

Genotype by management-system interaction on origin group of milk fatty acids for Holsteins

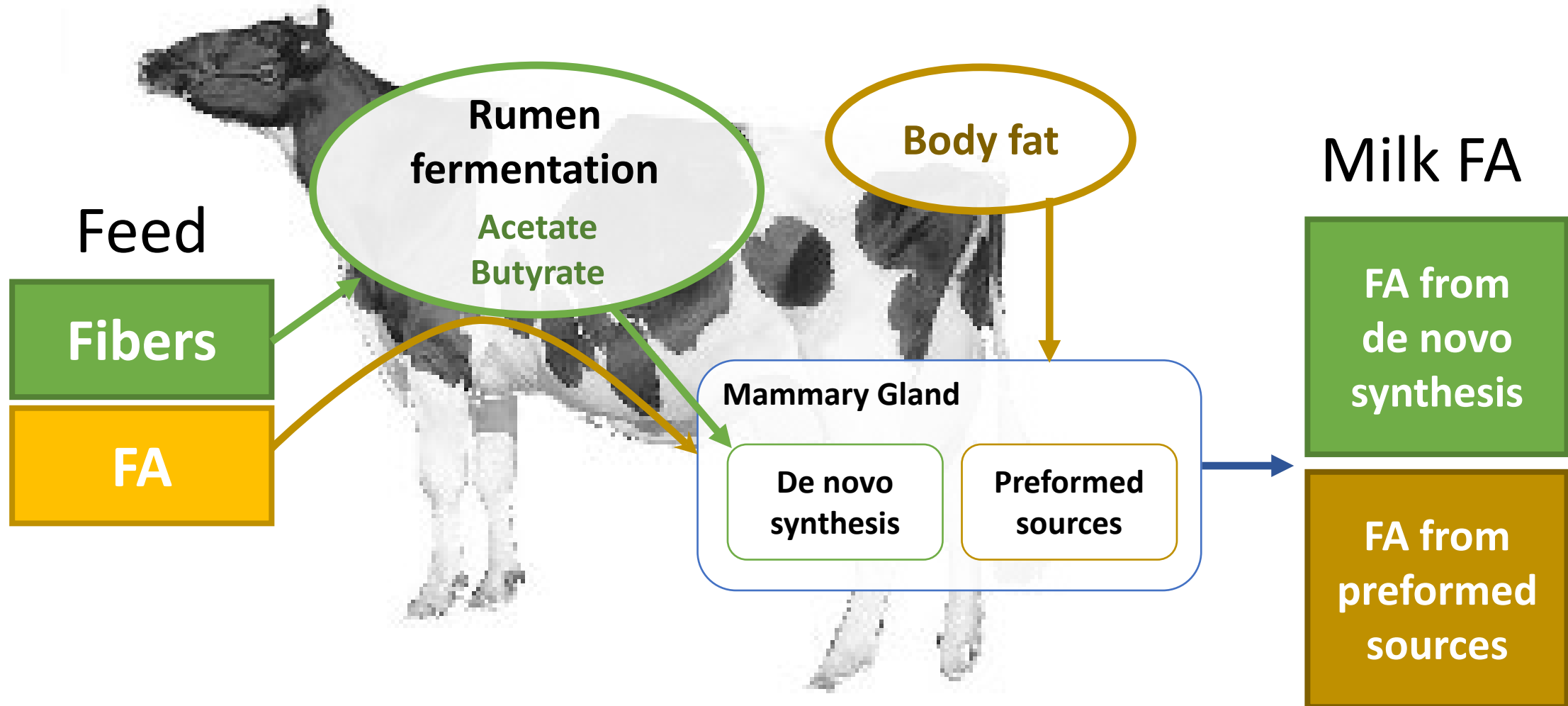
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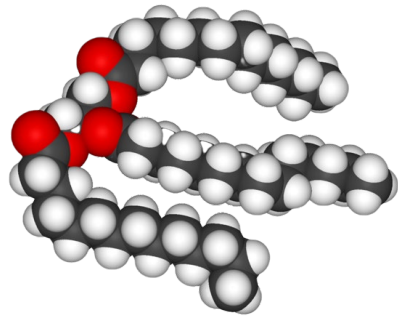
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Source of milk fatty acid (FA)



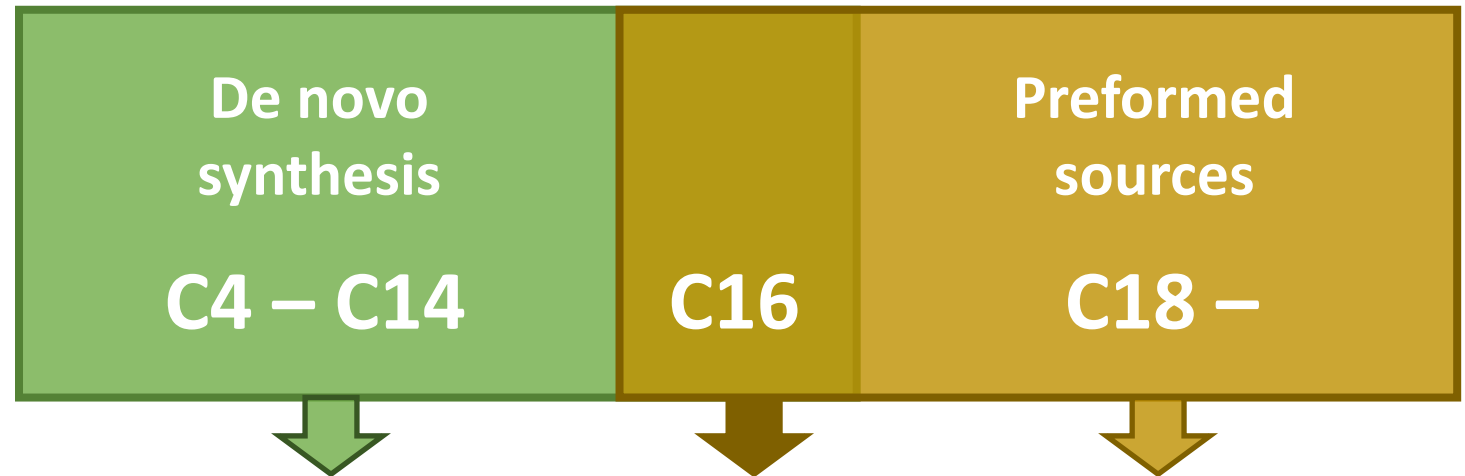
Milk fat and rumen health



Triglyceride
= Glycerol + 3 FA chains



MilkoScan FT1 (FOSS)
FA content predicted by FT-IR



De novo FA

Feed + Rumen
fermentation

Mixed FA

Preformed FA

Feed + Body
reserves

**Useful tool to monitor cow/rumen health
= indicator of negative energy balance**



Variety of management systems



Tie Stall-based
(Up to 60%)
Avg. > 8000kg



Free Stall-based
(Up to 30%)
Avg. > 9000kg



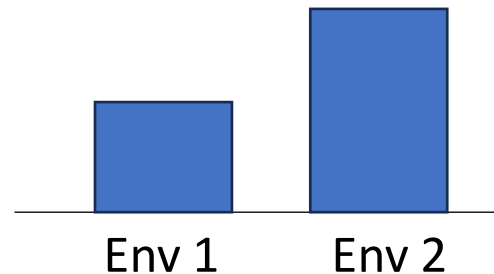
Pasture-based
(Up to 10%)
Avg. < 8000kg

**Different nutrition management
= Possible difference in milk FA by management (“environment”)**

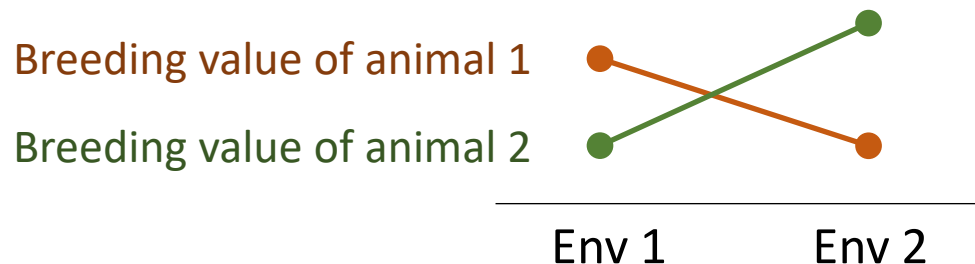
Motivation of this study

Models regarding management (environmental) effect on milk FA

Difference in average
[modeled as fixed effect]



Genotype by Env. interaction
[modeled as multiple-trait model]



Objectives

- To estimate genetic correlations among three management systems, i.e., tie stall, free stall, and pasture-based systems
- To perform GWAS to detect significant chromosome regions unique to each management system

* Results shown in the abstract + update

Data

- Test-day DHI records
 - Holstein cows in Hokkaido
From April 2021 to October 2022
 - 1st and 2nd lactation cows
 - DIM from 6 to 125
- Pedigree and genomic information
 - Up to 120,000 genotypes
 - >400K pedigree animals

	First Lactation	Second Lactation
No. of herds	3,027	3,029
No. of cows	211,462	100,865
No. of test-day records	1,448,373	1,012,756
No. of pedigree animals	402,418	309,539

Milk FA profiles

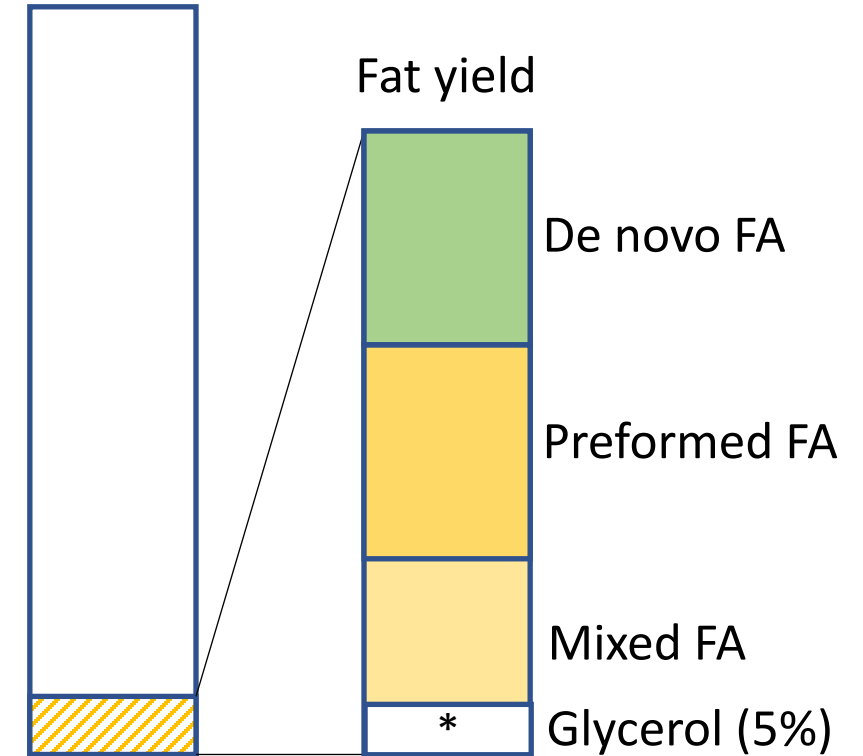
DnF(%): Test-day de novo FA % of FA yield

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

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

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

Milk yield



* 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 3: DIM 66 – 95
 - Stage 4: DIM 96 – 125
- Management system as different trait
 - Tie-stall, Free-stall, Pasture-based systems
- **Variance components**
 - 3-“trait” model for each FA by stage to estimate genetic correlations
 - BLUPF90+ (AI REML)
- **Genome-wide association study with all available genotypes**
 - Single-step GWAS with APY using blup90iod3 + accGS2 + postGSf90 (nonlinearA)
 - Only for stages with genetic correlations <0.99

Genetic correlations (1st lactation)

DnF%	Tie-Free	Tie-Pasture	Free-Pasture
Stage 1	>0.99	>0.99	>0.99
Stage 2	>0.99	>0.99	>0.99
Stage 3	>0.99	>0.99	>0.99
Stage 4	>0.99	>0.99	>0.99

PrF%	Tie-Free	Tie-Pasture	Free-Pasture
Stage 1	>0.99	>0.99	>0.99
Stage 2	>0.99	>0.99	>0.99
Stage 3	>0.99	>0.99	>0.99
Stage 4	>0.99	>0.99	>0.99

No GxE interaction in the first lactation

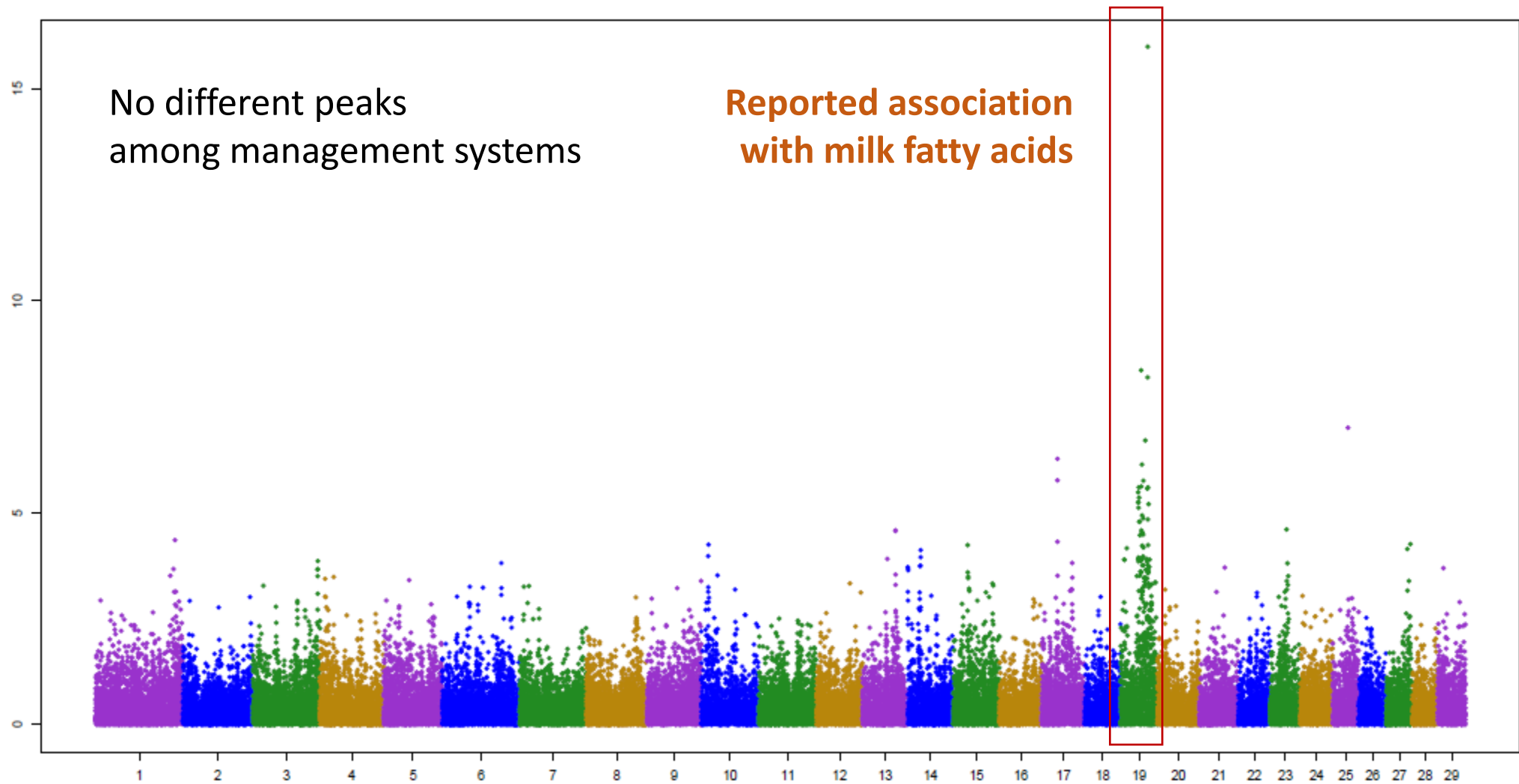
Genetic correlations (2nd lactation)

DnF%	Tie-Free	Tie-Pasture	Free-Pasture
Stage 1	>0.99	>0.99	>0.99
Stage 2	>0.99	>0.99	>0.99
Stage 3	>0.99	>0.99	>0.99
Stage 4	0.99	0.99	0.96

PrF%	Tie-Free	Tie-Pasture	Free-Pasture
Stage 1	>0.99	>0.99	>0.99
Stage 2	>0.99	>0.99	>0.99
Stage 3	>0.99	>0.99	>0.99
Stage 4	0.99	0.99	0.96

Almost no GxE interaction in the 2nd lactation

DnF%: Single-trait GWAS (no management systems) at stage 4 in the 2nd lactation



Results update

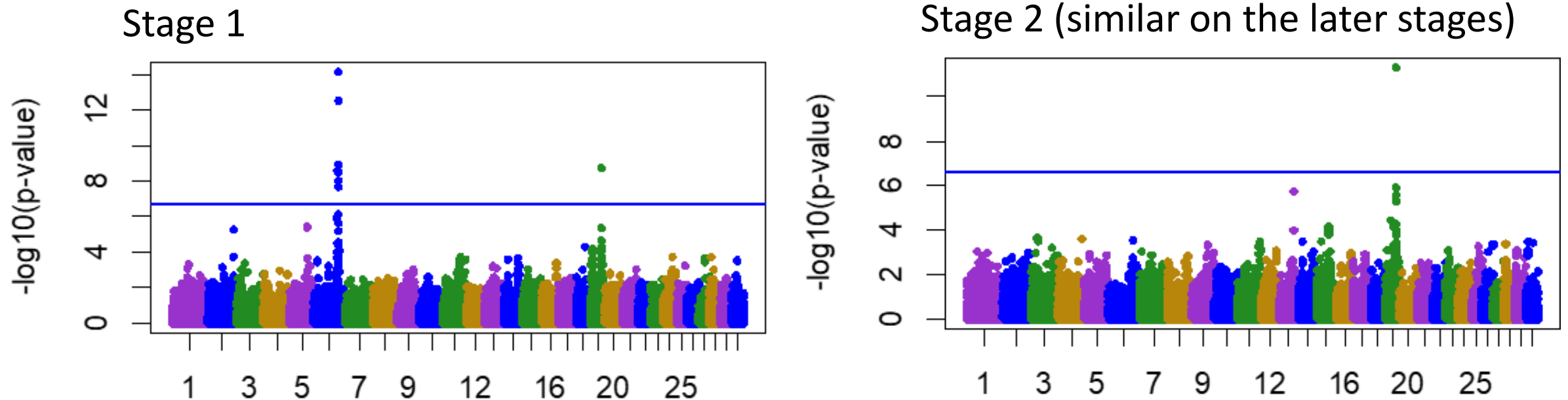
- More phenotypic data
 - Previous: Apr. 2021 – Oct. 2022
 - Updated: Apr. 2021 – Oct. 2023
- Genetic correlations among management systems
- GWAS
 - Without management systems using limited (21,013) genotypes (Regular ssGWAS, No APY)
 - APY GWAS in progress

1st Lactation

DnF%	Tie - Free	Tie - Pasture	Free - Pasture
Stage 1	0.96	0.99	0.97
Stage 2	0.97	0.97	0.89
Stage 3	0.99	0.99	0.99
Stage 4	0.97	0.93	0.87

PrF%	Tie - Free	Tie - Pasture	Free - Pasture
Stage 1	0.99	0.99	0.98
Stage 2	0.99	0.99	0.97
Stage 3	0.99	0.99	0.96
Stage 4	0.98	0.95	0.87

GWAS for DnF% (no GxE, limited genotypes)



Chr	Pos (MB)	Genetic Var. Explained (%)		QTL (or Association)
		Stage 1	Stage 2	
6	85.18 - 89.00	0.20	N/S	SLC4A4 etc. (Milk & fat yield, mastitis etc.)
19	51.32 – 51.32	0.12	0.18	BAHCC1 (Milk FA content etc.)

Summary

- **More data required to detect GxE interaction**

- Phenotypes from at least 3 year-period
- Ideal with at least 2 generations

- **GxE interaction in milk FA**

- Unclear at the very beginning of lactation
- Some interaction with pasture-based management on stage 2 or later

- **Single-step GWAS**

- APY-GWAS well with many more genotypes
- APY-GWAS in progress with GxE interaction
- Significant chromosome regions likely different by lactation stage = Different genetic control on metabolic status by stage

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HCAJ

