FACULTEIT DIERGENEESKUNDE
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DEPARTMENT OF REPRODUCTION, OBSTETRICS AND HERD HEALTH

GENOME-WIDE ASSOCIATION FOR DETECTING GENETIC MARKERS ASSOCIATED WITH METABOLIC ADAPTATIONS IN EARLY-LACTATION HOLSTEIN COWS

Hadi Atashi

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INTRODUCTION

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INTRODUCTION

The early-lactation cow needs comprehensive adaptive reactions to cope with the challenges caused by the transition period.

Dry matter intake (DMI) starts to decrease a few weeks before parturition, where its lowest level occurs at calving.

High-yielding dairy cows enter a state of negative energy balance (NEB) around calving when the energy demand for maintenance and lactation exceeds the dietary intake potential.

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INTRODUCTION

The NEB results in a mobilization of body reserves to provide energy requirements.

Lipid mobilization is a normal and necessary process to support lactation.

Metabolic disorders and decreased reproductive performance have been reported to be linked with longer and more severe periods of NEB.

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INTRODUCTION

Clustering early-lactation cows based on different blood or milk metabolites can be used to group individual cows based on their ability to cope with the altered metabolic challenges of lactation.

This clustering methodology can be used as a diagnostic or herd management tool and to identify superior animals with a high genetic value for genetic selection purpose.

INTRODUCTION

Although physiological adaptations of dairy cows in the transition period are well described, knowledge about the genetic background still remains insufficient.

The aim was to use GWAS to identify genetic markers linked with metabolic adaptation in early-lactation Holstein cows.

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MATERIALS & METHODS

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PHENOTYPIC DATA

4,267 second-parity Holstein cows distributed in 50 herds.

Milk samples collected starting from the first week in milk until 50 days in milk.

Fourier-transform mid-infrared (FT-MIR) spectra of milk samples were determined and used to predict metabolic cluster of the cows (De Koster et al., 2019).

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(De Koster et al., 2019. Journal of Dairy Science 102(3):2631-2644.

GENOTYPIC DATA

Individuals were genotyped using the Bovine LD, Bovine SNP50K or Bovine HD SNP panel.

Genotypes of animals were imputed to HD with a reference population of 795 (46 M and 749 F) HD individuals.

Quality control:
MAF, HWE, Mendelian error.

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VARIANCE COMPONENT ESTIMATION

BLUPF90 family of programs were used.

Pedigree file contained 43,181 individuals.

The variance components were estimated by Bayesian inference.

The analysis
consisted of a single chain of 350,000 cycles
with a burn-in of 100,000 cycles
taking a sample every 50 iterations
THRGIBBS1F90

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SINGLE-STEP GENOME WIDE ASSOCIATION STUDY

Different window types and variable window sizes can be used.

What window size is optimal?

Single-step GWAS was used to estimate genetic variance explained by windows of 1, 5, 10, 15, 20, and 25 consecutive SNPs.

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RESULTS & DISCUSSION

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RESULTS AND DISCUSSION

The cows (n = 4,267) were grouped in either BALANCED (28%) or OTHERBAL (72%) metabolic cluster.

The heritability for metabolic clustering was 0.17.

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RESULTS AND DISCUSSION

Item	BALANCED	OTHER
Milk yield (kg/d) LSM (SE)	32.8 (1.89)^{b}	33.5(1.89)^{a}
FPCM (kg/d) LSM (SE)	35.0 (1.70)	34.7 (1.69)
Fat yield (kg/d) LSM (SE)	1.46 (0.07)^{a}	1.40 (0.07)^{b}
Protein yield (kg/d) LSM (SE)	1.18 (0.06)	1.19 (0.06)
Fat+Protein yield (kg/d) LSM (SE)	2.64 (0.12)^{a}	2.59 (0.12)^{b}
Fat percentage (%)	4.51 (0.17)^{a}	4.24 (0.17)^{b}
Protein percentage (%)	3.64 (0.09)^{a}	3.61 (0.09)^{b}
Milk SCS	3.72 (1.07)	3.73(1.07)

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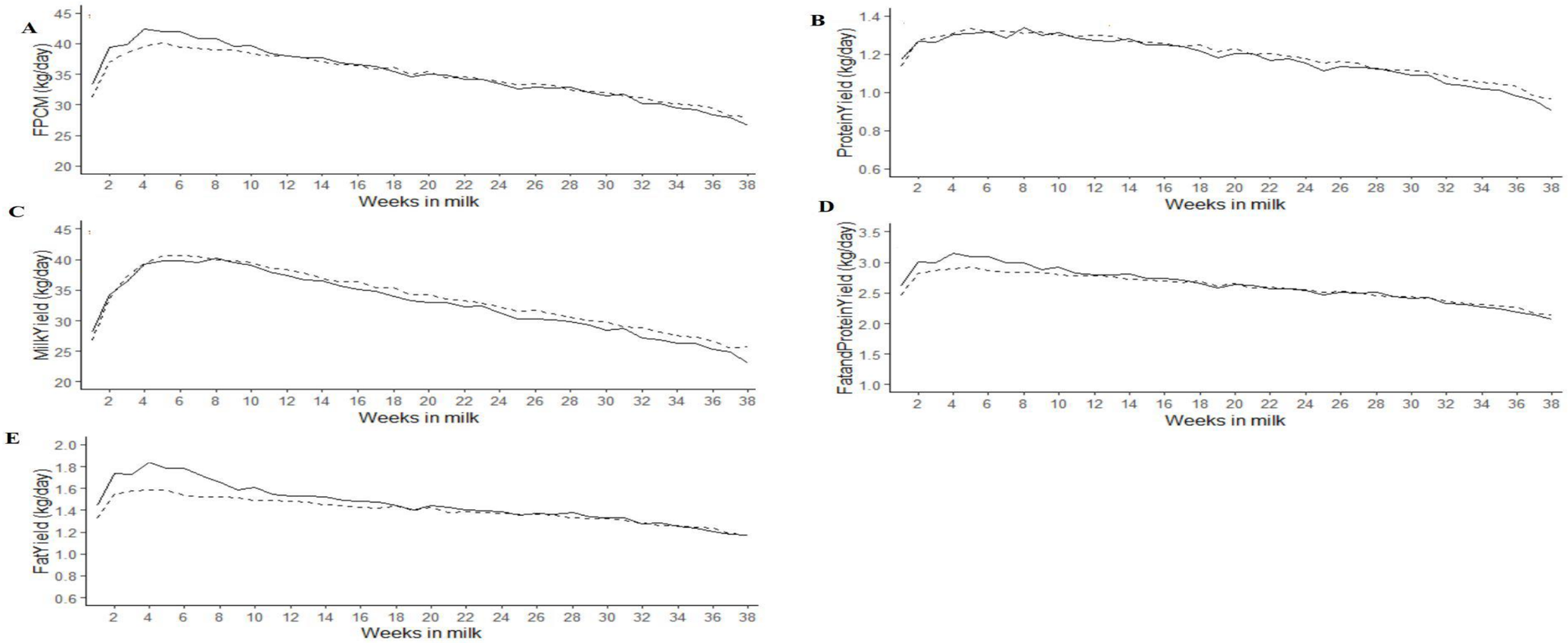
RESULTS AND DISCUSSION



Association between the predicted metabolic cluster [BALANCED (line) and OTHER (dashed line)] and production performance.

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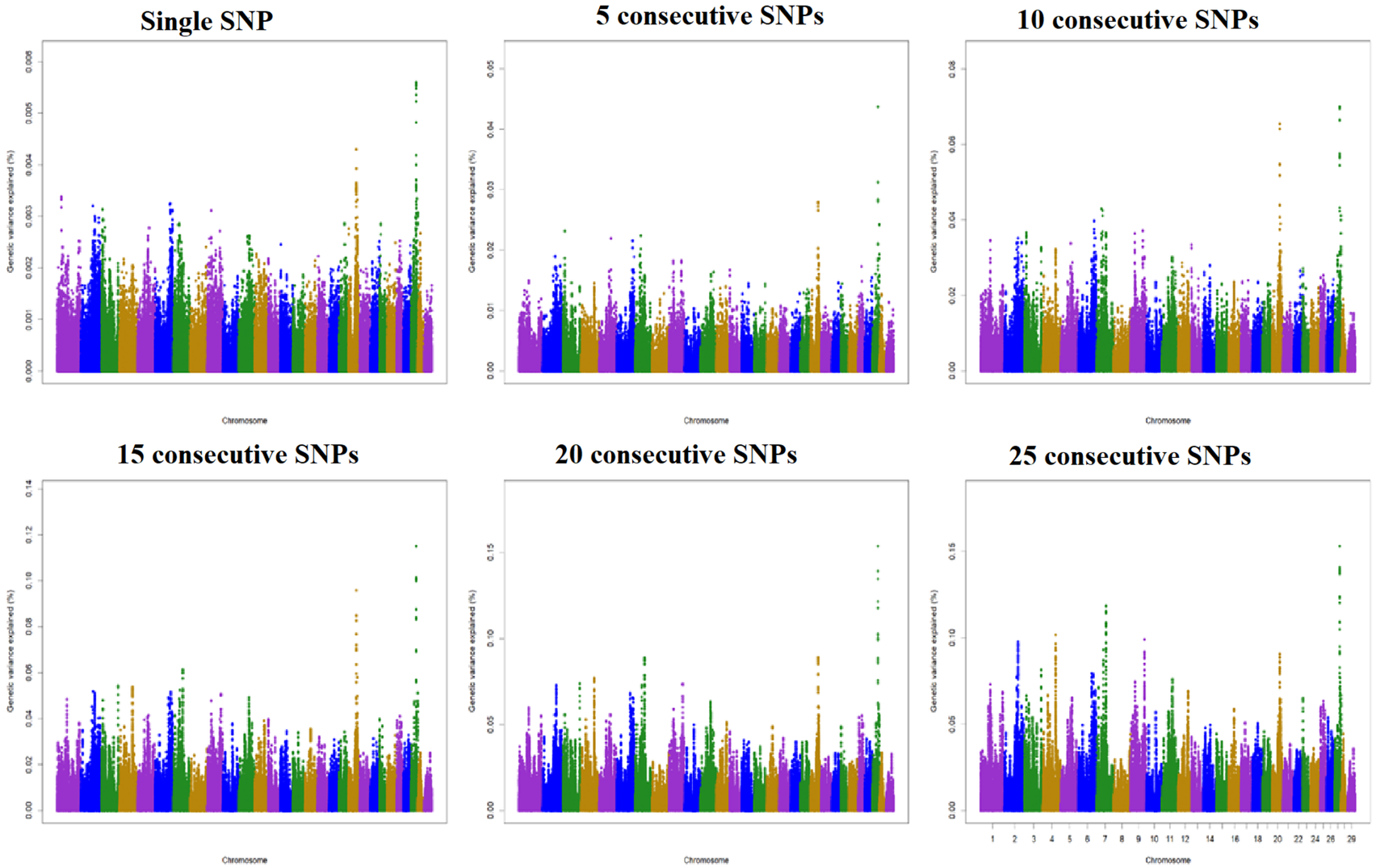
RESULTS AND DISCUSSION



Additive genetic variance explained by windows of 1, 5, 10, 15, 20, and 25 consecutive SNP

RESULTS AND DISCUSSION

The identified region (with length < 38,000 bp) overlaps with QTLs reported for meat quality, milk fatty acid profiles, and dry matter intake (DMI) in cattle.

The region was mapped inside *ANK1* and *miR-486* genes.

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RESULTS AND DISCUSSION

ANK1 is a large gene that encodes protein ankyrin-1which plays role in cell motility, proliferation, and activation.

Tetens et al. (2014) reported a QTL for dry matter intake mapped inside *ANK1*.

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Tetens et al., 2014. Journal of dairy science 97(1):520-531

RESULTS AND DISCUSSION

miRNAs are small (~22 nucleotides) non-coding RNAs that regulate many fundamental biological processes through affecting both the stability and translation of mRNAs

Mammary gland development is controlled by several genes including miRNAs and *miR-486*.

Significant association between residual feed intake (RFI) and expression level of miR-486 has been reported in cattle and pig.

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CONCLUSION

The aim was to identify genetic markers linked with metabolic adaptation in early-lactation Holstein cows.

A region on BTA27 was identified to be associated with the predicted metabolic cluster

The findings may help to better understand the genetic mechanisms regulating metabolic adaptation, and might be useful for future genomic studies.

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Hadi Atashi

Scientific staff

DEPARTMENT OF REPRODUCTION,
OBSTETRICS AND HERD HEALTH

E hadi.atashi@ugent.be
T +32 9 264 75 61
M +32 465 199 201

www.ugent.be

Ghent University
@ugent
Ghent University

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