

# Subacute ruminal acidosis and the global profile of ruminal and fecal microbiota of dairy cows

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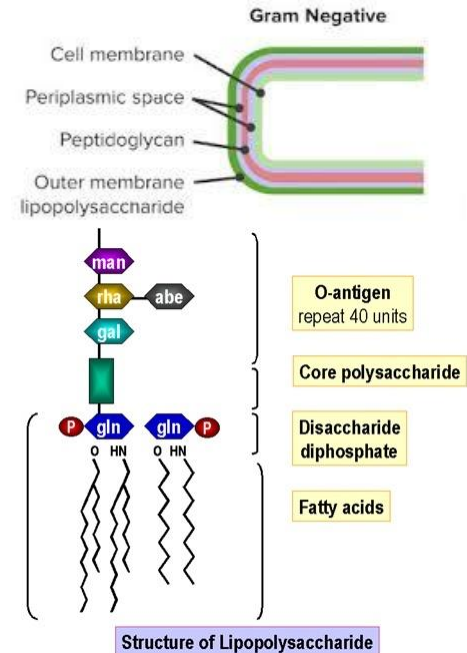
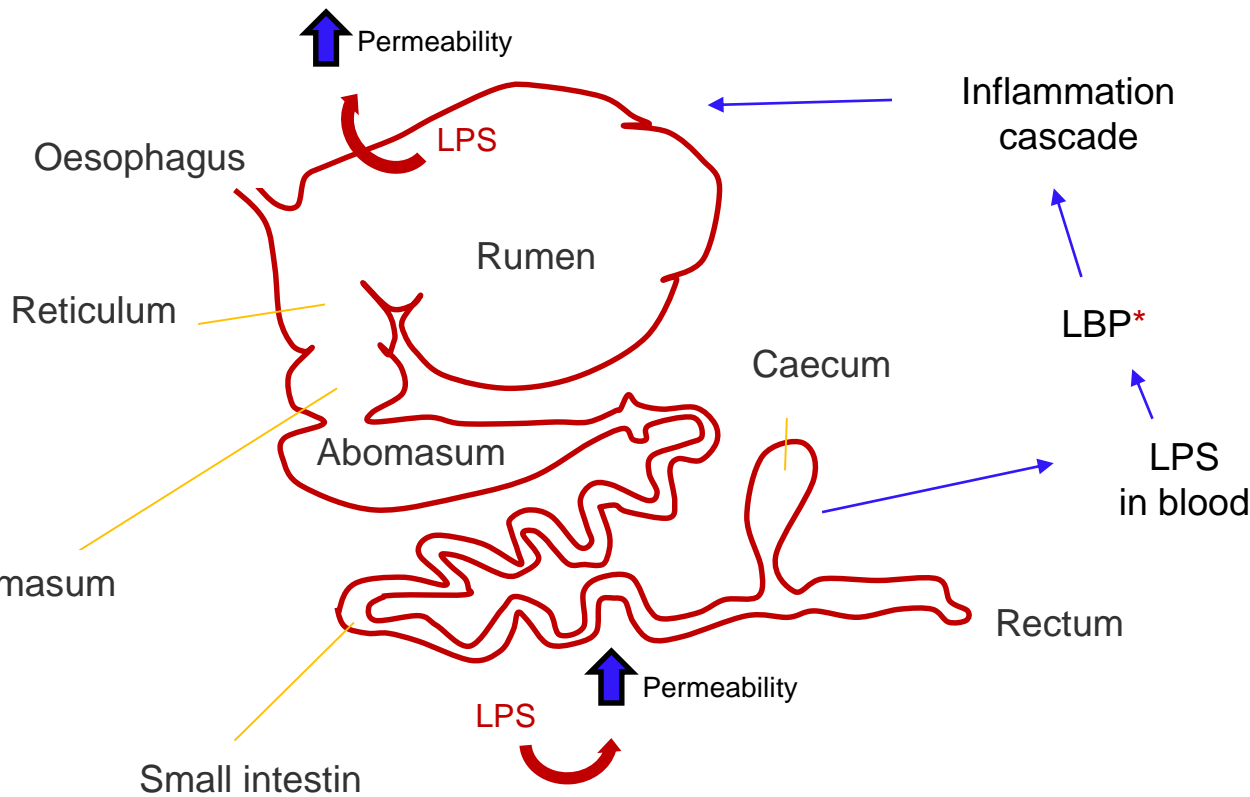
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# Subacute ruminal acidosis (SARA) and inflammation

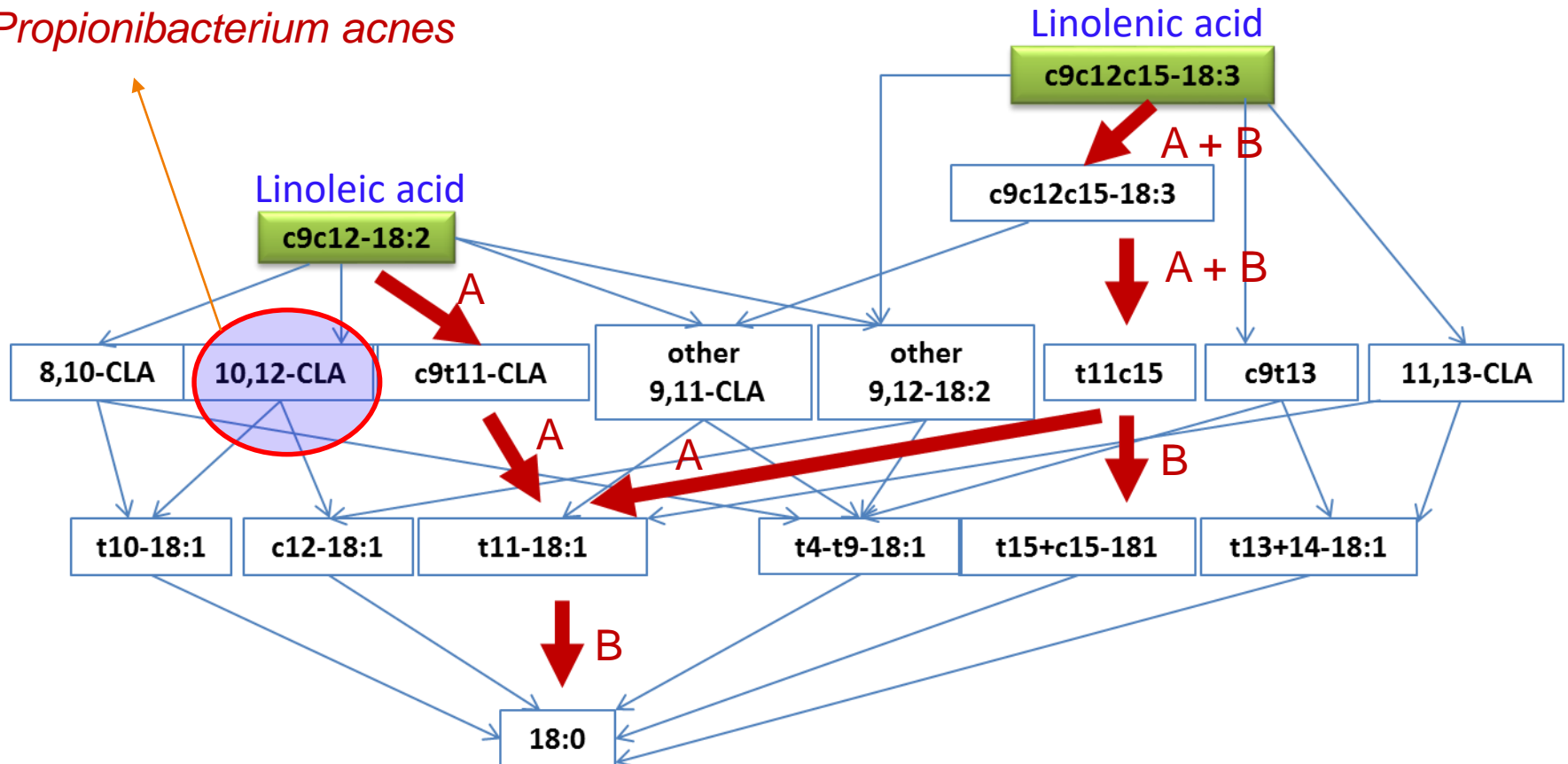


\*Lipopolysaccharide binding protein



# Ruminal biohydrogenation of PUFA

*Propionibacterium acnes*



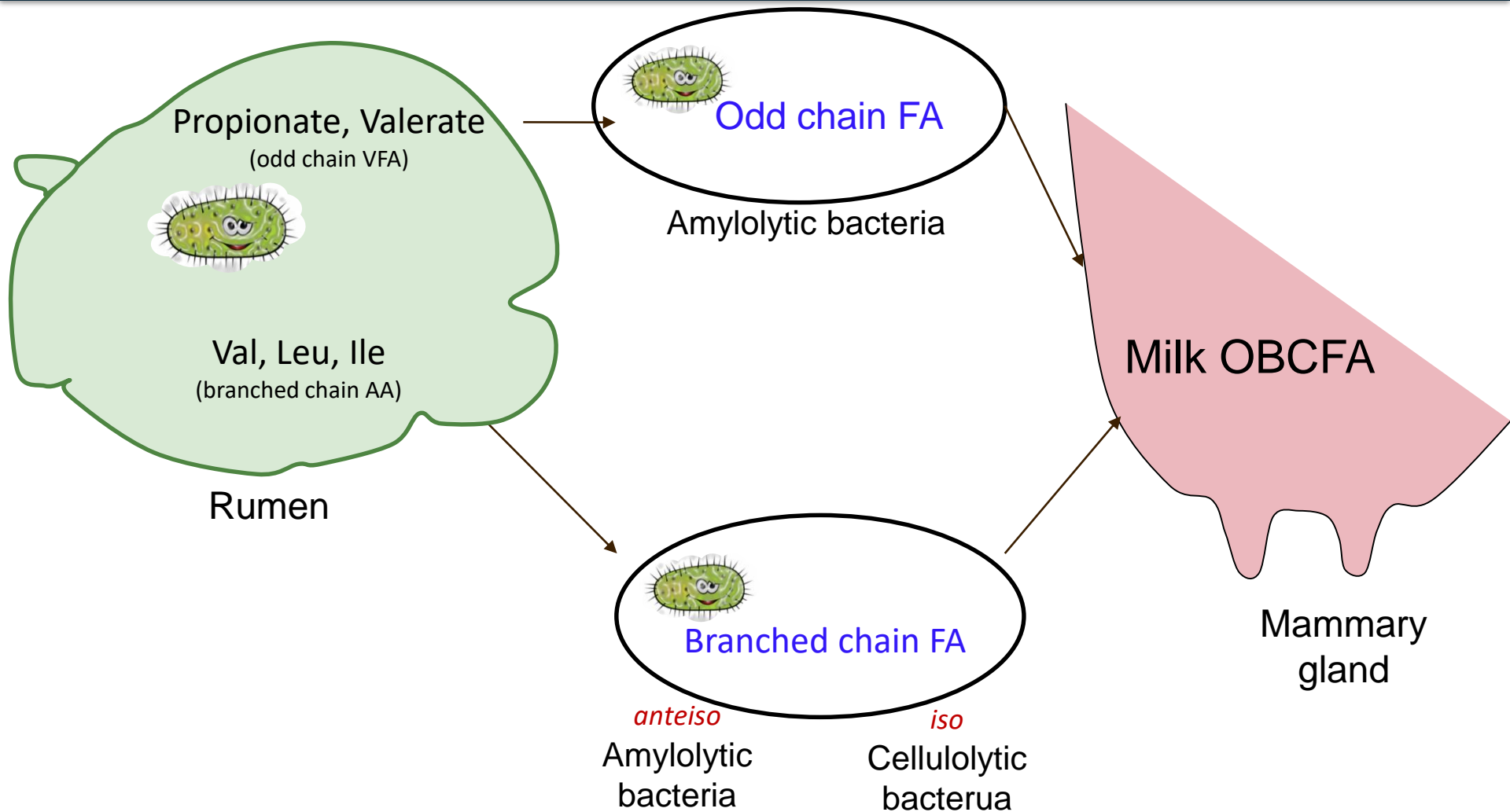
\*Group A B

Hartfoot and Hazlewood, 1997

*Lourenço et al., 2010*

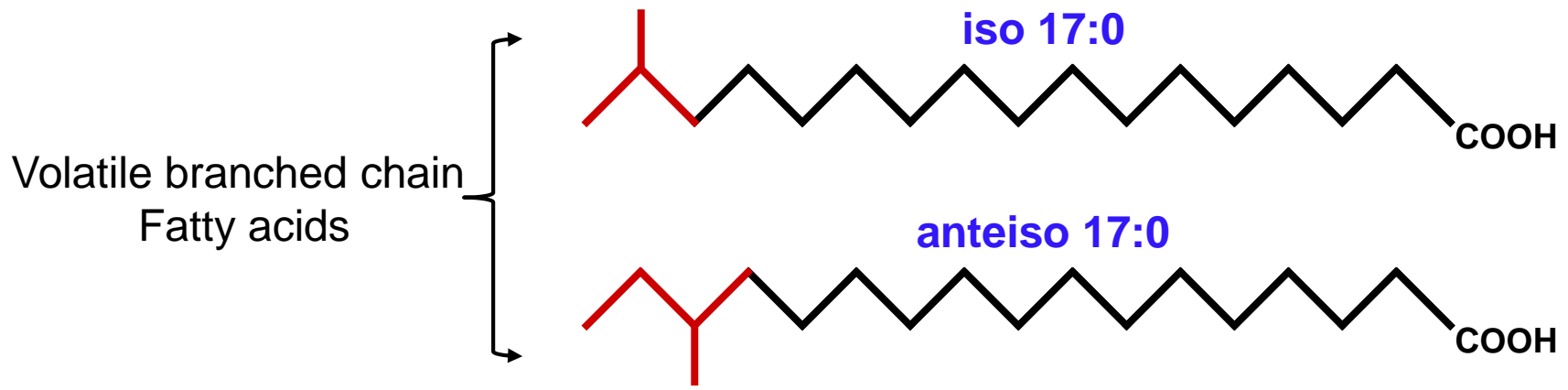


# Odd and branched chain fatty acids





# Odd and branched chain fatty acids





# Materials and methods

Twelve ruminally cannulated cows ( $120 \pm 52$  DIM;  $35.5 \pm 8.9$  kg of milk/d; mean  $\pm$  SD)

1) SARA induction; (29% starch, 24% NDF, and 2.8% fatty acids)

2) Control / Recovery ; (20% starch, 31% NDF, and 2.3% fatty acids)

Cow	Pre-Exp.	Period 1	Period 2	Period 3
1	Control	Control	Induction	Recovery
2	Induction	Recovery	Control	Induction
3	Control	Induction	Recovery	Control



# Materials and methods

pH recorded every 5 min over a 24h period on d 0, 3, 7, 14, 21



- Milk fat (d 0, 3, 7, 14, 21) extracted and profile determined by gas chromatography
- Genomic DNA from whole rumen digesta (liquid and solid fractions; d 7 and 21) were extracted and subjected to Illumina sequencing of 16S rRNA (V3-V4 region).
- Default QIIME pipeline was used to identify operational taxonomic units
- Data analyzed using MicrobiomeAnalyst



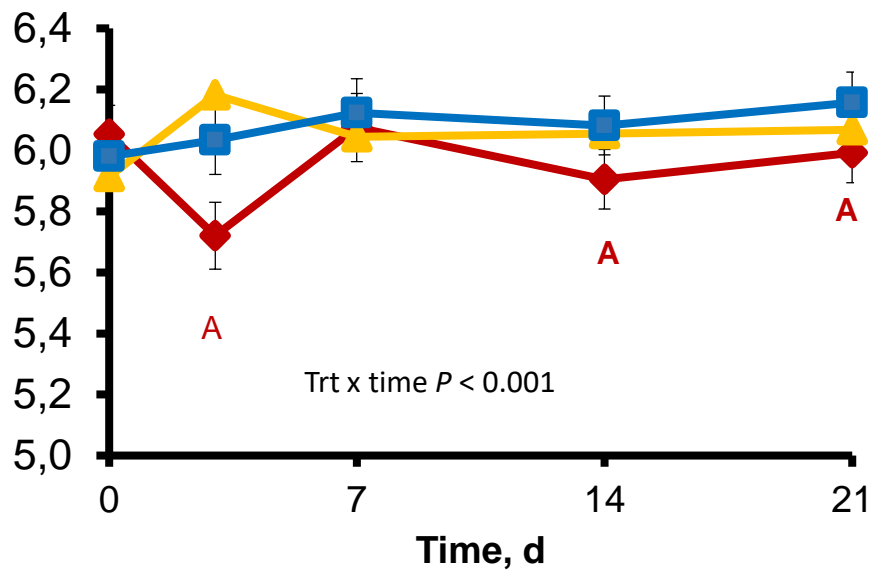
# Ruminal pH



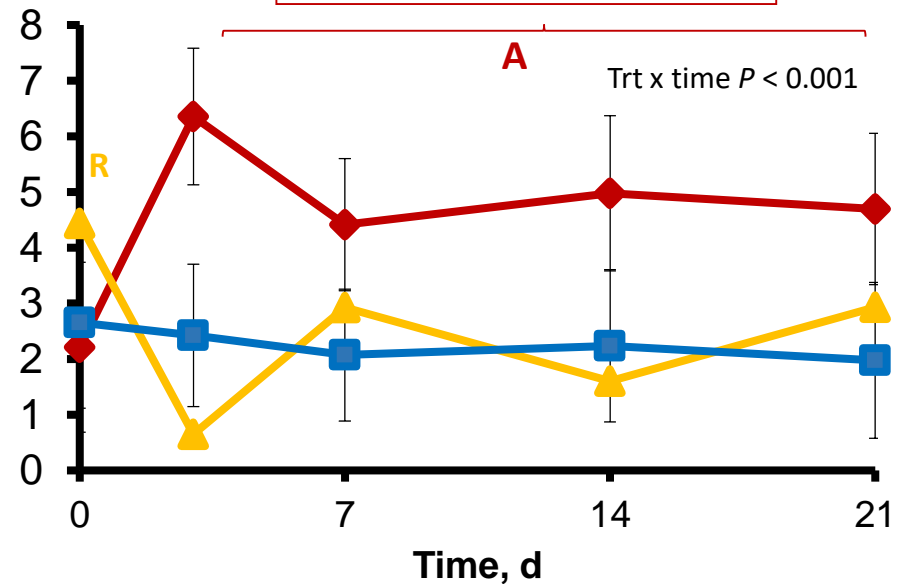
Ecow, UK

SARA  Recovery  Control 

Mean rumen pH



Time below 5.6, h/d



CON vs. SARA (A =  $P < 0.05$ ; a =  $P < 0.10$ )

CON vs. Recovery (R =  $P < 0.05$ ; r =  $P < 0.10$ )

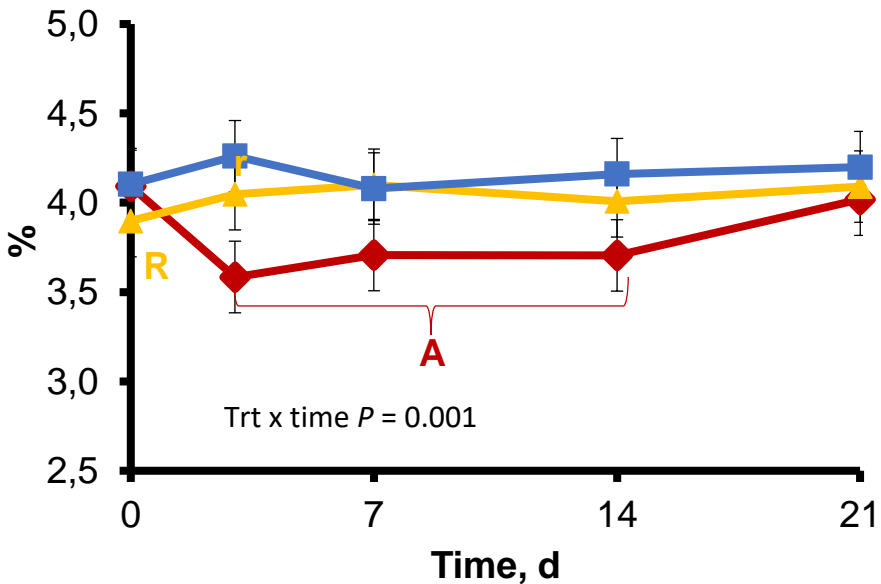




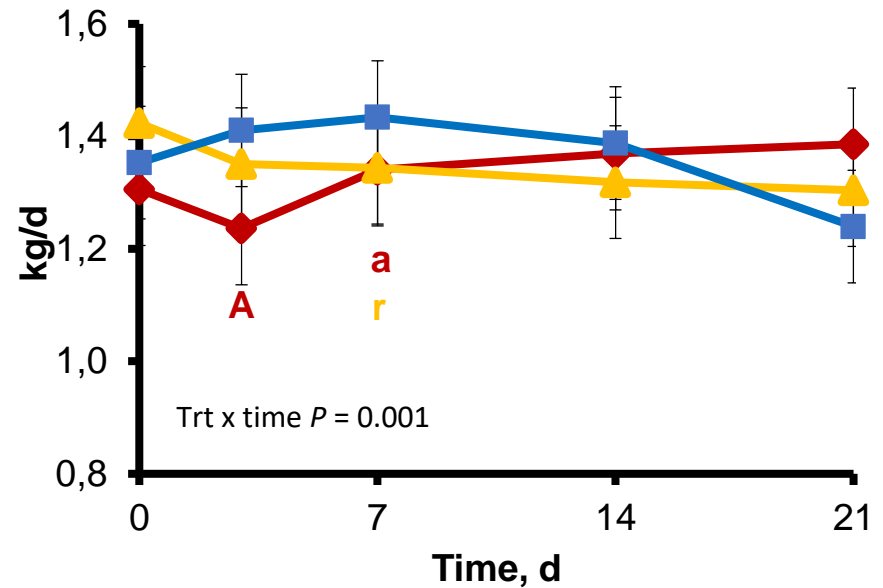
# Milk fat synthesis

SARA ◆ Recovery ▲ Control ■

Milk fat concentration



Milk fat yield

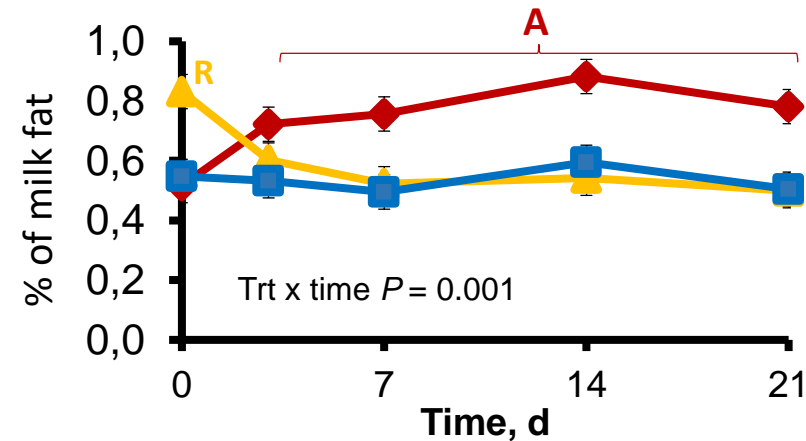




# Biohydrogenation pathways

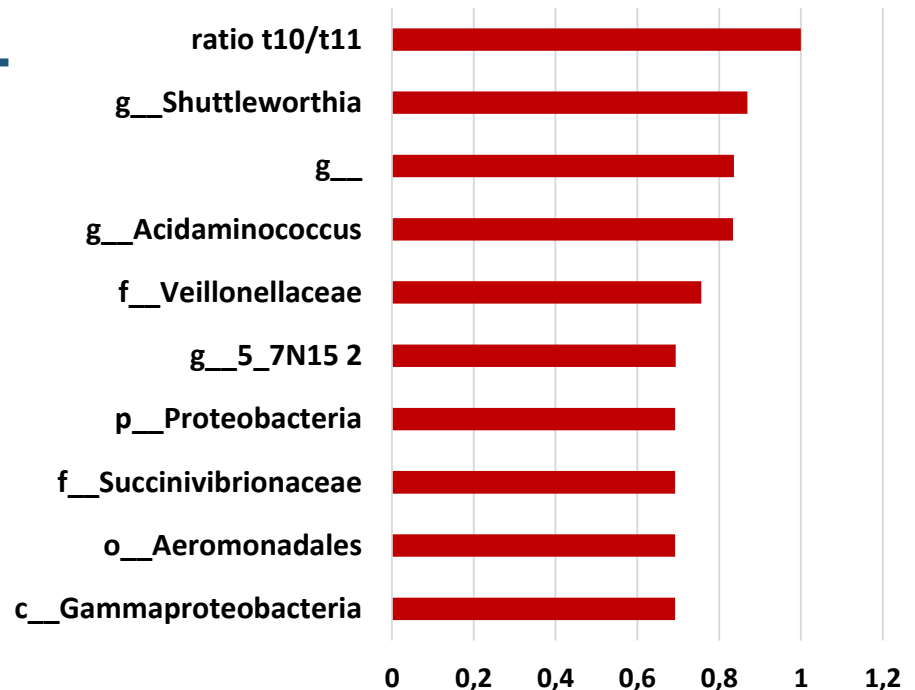
SARA ◆ Recovery ▲ Control ■

*trans*-10/*trans*-11 ratio



*trans*-10, *cis*-12 CLA not detected

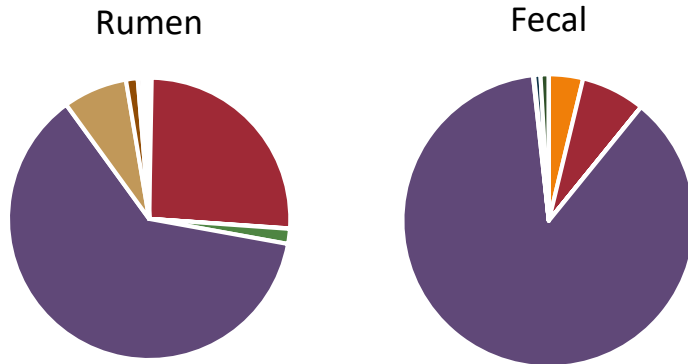
Ratio *trans*-10/*trans*-11 18:1



Positively associated with the *trans*-10/*trans*-11 ratio ( $r=0.70$  to  $0.83$ )

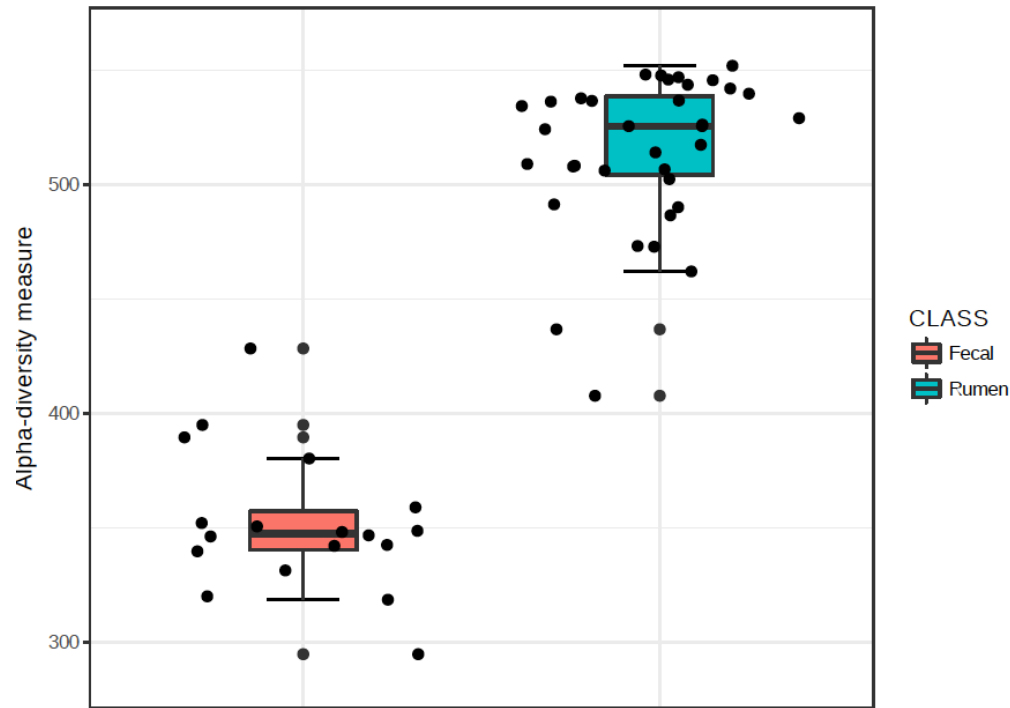


# Ruminal and fecal microbiota composition



- \* p\_\_Actinobacteria
- \* p\_\_Bacteroidetes
- p\_\_Elusimicrobia
- \* p\_\_Fibrobacteres
- p\_\_Firmicutes
- \* p\_\_Proteobacteria
- p\_\_Spirochaetes
- p\_\_SR1
- p\_\_TM7
- p\_\_Verrucomicrobia
- p\_\_WPS\_2

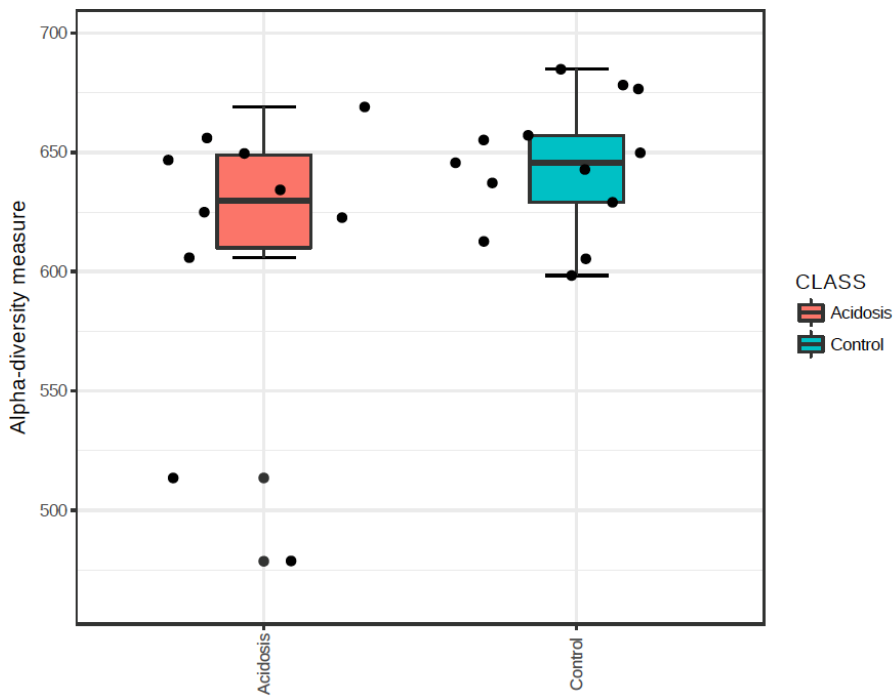
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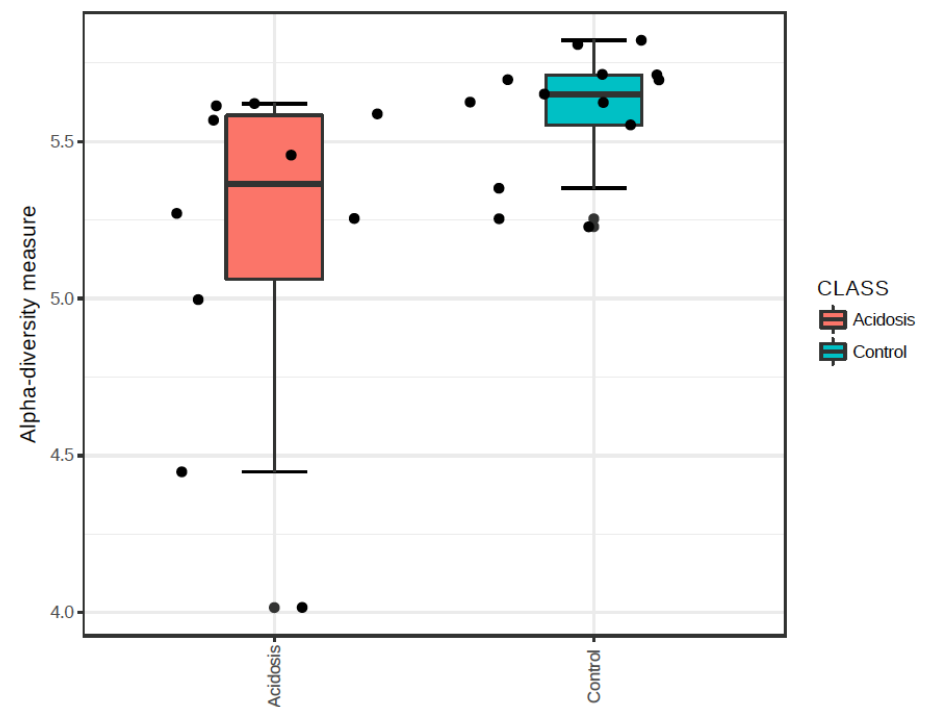
Chao 1 diversity.  
*P* value: < 0.0001



# Effects of acidosis on alpha diversity of rumen microbiota



Chao 1 diversity.  $P$  value = 0.13



Shannon diversity.  $P$  value < 0.05

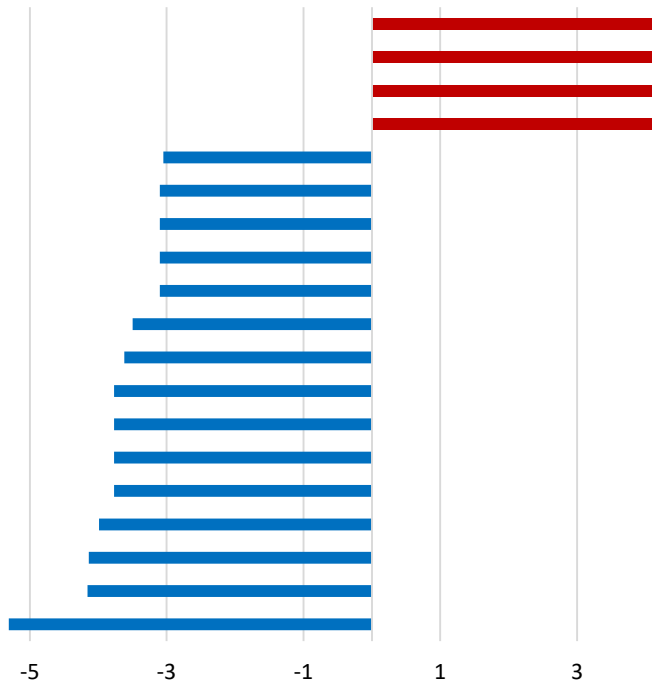


# Discriminant analysis of rumen and feces microbiota

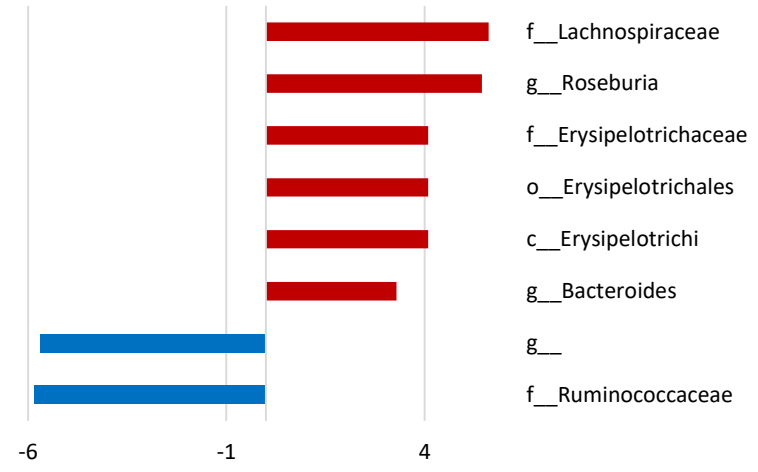
Rumen

SARA ■ Control ■

Feces



- f\_\_Bifidobacteriaceae
- o\_\_Bifidobacteriales
- c\_\_Actinobacteria
- p\_\_Actinobacteria
- g\_\_Mogibacterium
- f\_\_WCHB1\_25
- o\_\_WCHB1\_41
- c\_\_Verruco\_5
- p\_\_Verrucomicrobia
- g\_\_Selenomonas
- g\_\_CF231
- f\_\_F16
- o\_\_CW040
- c\_\_TM7\_3
- p\_\_TM7
- f\_\_Christensenellaceae
- f\_\_Paraprevotellaceae
- p\_\_SR1
- f\_\_



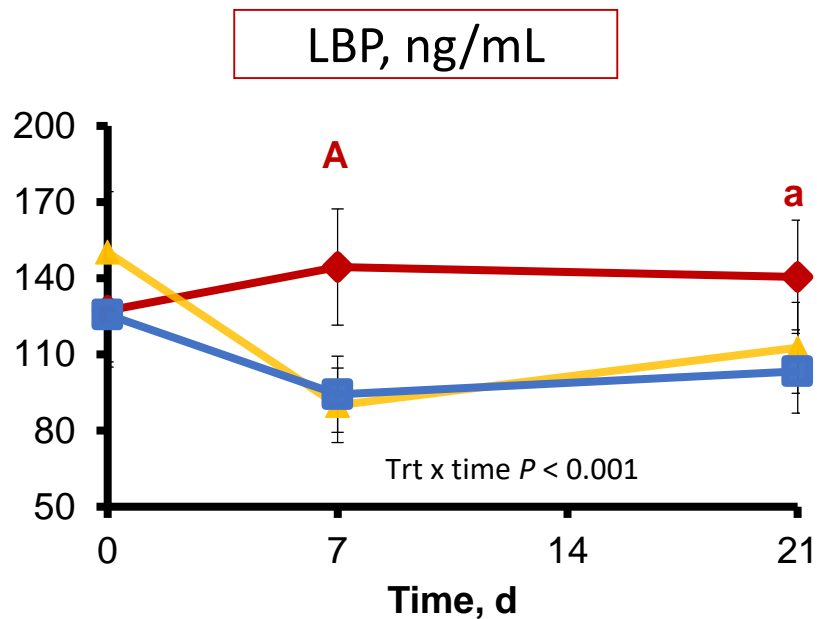
LDA score, Log 10

LDA score, Log 10

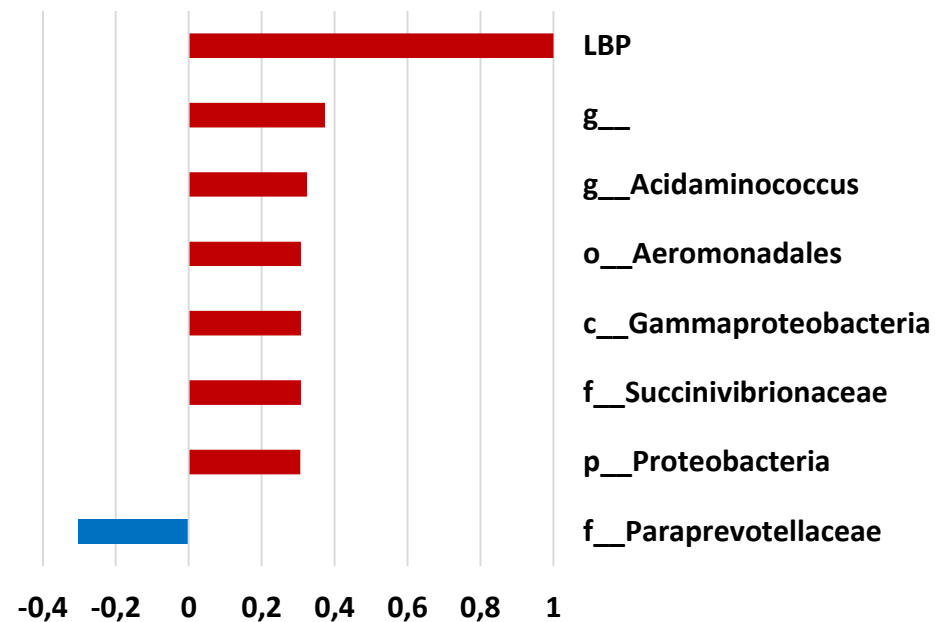


# Lipopolysaccharide binding protein and gut microbiota

SARA ◆ Recovery ▲ Control ■



## LBP and rumen microbiota

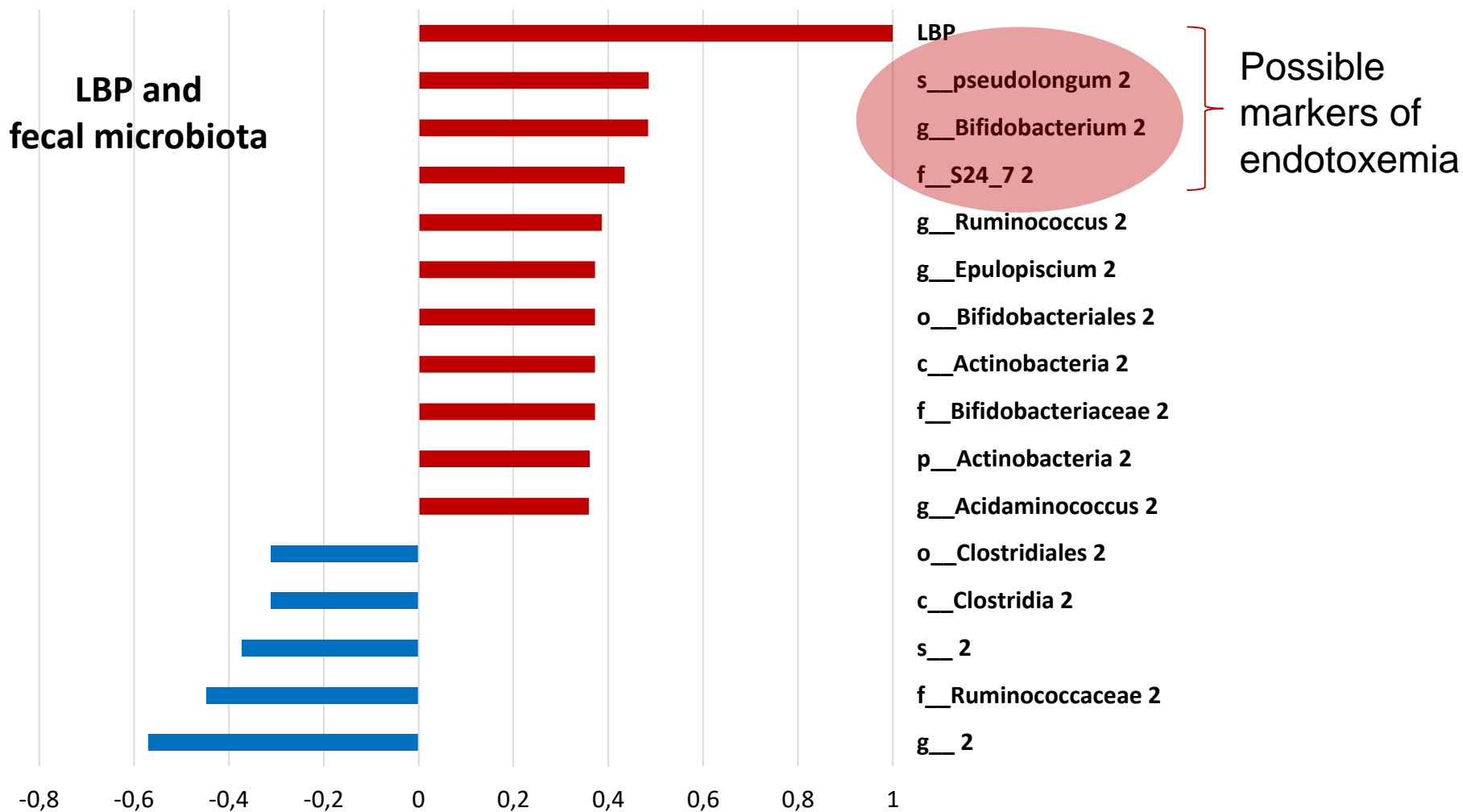


**No effects detected on plasma cytokines:**

IFN $\alpha$ , IFN $\gamma$ , IL-13, IL-1 $\alpha$ , IL-1 F5, IL-21, IP-10, MIG, MIP-1 $\beta$ , and TNF $\alpha$

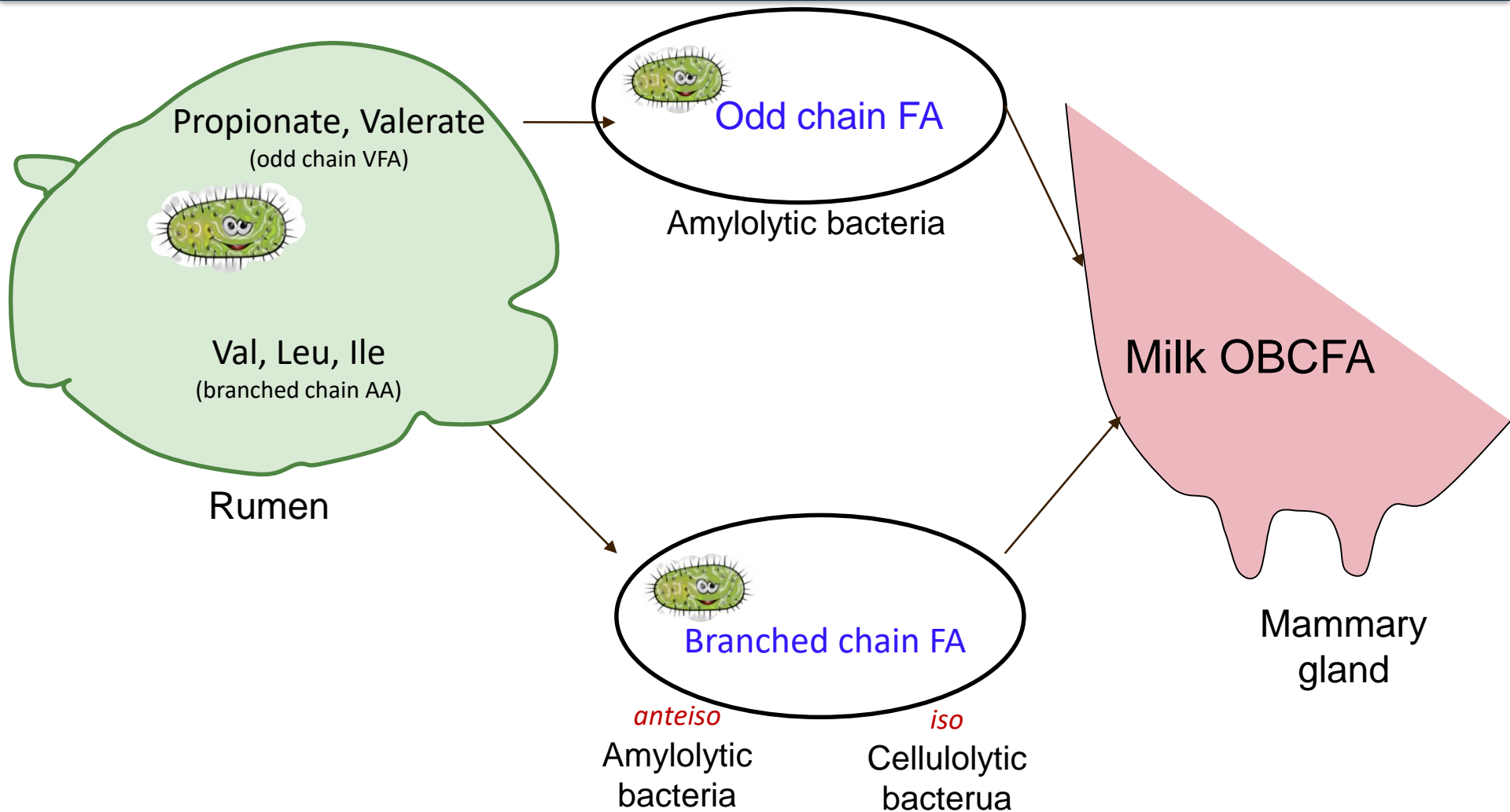


# Lipopolysaccharide binding protein and gut microbiota





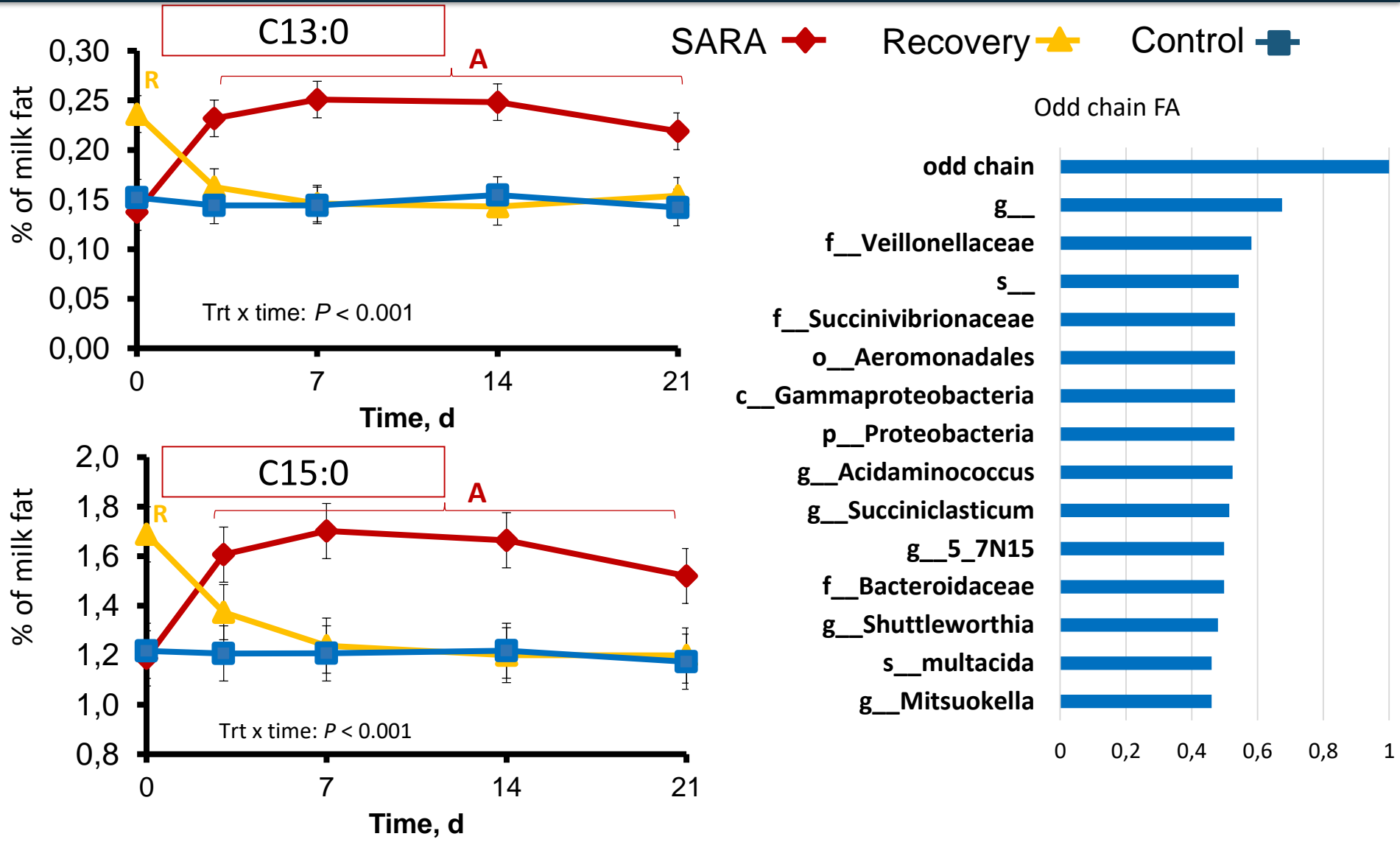
# Odd and branched chain fatty acids





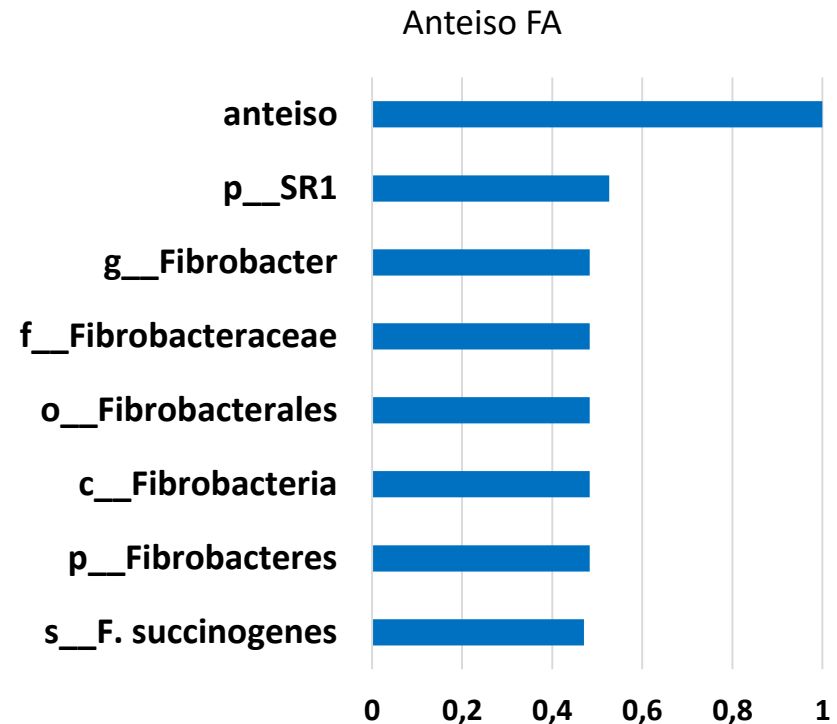
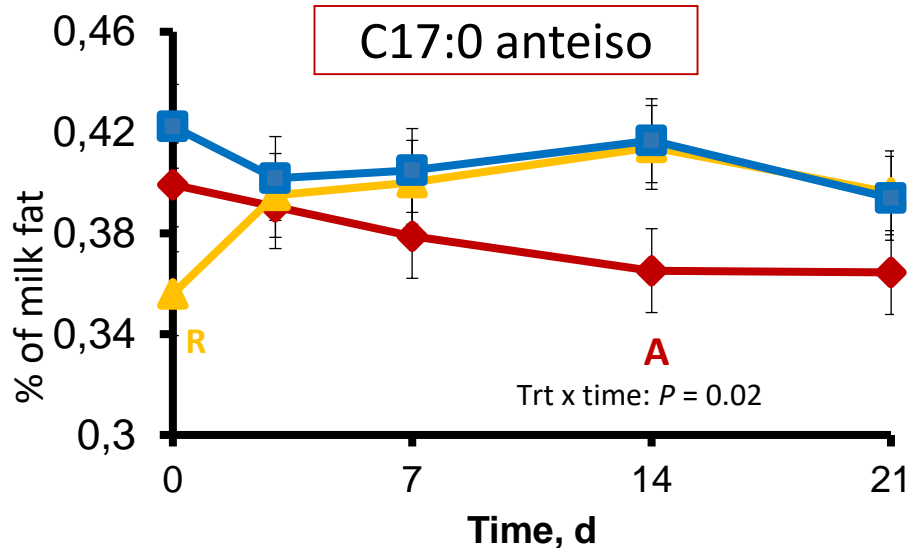
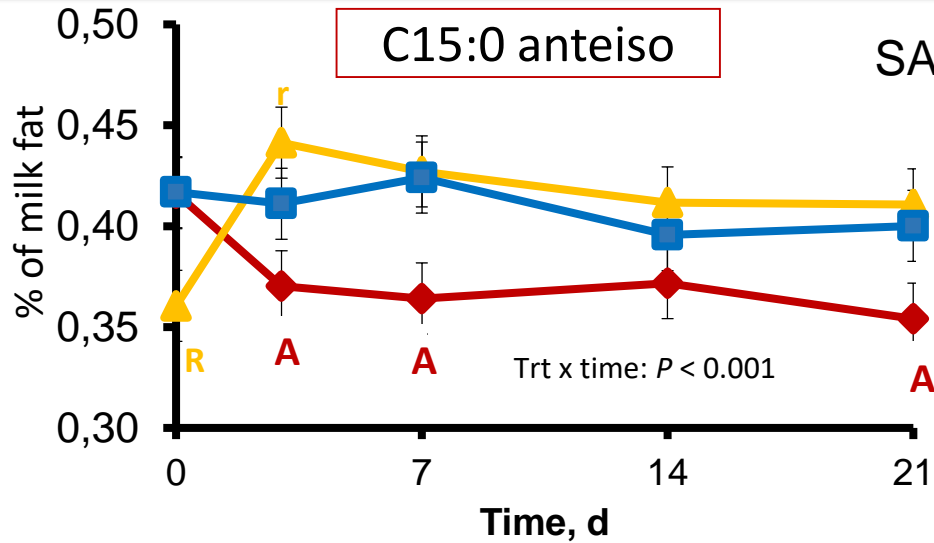


# Odd chain fatty acids and rumen microbiota



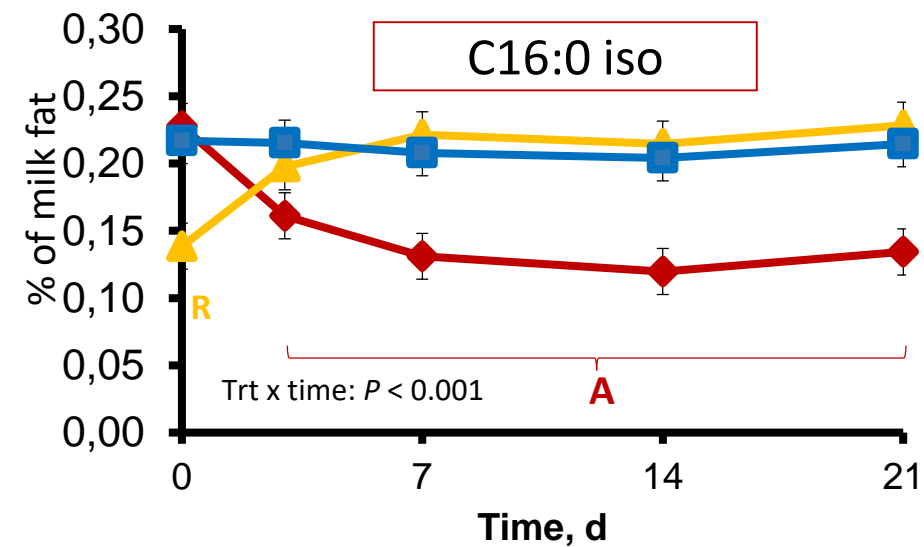
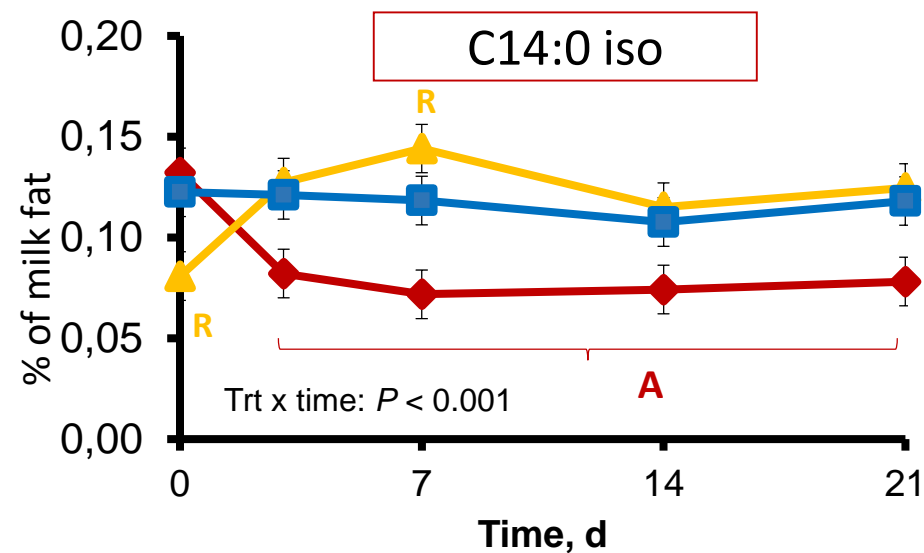


# Branched chain fatty acids (anteiso) and rumen microbiota

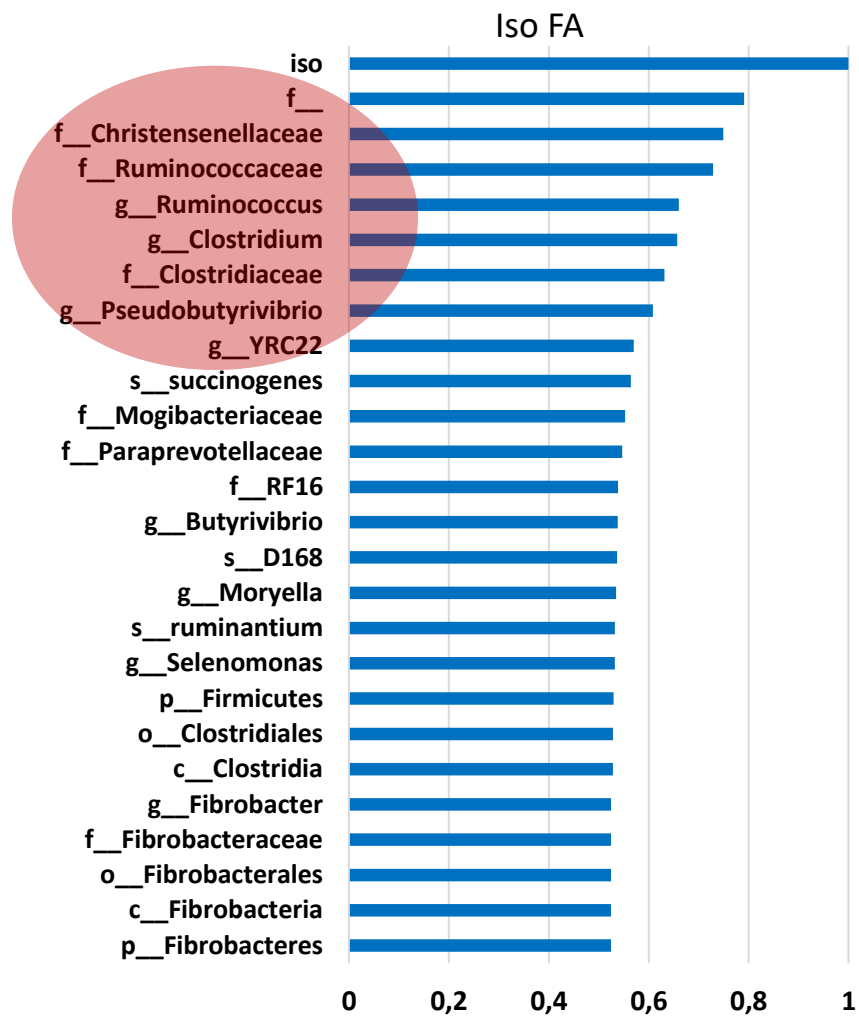




# Branched chain fatty acids (iso) and rumen microbiota



SARA Recovery Control





# Conclusions

- Induction of SARA resulted in a rapid and transient reduction in milk fat synthesis, which was not strongly associated with ruminal biohydrogenation .
- Milk odd and branched fatty acids closely followed acidosis.
- Ruminal and fecal microbiota were affected by SARA and may be used as predictors of observed responses.

An aerial photograph of a large farm or research facility. The complex consists of numerous buildings, including several large white barns with green roofs, smaller green and white structures, and a central brick house with a red roof. The buildings are situated on a green lawn with scattered trees, some showing autumn foliage. In the foreground, there is a dirt road and a fenced-in area. The background features a wide, calm body of water, likely a lake or a large river, under a clear blue sky. The overall scene is peaceful and well-maintained.

Thanks!

# Questions?

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CRSAD, Deschambault, QC, Canada



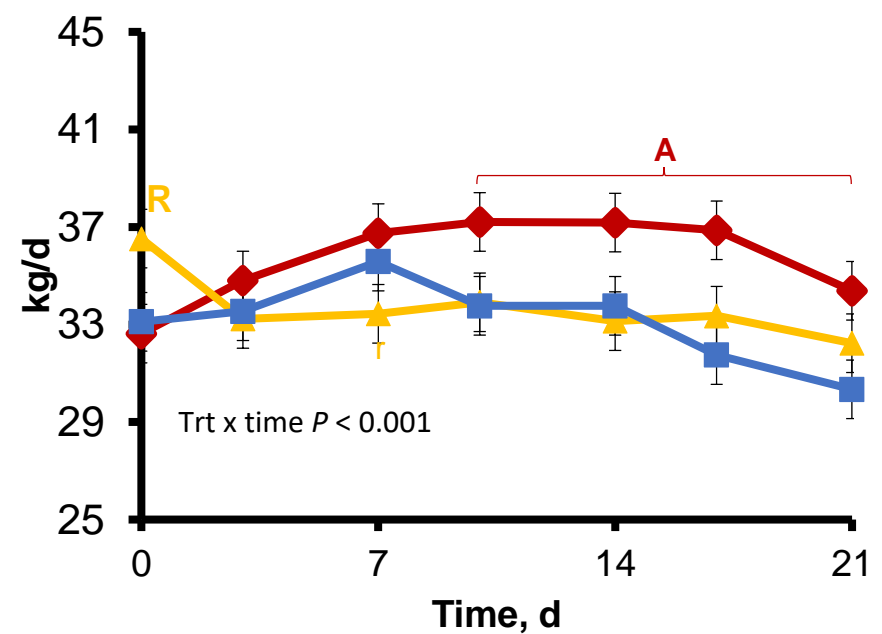
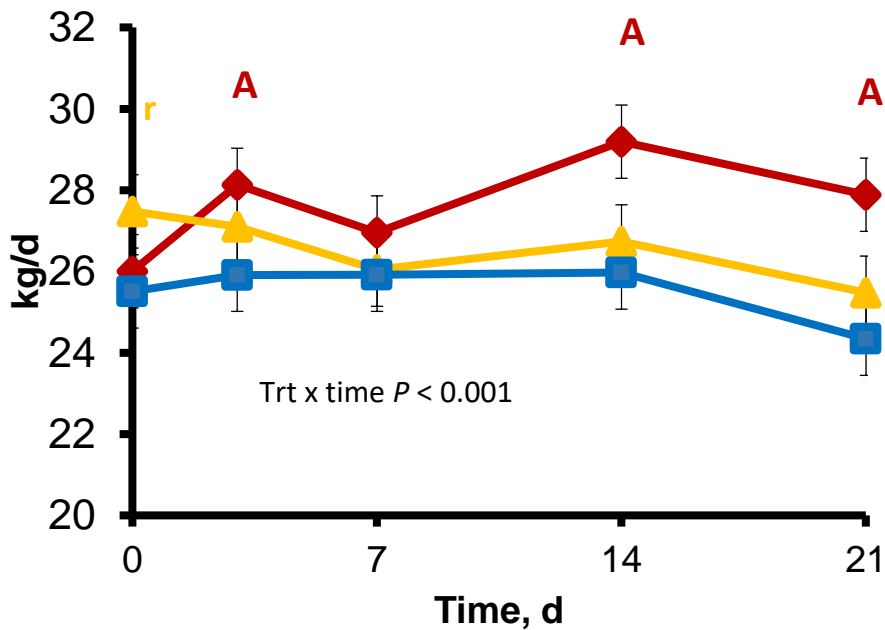


# Dry matter intake and milk yield

SARA ◆ Recovery ▲ Control ■

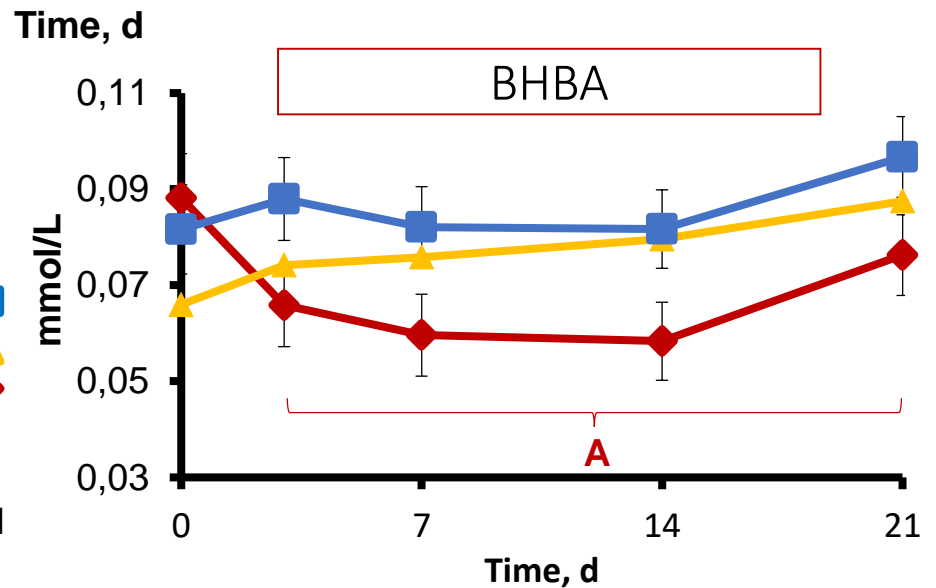
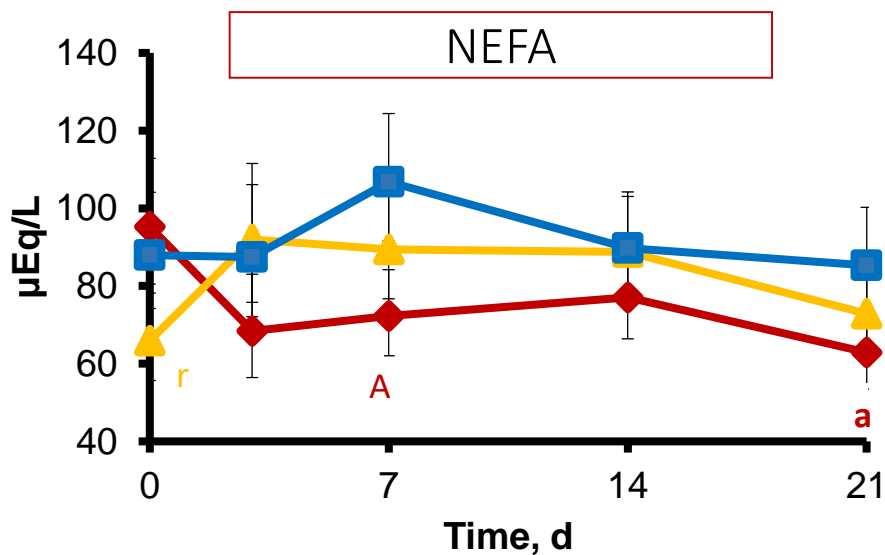
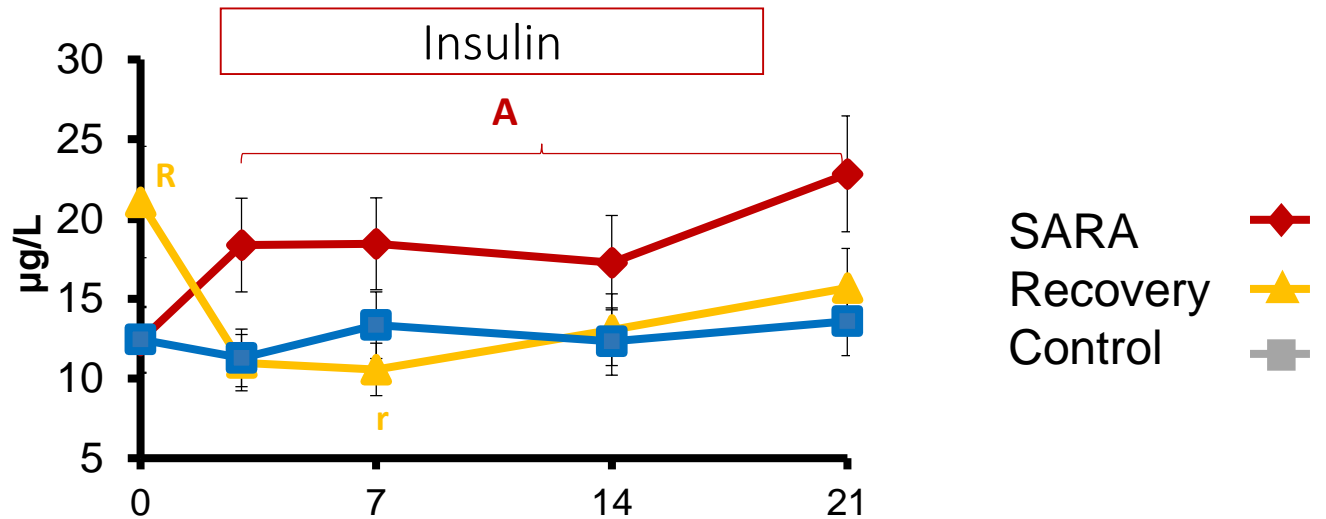
Dry matter intake

Milk yield





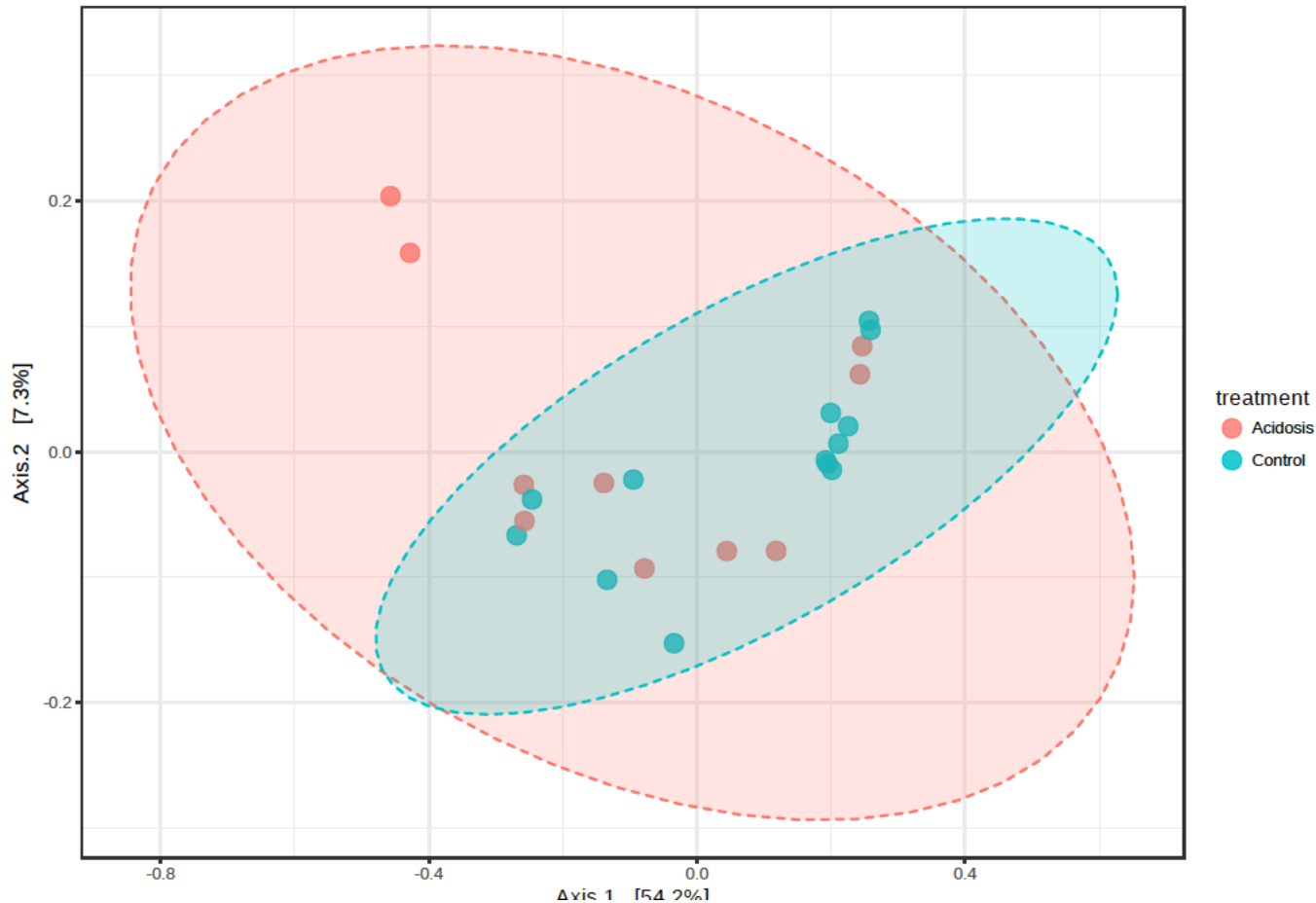
# Plasma insulin, NEFA and milk BHBA







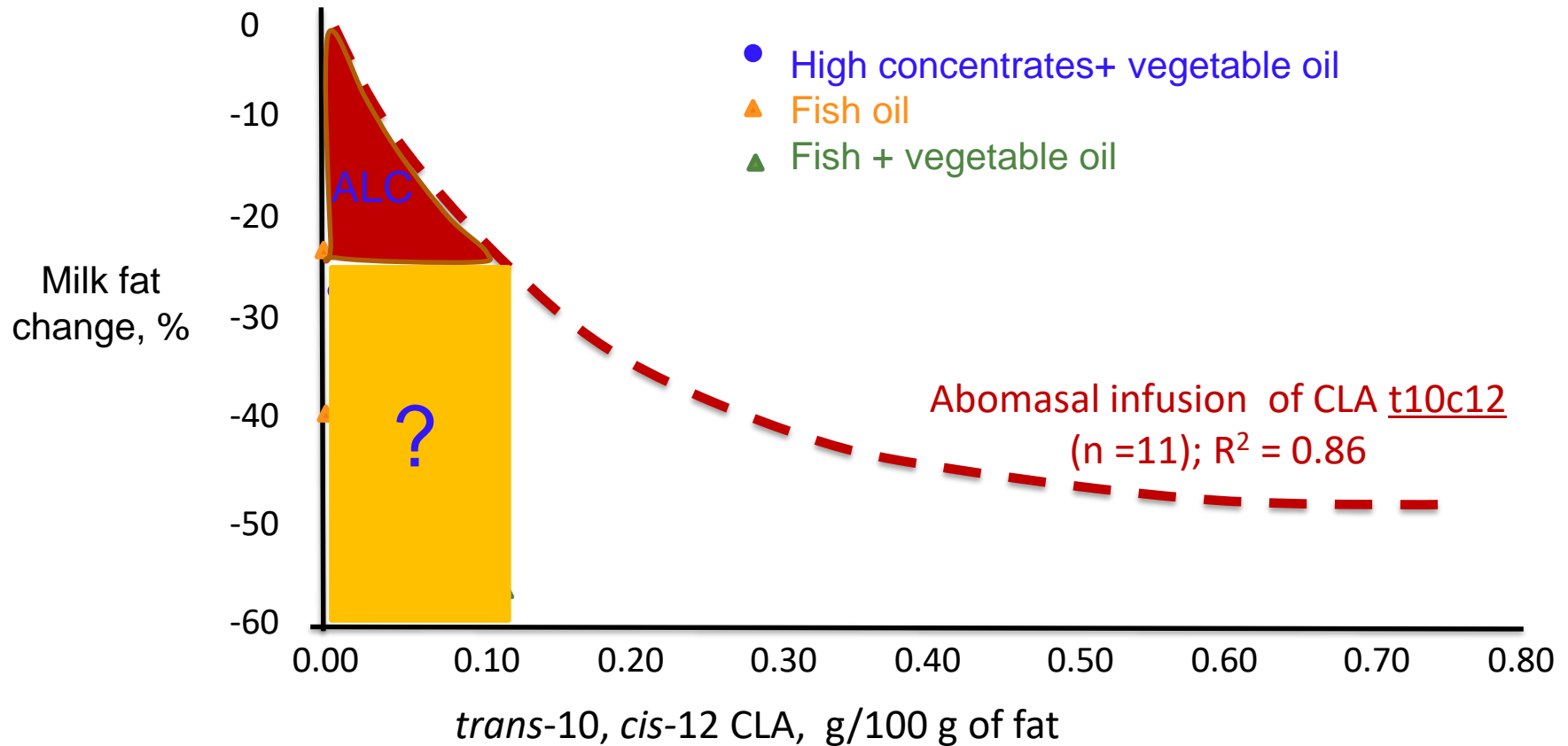
# Effects of acidosis on rumen OTU Beta diversity



**[PERMANOVA] R-squared: 0.11; p-value < 0.057**



# Prediction of milk fat using *trans*-10, *cis*-12 (CLA)



Adapted from Shingfield and Griinari, 2007



# Acidosis and inflammation

