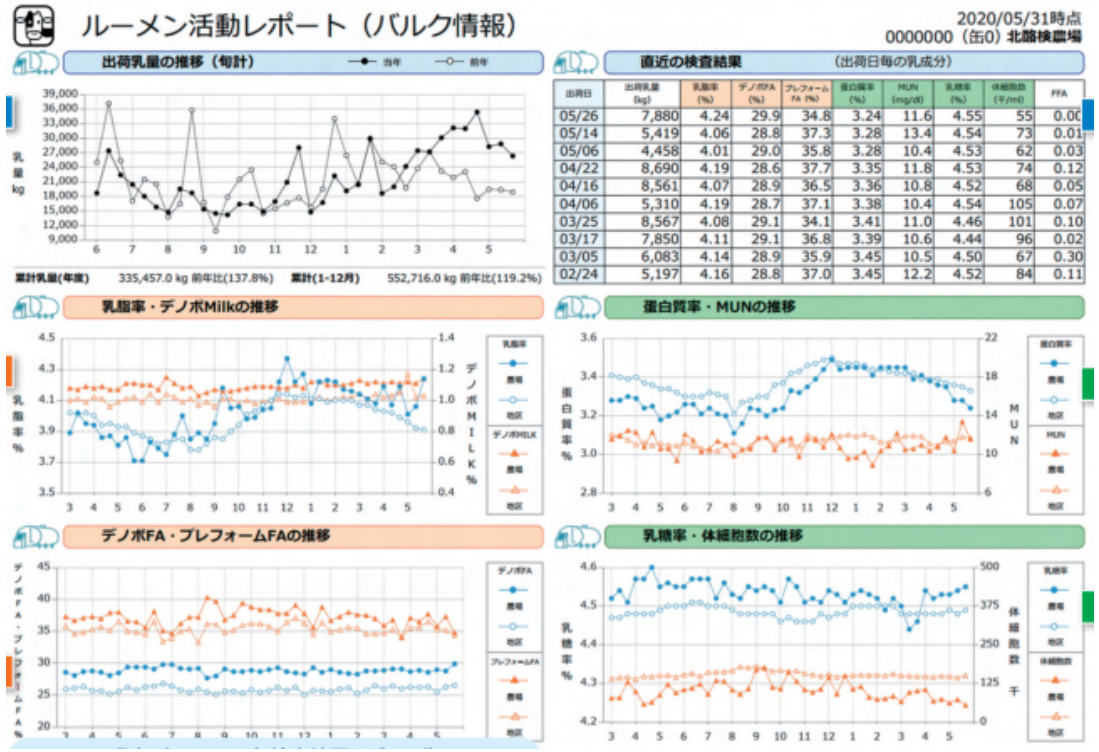
Triglyceride
= Glycerol + 3 FA chains



Useful tool to monitor rumen health

Milk FA records in Japan

- Milk FA content collected in the DHI program since 2021
  - Using FT-IR
  - De novo FA, Mixed FA, and Preformed FA
- For monitoring purpose
  - Individual measurements
  - Herd average
- No genetic analysis yet



Objectives

- For test-day de novo FA & preformed FA content for Holsteins in Japan
  - To estimate genetic parameters.
  - To determine covariance structures.
- FA content predicted by FT-IR

MilkoScan FT1 (FOSS)

Data

- Test-day records
  - Holstein cows in Hokkaido (collected by Hokkaido Milk Test & Recording Association)
  - From April 2021 to October 2022
  - DIM from 6 to 365
  - First lactation cows
- Pedigree information
  - Collected by Holstein Cattle Association Japan

	First Lactation
No. of herds	1,651
No. of cows	211,462
No. of test-day records	1,448,373
No. of pedigree animals	402,418

Test-day milk FA profiles

DnM(%): Test-day de novo FA % of milk yield

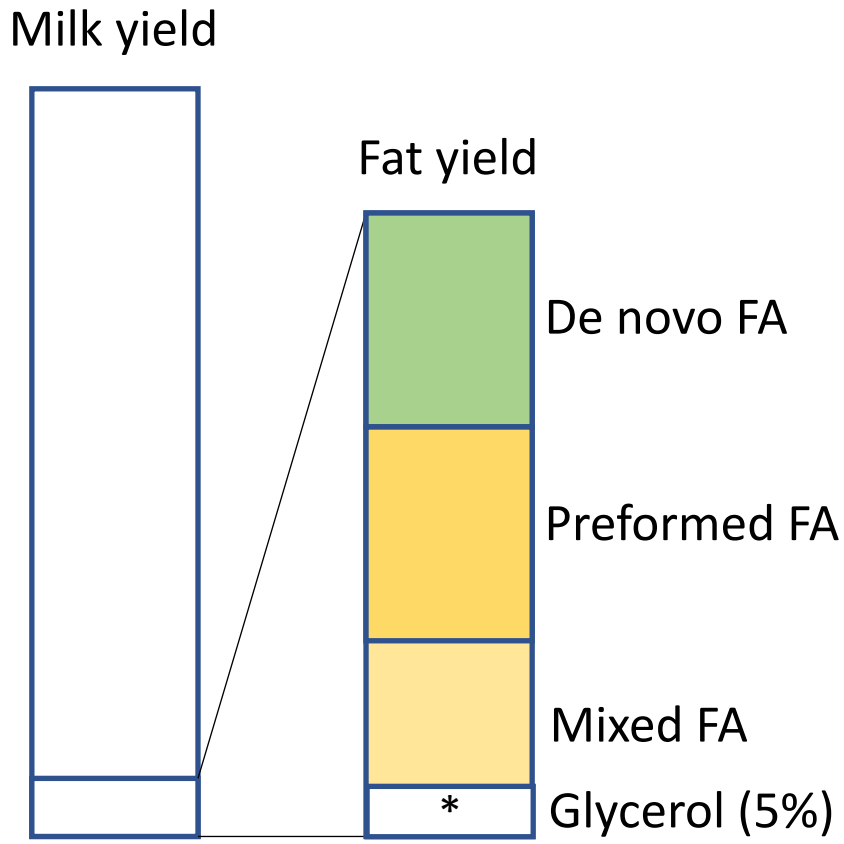
$$\mathrm{DnM}(\%) = \frac{\text{De novo FA yield}}{\text{Milk yield}} \times 100$$

DnF(%): Test-day de novo FA % of FA yield

$$\mathrm{DnF}(\%) = \frac{\text{De novo FA yield}}{\text{Fat yield} \times 0.95^{*}} \times 100$$

PrF(%): Test-day preformed FA % of FA yield

$$\mathrm{PrF}(\%) = \frac{\text{Preformed FA yield}}{\text{Fat yield} \times 0.95^{*}} \times 100$$



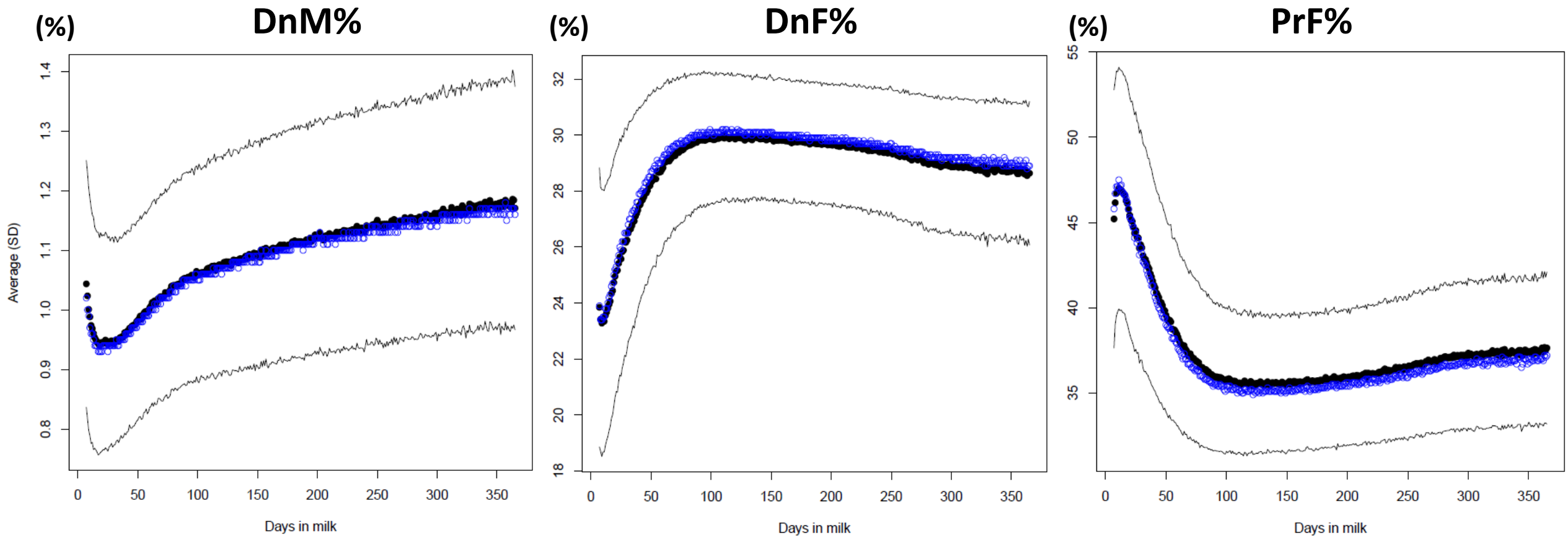
* Assuming 5% for glycerol in the total milk fat yield (triglyceride)

Analysis by lactation stage

- Data division by lactation stage (30-day interval)
  - Stage 1: DIM 6 – 35
  - Stage 2: DIM 36 – 65
  - …
  - Stage 12: DIM 336 – 365

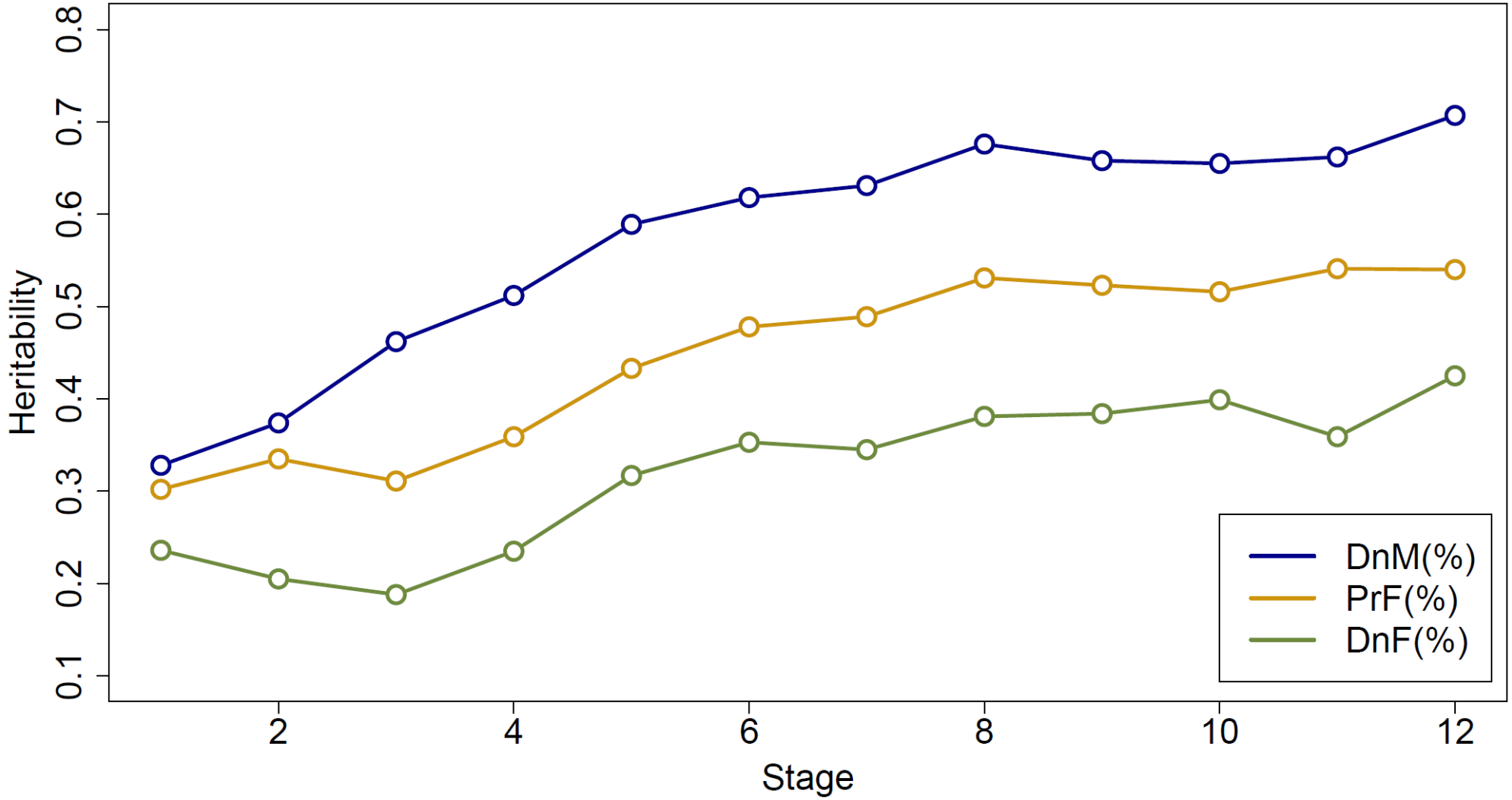
- **Model in each stage**
  - **Fixed**: Herd-year, Year-month of calving (intercept + reg. on DIM), Age of calving (intercept + reg. on DIM)
  - **Random**: Additive genetic + Residual effects
- **AI REML analyses**
  - Heritability (single-trait model)
  - Genetic/phenotypic correlations among stages (repeated bivariate analyses)

Average/median of milk FA at each DIM



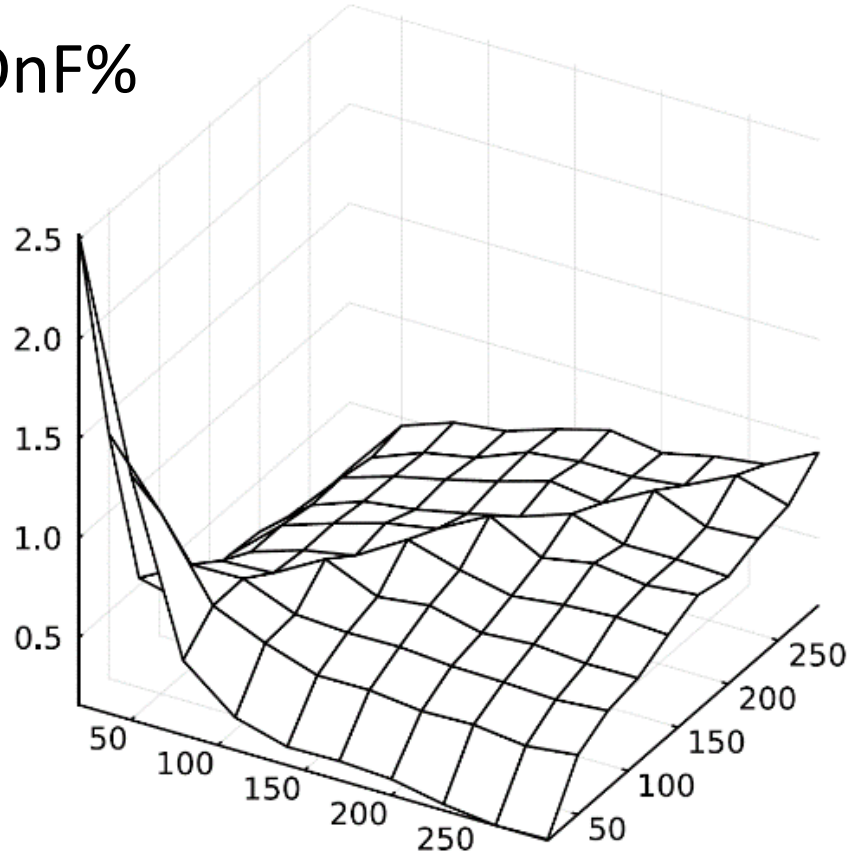
●: Average; ●: Median; —: Average±SD

Heritability

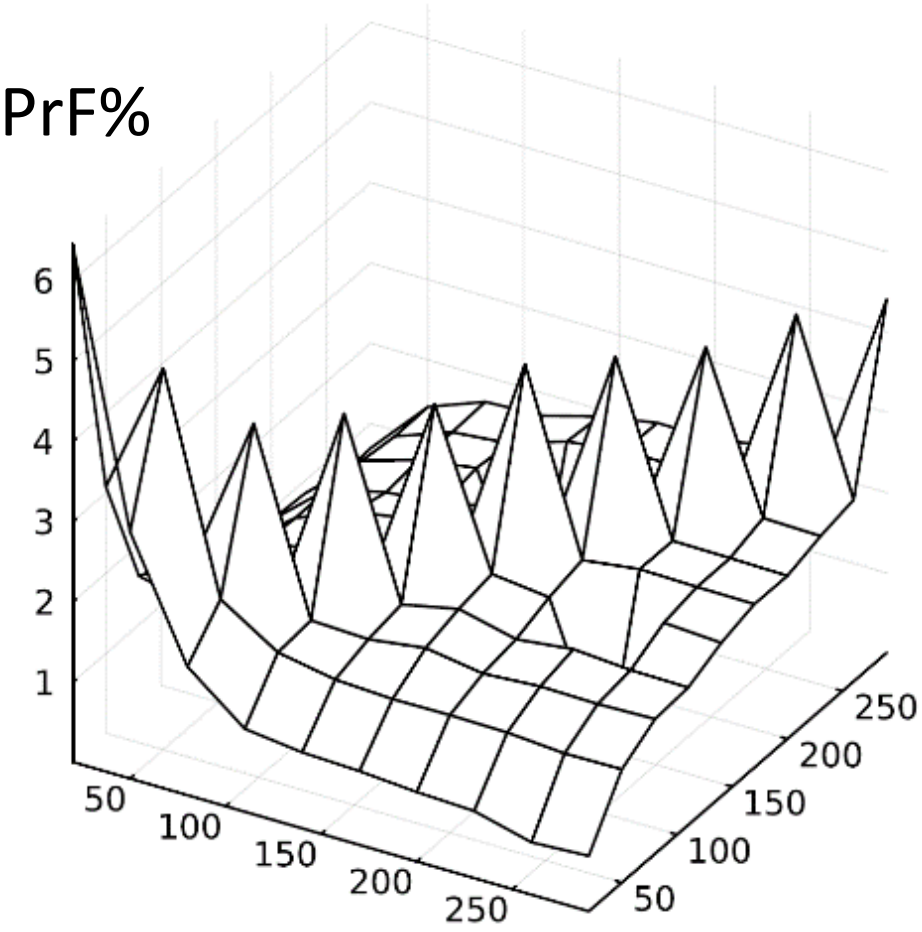


Genetic covariance structure

DnF%

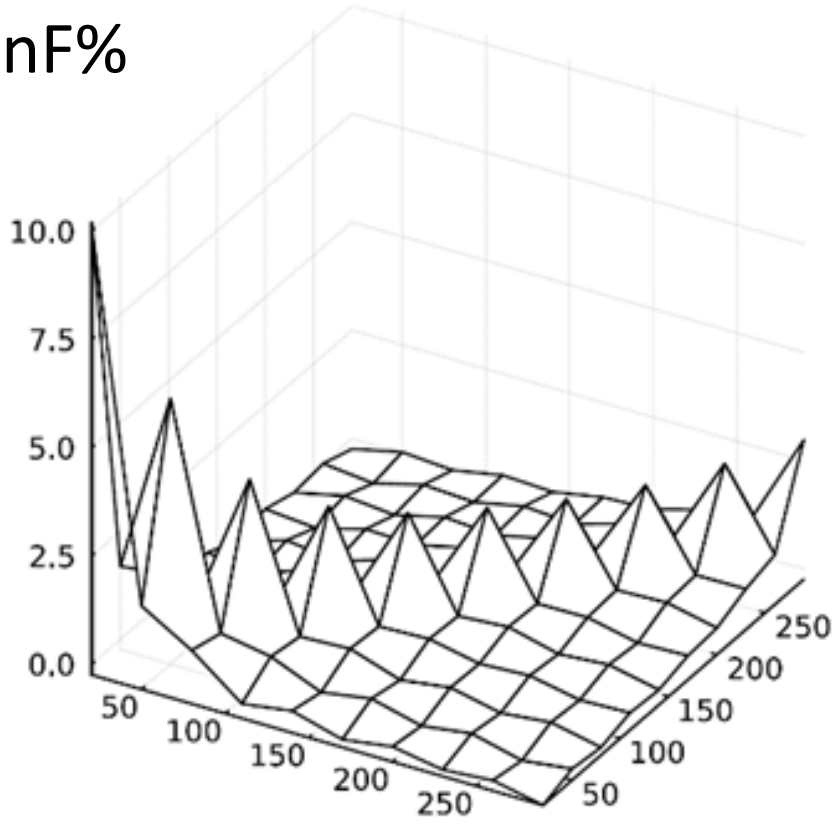


PrF%

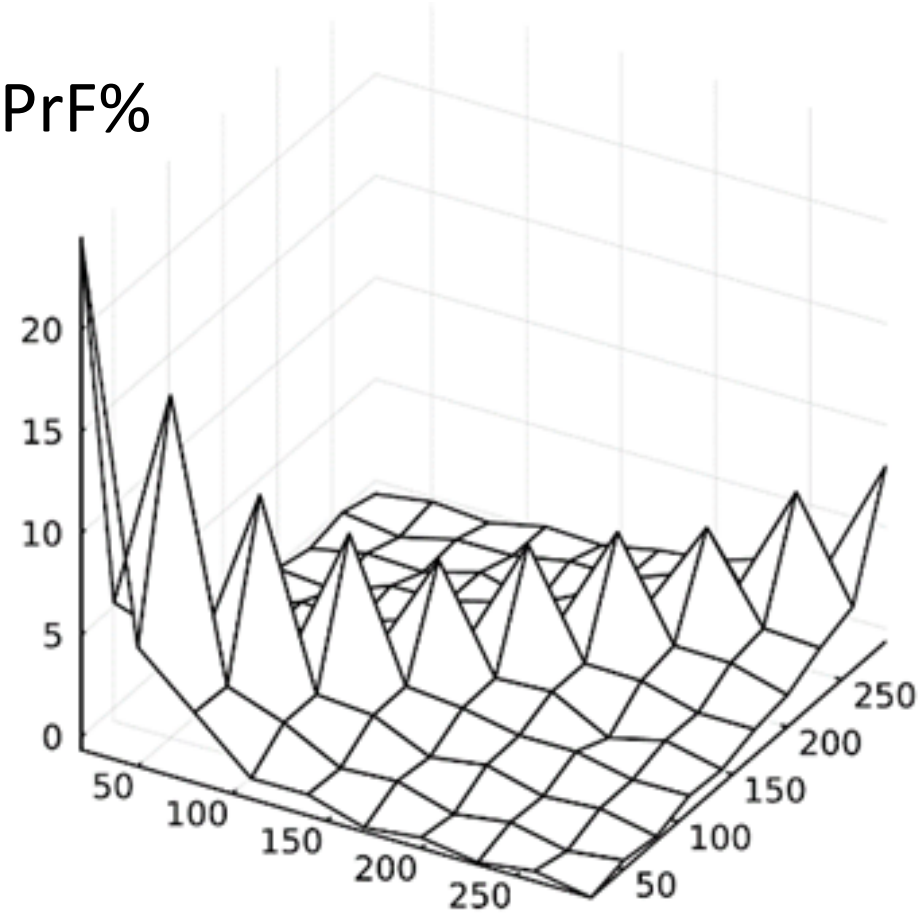


Residual covariance structure

DnF%



PrF%



Genetic parameters: DnF(%) and PrF(%)

DnF (%)	ST 1 6-35	ST 2 36-65	ST 3 66-95	ST 4 96-125	ST 5 126-155
ST1	0.24	0.84	0.46	0.27	0.21
ST2	0.22	0.21	0.89	0.73	0.63
ST3	0.16	0.17	0.19	0.98	0.94
ST4	0.02	0.15	0.15	0.23	0.99
ST5	0.05	0.03	0.18	0.18	0.32

PrF (%)	ST 1 6 - 35	ST 2 36 - 65	ST 3 66 - 95	ST 4 96 - 125	ST 5 126 - 155
ST1	0.30	0.86	0.58	0.39	0.34
ST2	0.27	0.34	0.92	0.79	0.70
ST3	0.17	0.21	0.31	0.97	0.94
ST4	0.03	0.15	0.18	0.36	0.99
ST5	0.03	0.03	0.17	0.20	0.43

Diagonal: heritability; **Upper**: genetic correlation; **Lower**: phenotypic correlation

Summary

- Heritability
  - Moderate to high (0.2 – 0.7)
  - DnF(%)&PrF(%): Stable up to stg 4
  - Increasing up to stage 8
- Genetic correlations
  - Stage 1 & 2: low with later lactations
  - Possible different background before DIM 65
- Covariance structure
  - High peak at the beginning of lactation
  - Legendre polynomials not suitable to account the structure
    = Spline functions
    Or, early stages as separate traits
- Future study
  - Random regression model
  - Correlations with other traits
  - Genomic prediction

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