

# Differences in bovine milk fat composition among dairy breeds in The Netherlands

Myrthe Maurice – Van Eijndhoven, Henk Bovenhuis, H el ene Soyeurt, and Mario Calus



# Background

- **Differences in milk fatty acid (FA) composition between breeds** is of interest because it is associated with
  - Processability
  - Human health
  - Methane emission
  - **Unique breed characteristic (selection / conservation)**
- Different cattle breeds used in dairy industry in the Netherlands:

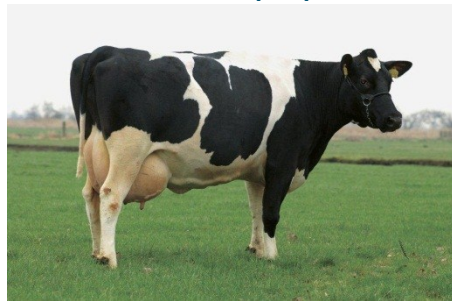
Holstein Friesian (HF)  
Jersey (JER)



Meuse-Rhine-Yssel (MRY)



Dutch Friesian (DF)



Groningen White Headed (G)



# Measuring FA composition

- Gas chromatography (GC)
  - Highly accurate
  - High cost per sample
- Mid-infrared (MIR) profiles
  - (Somewhat) lower accuracy
  - Very low cost per sample (measured during routine milk recording)

=> MIR is optimal for large-scale breeding applications

# Aim of this study

Investigate differences in bovine milk fat composition between different cattle breeds in the Netherlands

=> Milk fat composition predicted from MIR spectra using RobustMilk prediction equations (**Soyeurt et al., 2011**)

# Data

MIR profiles obtained during routine milk recording

On farms with MRY, DF, GWH, and JER (and HF):

- 24,445 cows (41,404 records) from 445 farms
- 7,626 cross-bred cows
- 1,769 purebred ( $\geq 87,5\%$ ) MRY, DF, GWH, and JER
- 15,050 purebred ( $\geq 87,5\%$ ) HF

Holstein Friesian (HF)

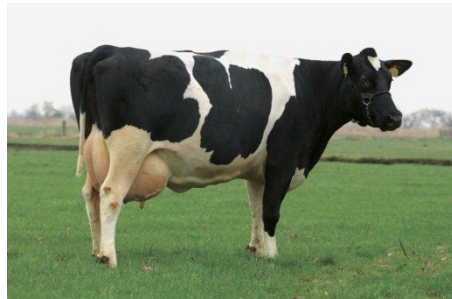
Jersey (JER)



Meuse-Rhine-Yssel (MRY)



Dutch Friesian (DF)



Groningen White Headed (G)



# Model

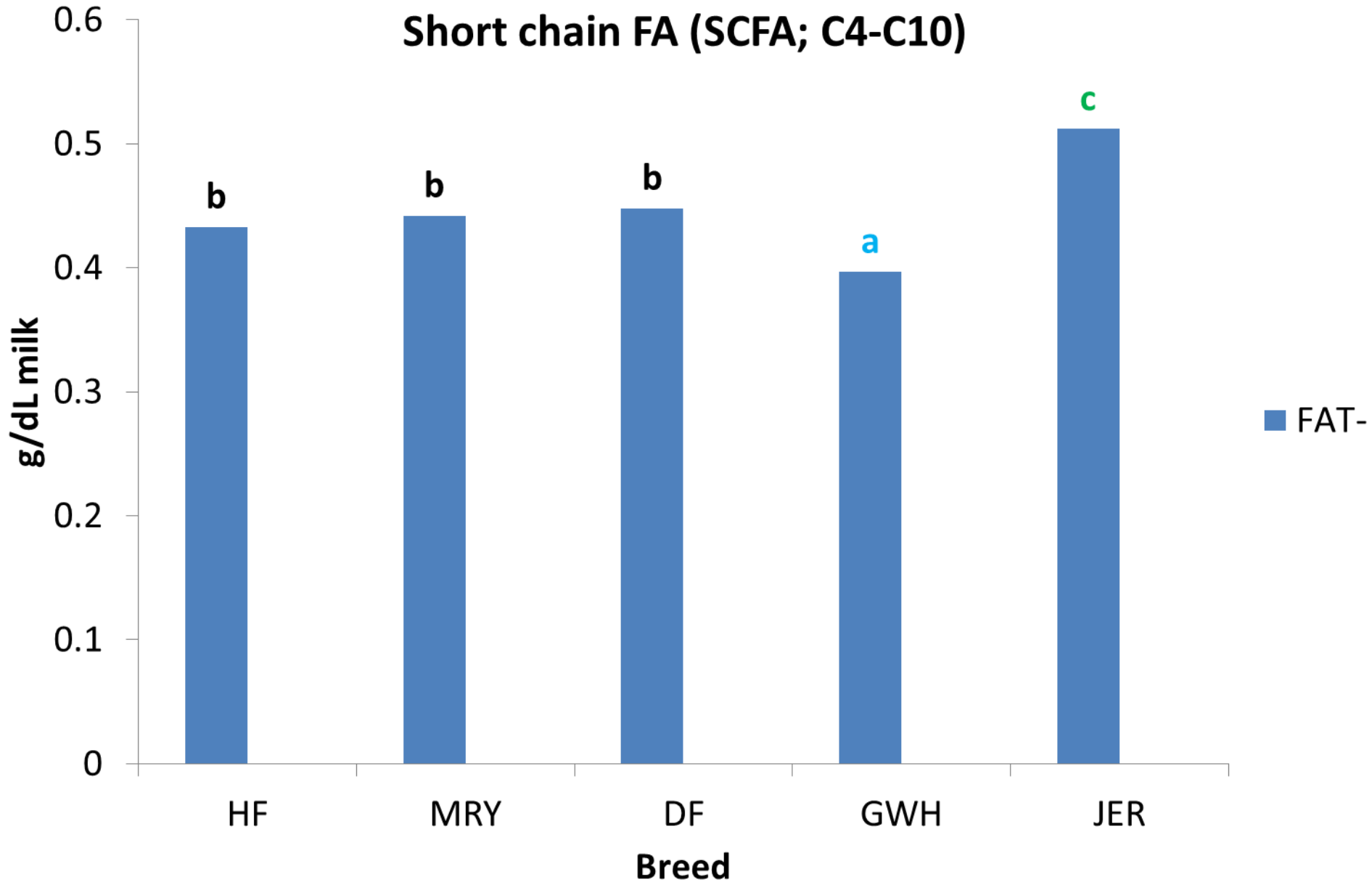
- Only FA included that were predicted accurately
  - validation  $R^2 > 0.6$  (on Dutch data)
- All FA components analysed as g/dL milk
- FA+ & FA- model
  - FA- includes no regression on fat%
  - FA+ includes regression on fat%
    - => To correct for differences in total Fat%
- Fixed effects
  - Regression on breed fractions
  - Heterosis & recombination
  - Further: age, hys, dim, etc.

# Results – groups of FA

- Generated through de novo synthesis
  - short and medium chain FA
- Affected by  $\Delta 9$ -desaturases
  - C14:1
- Arising in milk directly from cows diet
  - C18:2cis9,12 and C18:3cis9,12,15

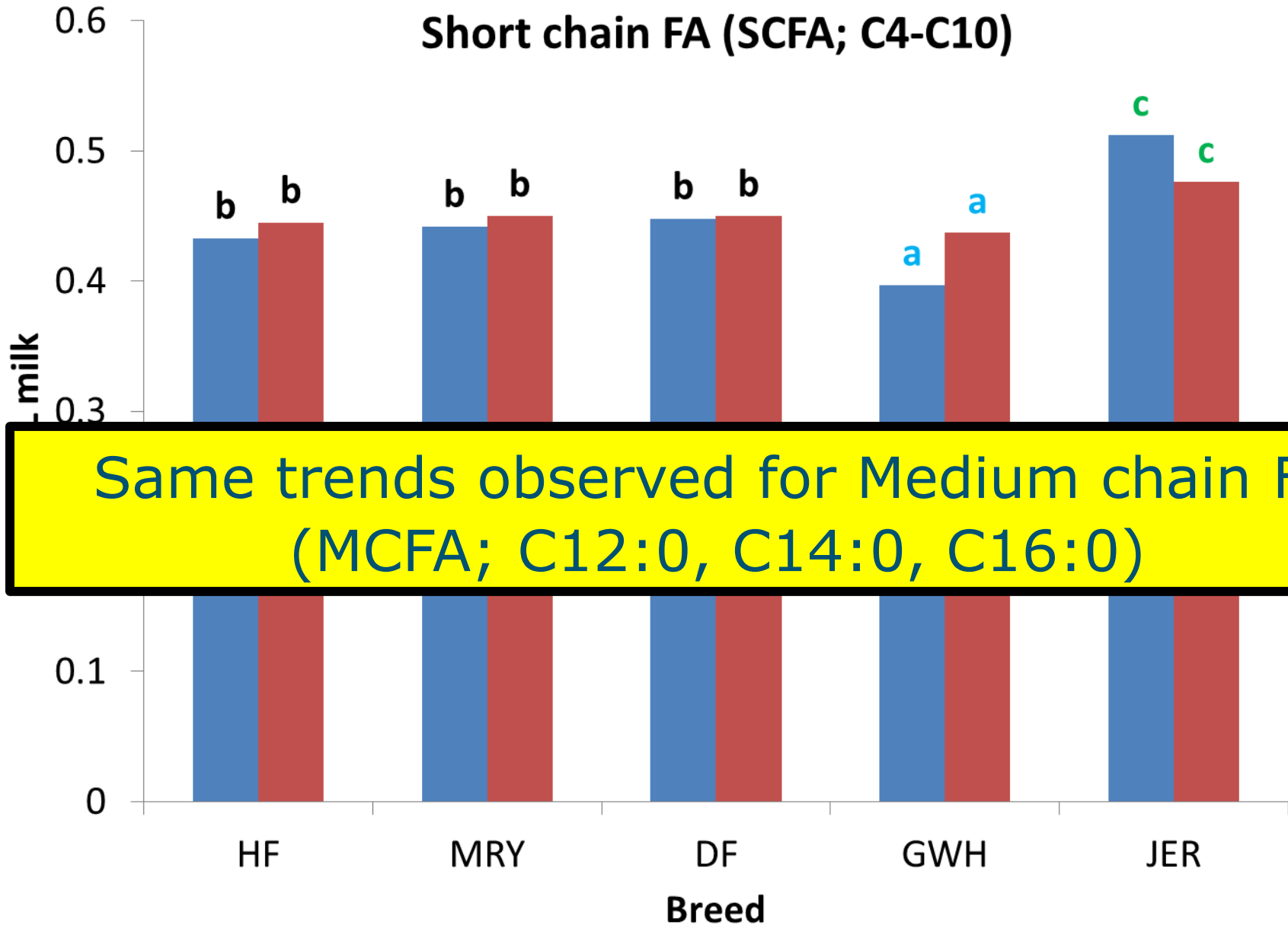


# FA generated through de novo synthesis

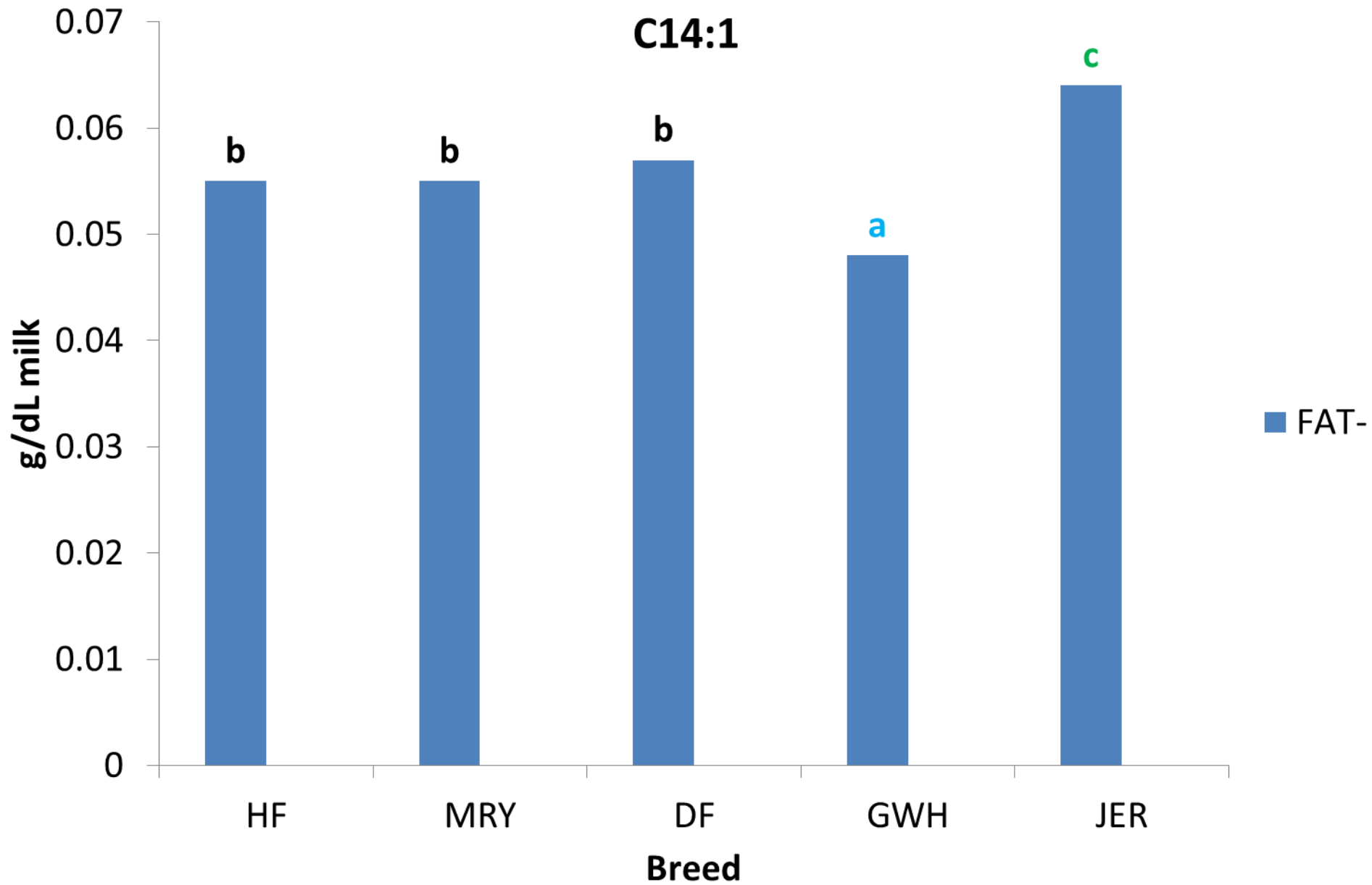




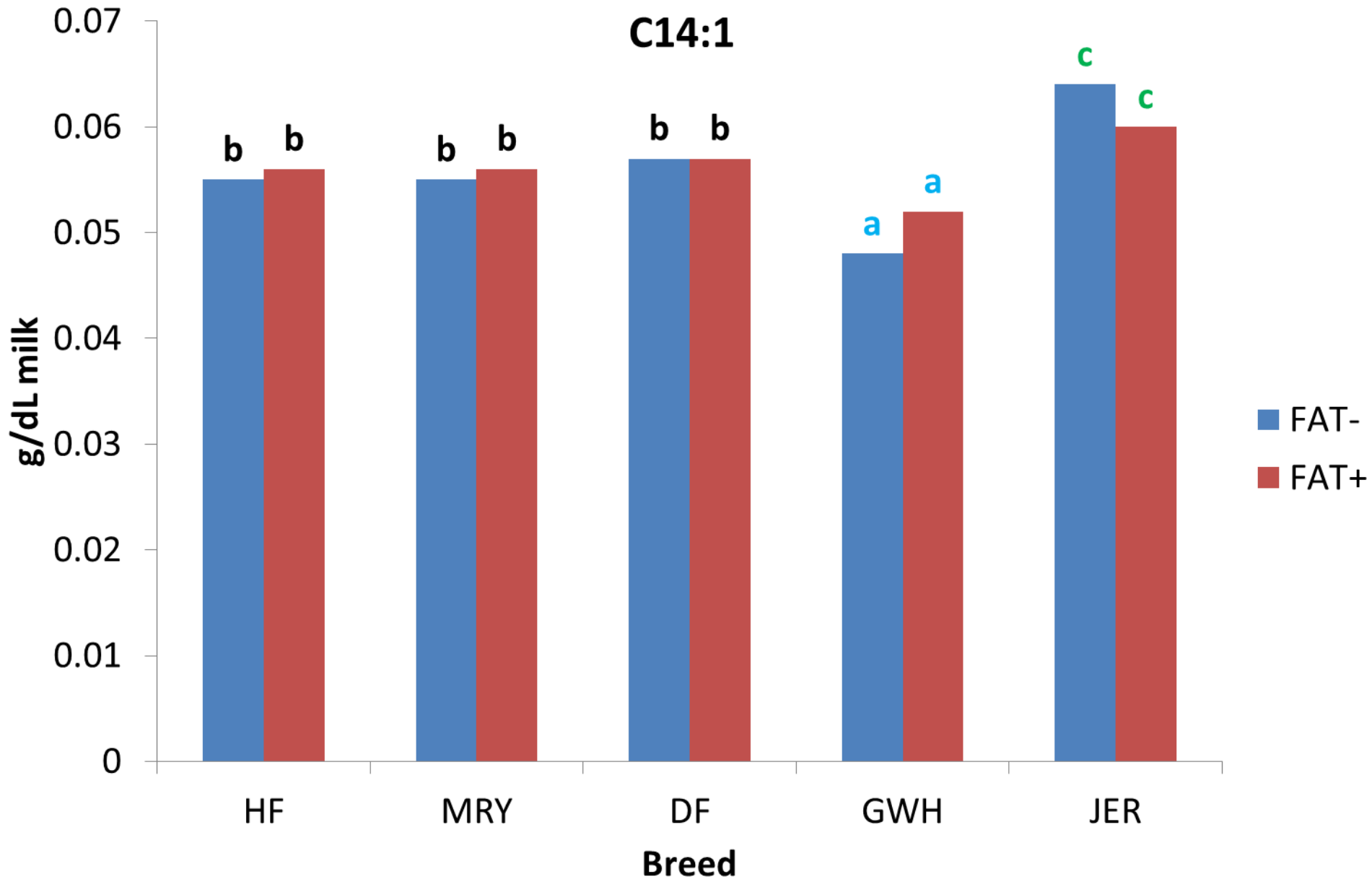
# FA generated through de novo synthesis



# FA affected by $\Delta 9$ -desaturases (C14:1)



# FA affected by $\Delta 9$ -desaturases (C14:1)



# FA arising from the cows diet

- Some significant differences, despite low concentration in milk

Using FAT+ model (correcting for Fat%):

- C18:2cis9,12
  - JER: Lower compared to other breeds
- C18:3cis9,12,15
  - Results inconsistent with other studies

# Conclusions

FA composition:

- Similar for HF, MRY, and DF; different for GWH & JER
- Short & medium chain FA:
  - GWH: lowest concentration
  - JER: highest concentration
- Is related to total fat percentage in all breeds; especially short and medium chain FA
  - FA- or FA+ model



# Acknowledgements

Melk op Maat

Dutch Milk Genomics  
Initiative

