



Genome-wide association of myristic and palmitic acid in milk of Dutch dairy cattle

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Aim

Identify genomic regions associated with myristic (C14:0) and palmitic (C16:0) acid

Introduction

- C14:0 and C16:0 are believed to increase cholesterol levels and should be reduced in human diets
- Together they make up for 40-50% of fat in bovine milk
- Discovering the genetic background of fatty acids will help
 - to understand fat metabolism of dairy cows
 - to select for animals with desired milk fat composition

Data

- 2,000 first lactation Holstein Friesian cows
- C14:0 and C16:0 measured by gas chromatography
- 50,000 SNP genotypes

	Mean (wt%)	σ_p	h^2
C14:0	11.61	0.78	0.62
C16:0	32.59	2.15	0.43

Method

Two step single SNP association

1. General linear model: $y^* = \mu + \text{sire} + \text{SNP} + e$
2. Animal model: regions with false discovery rate (FDR) < 0.1% reanalyzed with inclusion of pedigree

Results

Regions highly significant (FDR<0.1%) with animal model:

C14:0

- BTA 14: DGAT1 SNP explains 18% of genetic variation
- BTA 19: SNP (52Mbp) explains 14% of genetic variation
 - SNP located near FASN gene
- BTA 26: SCD1 SNP explains 5% of genetic variation

C16:0

- BTA14: DGAT1 SNP explains 40% of genetic variation

Other interesting regions such as BTA 1, 8, 27 for C14:0 and BTA 26, 27 for C16:0 explain 2-3% of genetic variation

Conclusion

Major regions associated with C14:0 and C16:0 harbor candidate genes involved in fat synthesis

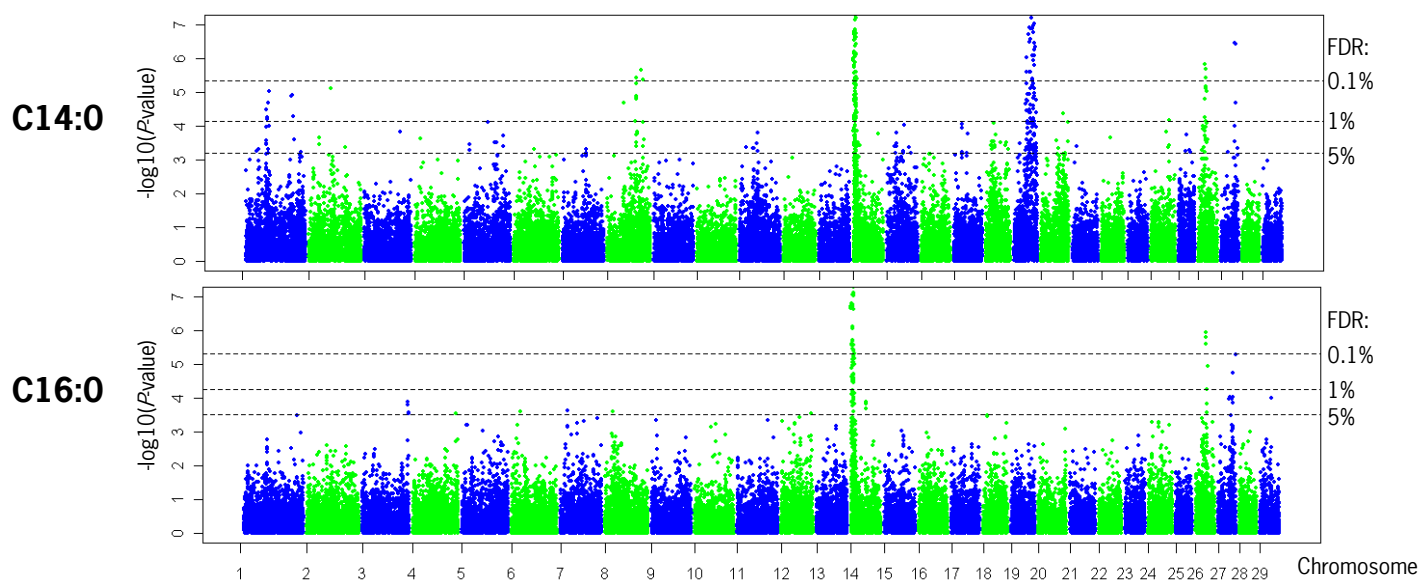


Figure: Genome-wide plots of $-\log_{10}(P\text{-values})$ (y-axis cut off at 7) for association with C14:0 and C16:0 using the general linear model. The genomic position is represented along the x-axis and chromosome numbers are given on the x-axis. The dotted horizontal lines represent the false discovery rate thresholds.