AARHUS UNIVERSITY

CENTER FOR QUANTITATIVE GENETICS AND GENOMICS QGG

The impact of the rumen microbiome on the detailed milk fatty acid profile in Danish Holstein

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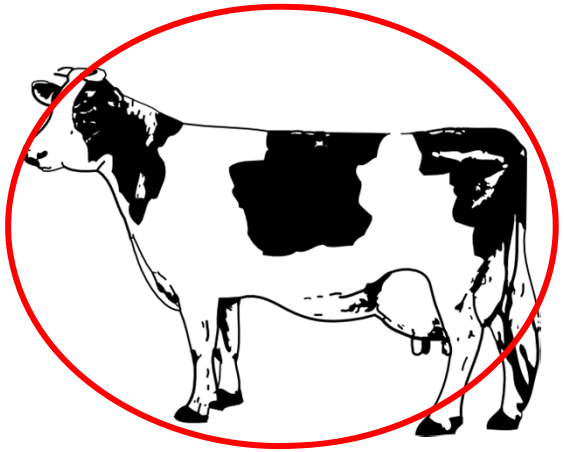
Introduction

- **What factors influence the milk composition**
  - Focus on milk fatty acids

Feed



Milkfat

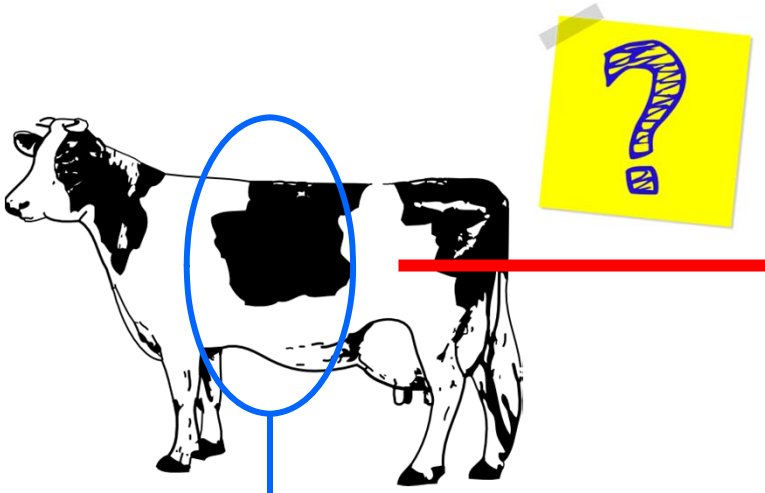
Unsaturated FA

Saturated FA

E

G

Introduction



Milk fat composition

Community of living organisms in the rumen

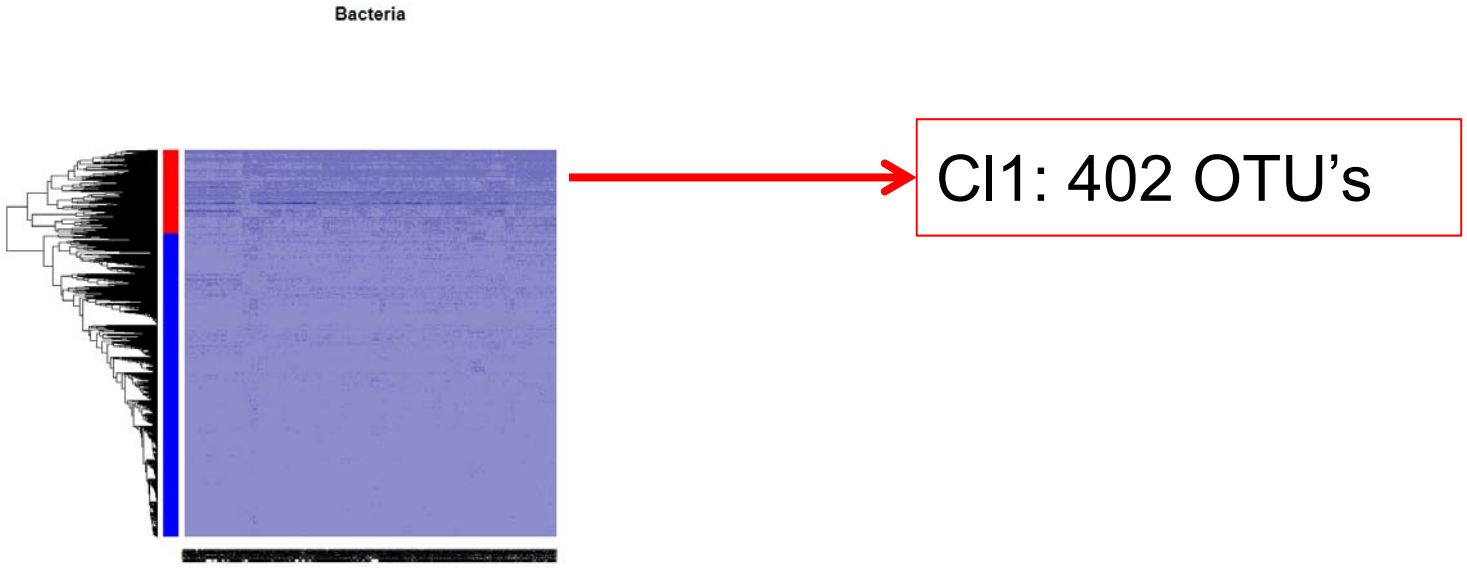
Data

- **292 cows from 3 herds, 1-3 parity, 3-398 DIM**
- **50k bovine SNP information**
- **Morning milk sample → detailed milk fatty acid profile (Gass Chromatochraphy)**
- **Rumen sample → sequenced using 16S approach**

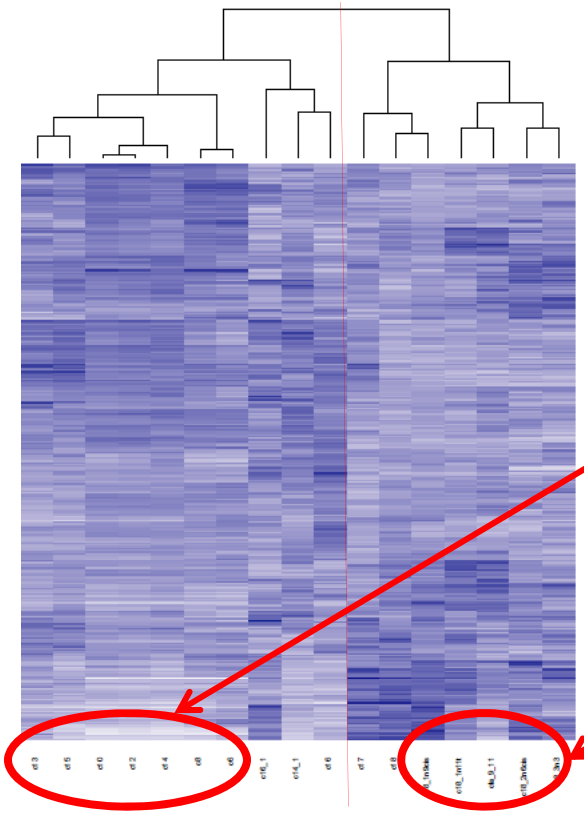
Results: Rumen data

- **8,515 bacterial and 168 archeal OTU's detected**

Center scale the data and perform a hierarchical clustering



Results: fatty acids



Hierarchical clustering of the fatty acids:

Extremes are separated into

saturated FA or unsaturated FA

Influence of bacterial cl1 on fatty acids

- **Made a genomic relationship matrix based on 50K SNP data**
- **Made a bacterial relationship matrix based on bacterial cl1 (402 OTU's)**
- $Y_{ijk} = \mu + herd_j + parity_k + b_1*DIM_i + b_2*e^{-0.05*DIMi} + B_i + G_i + e_{ijk}$
- $h_B = V_B/(V_B + V_G + V_e)$

Results: Influence of bacterial cl1 on fatty acids

- **SE were relative large, but it was shown that:**

Saturated FA	Unsaturated FA
• C6:0	• C18:1n11t
• C8:0	• C18:2n6c
• C10:0	• C18:3n3
• C12:0	• CLA
• C16:0	
h_B close to 0	h_B > 0.50

Conclusion

- **Necessary to reduce the number of rumen bacteria before making a relationship matrix**

- **Rumen bacteria explain the largest variance of the unsaturated fatty acids**

Acknowledgements

- Milk Levy Fund, Denmark
  - o “Metagenomets betydning for mælkens sammensætning og kvalitet”