Time course of changes in lactation performance, blood metabolites, inflammation and milk fatty acids during subacute ruminal acidosis induction and recovery in dairy cows

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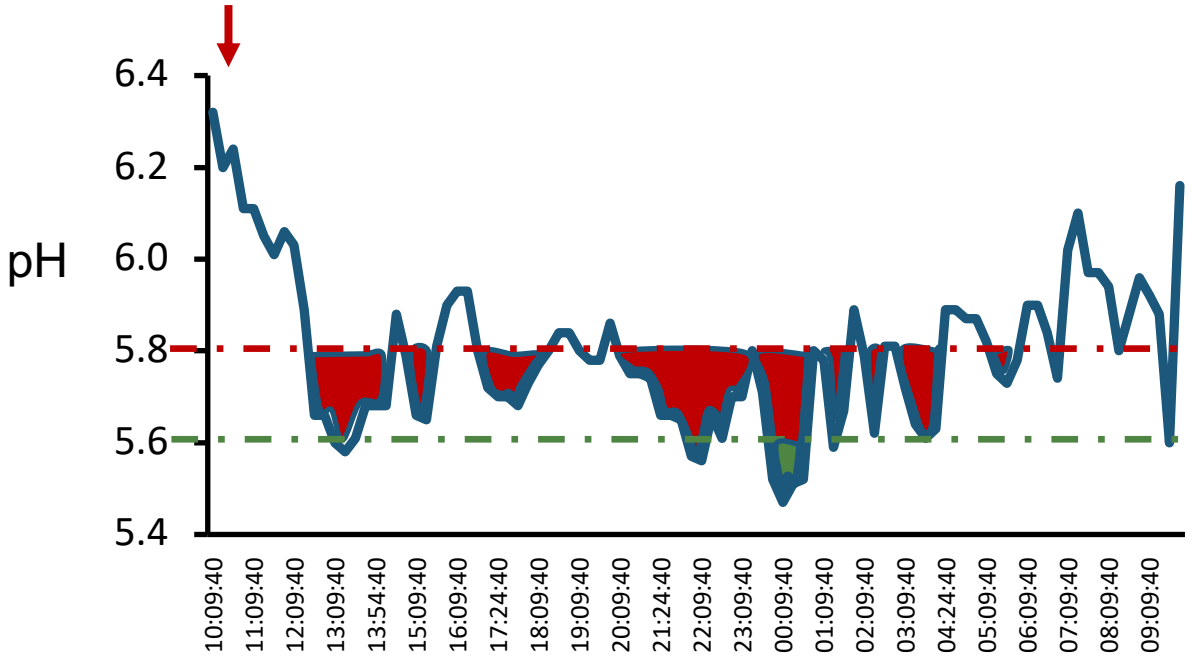
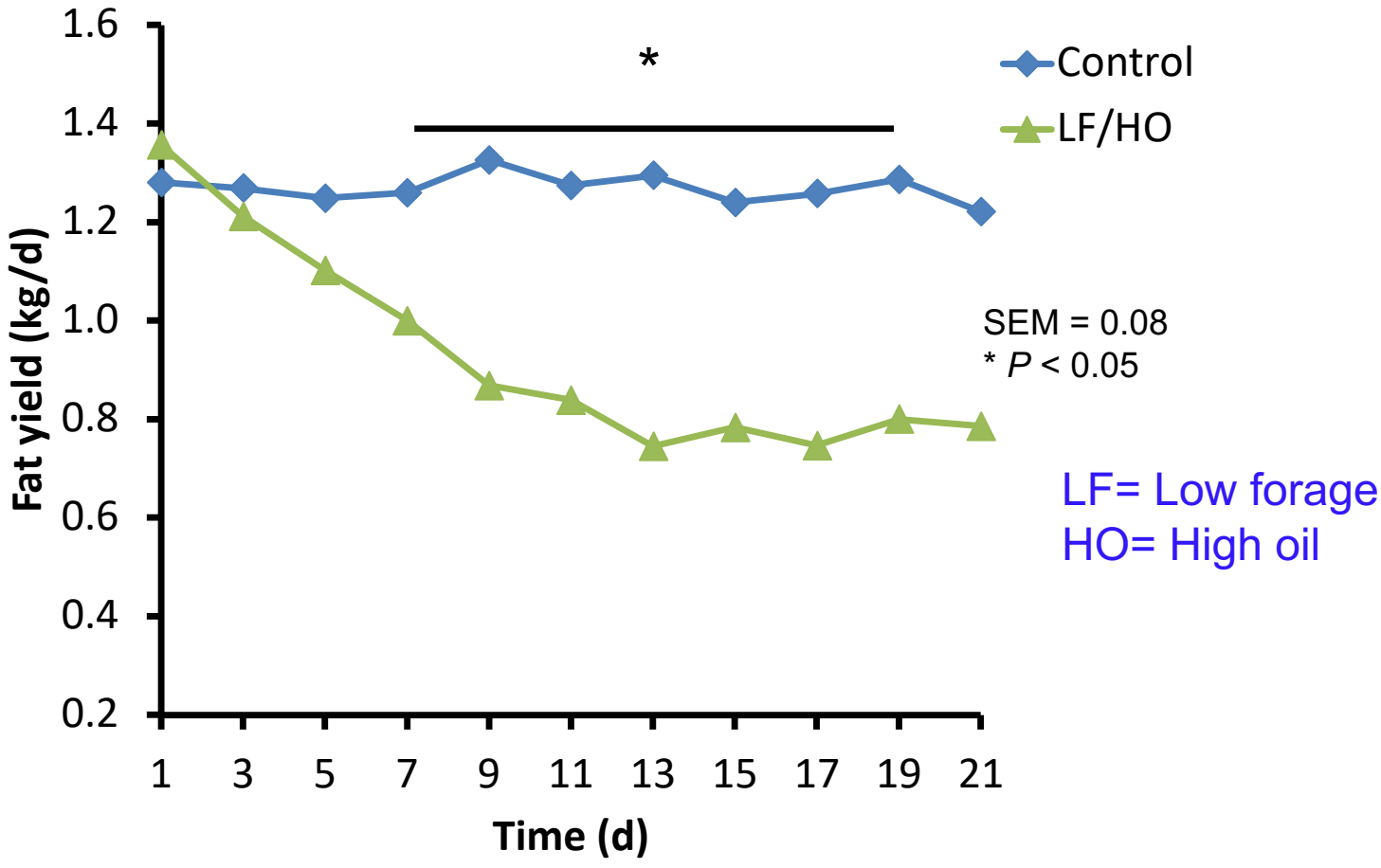
Subacute ruminal acidosis



Sometimes accompanied by milk fat depression (MFD)

1) Time below pH 5.6 > 180 min (Gozho et al., 2005; Castillo-Lopez et al., 2004)
2) Time in acidosis + systemic inflammation (Khafipour et al., 2012). pH 5.6 > 180 min + increase in acute phase proteins

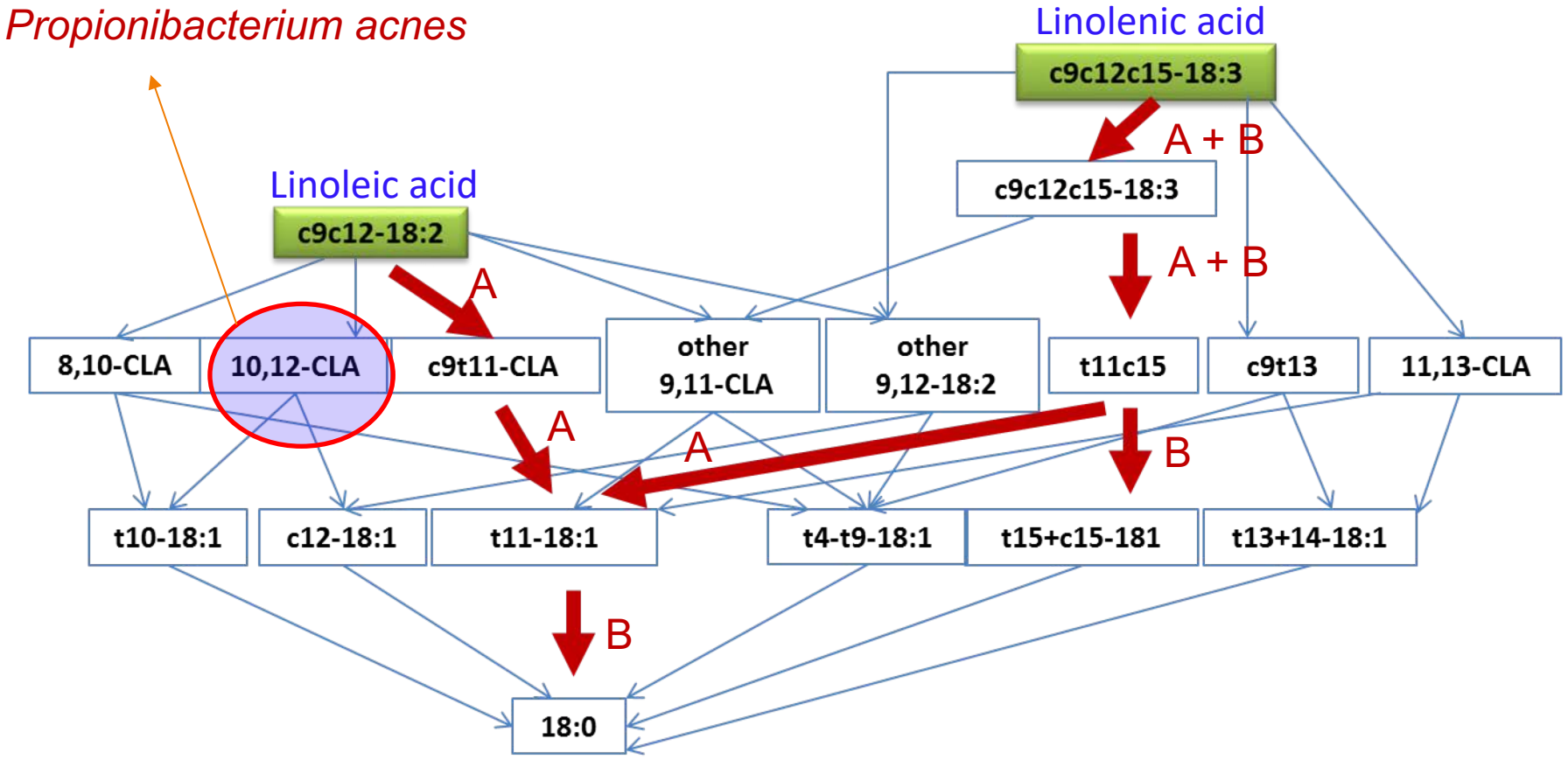
Progressive MFD under High PUFA-low fiber diets



LF= Low forage
HO= High oil

Rico and Harvatine, 2013

Ruminal biohydrogenation of PUFA

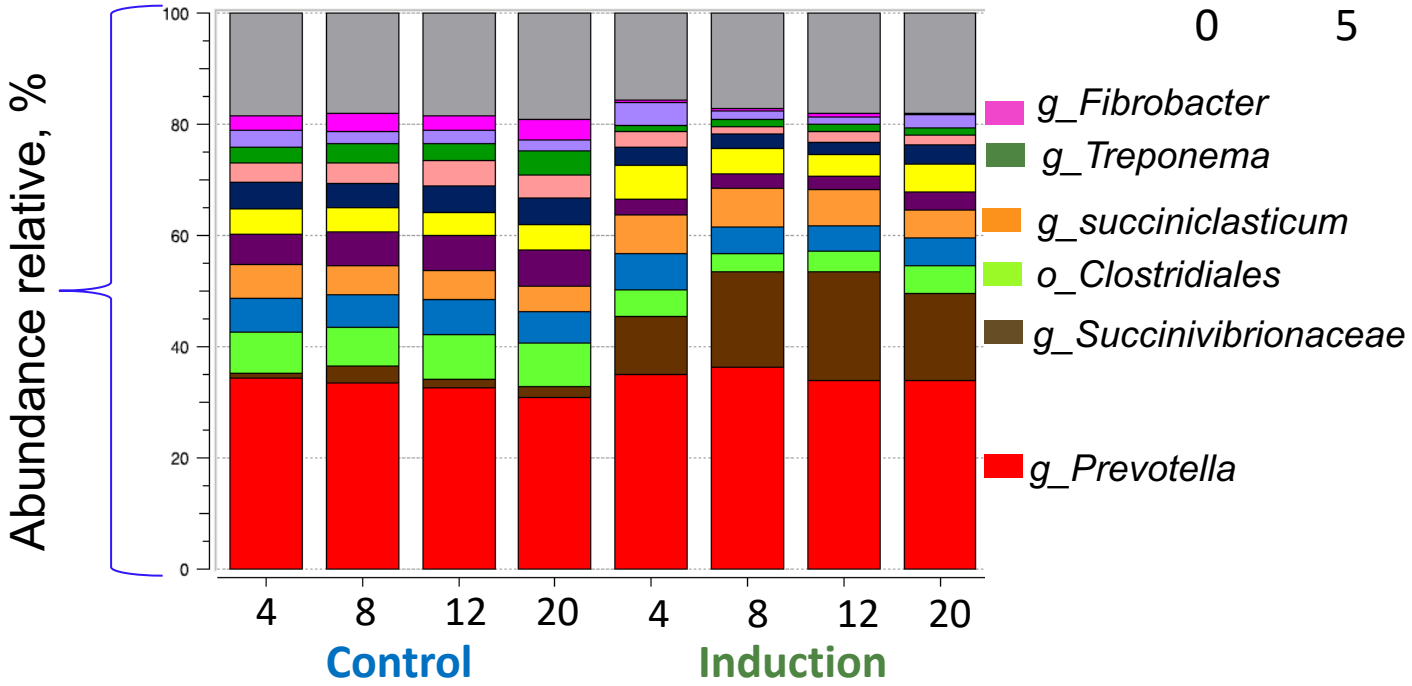


*Group A B

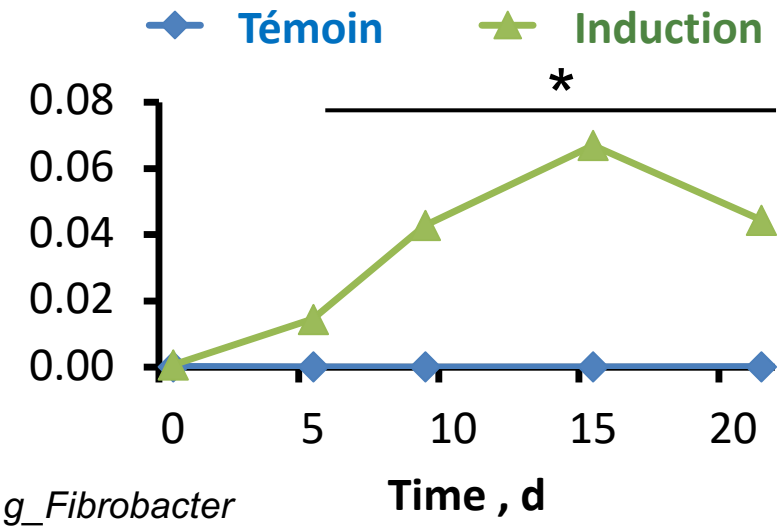
Hartfoot and Hazlewood, 1997

Lourenço et al., 2010

Microbiota transformation during BH induced MFD



trans-10, cis-12, CLA, %



16S rRNA sequencing

UNIVERSITY OF MANITOBA

Azad et al., 2015

Odd and branched chain fatty acids

Propionate, Valerate
(odd chain VFA)

Val, Leu, Ile
(branched chain AA)

Rumen

Odd chain FA

Amylolytic bacteria

Milk OBCFA

Mammary gland

Branched chain FA

anteiso

Amylolytic bacteria

iso

Cellulolytic bacterua

Vlæminck *et al.* 2005
Fievez *et al.* 2012

Materials and Methods

Twelve ruminally cannulated cows (120 ± 52 DIM; 35.5 ± 8.9 kg of milk/d; mean ± 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

Experimental sampling on d 0, 3, 7, 10, 14, 17, and 21 of each period.

$$Y_{ijk} = \mu + C_i + P_j + T_k + D_l + T_k*D_l + e_{ijkl}$$

Where:

- μ = Overall mean
- C_i = Random effect of cow
- P_j = Random effect of period
- T_k = Treatment
- D_l = Day
- e_{ijk} = Residual error

Preplanned contrasts:

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

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

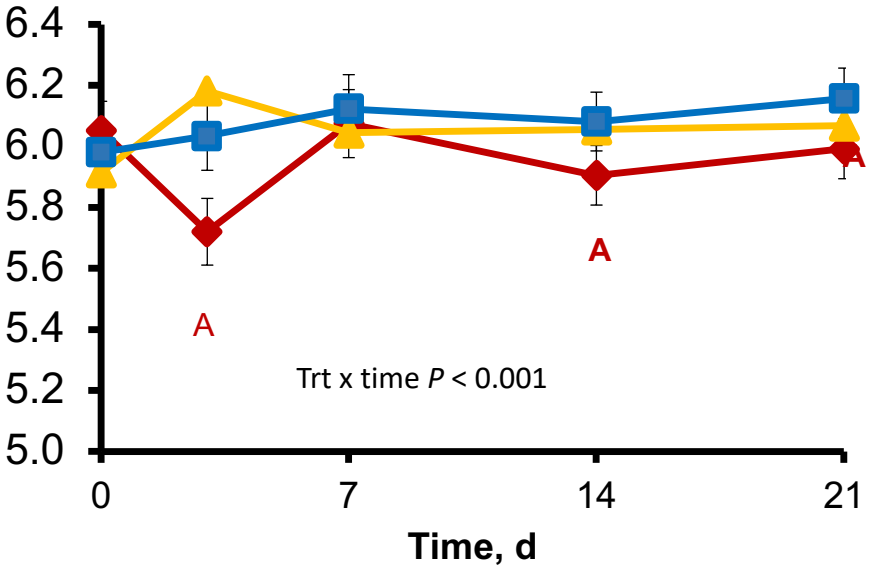
at each time point

Ruminal pH

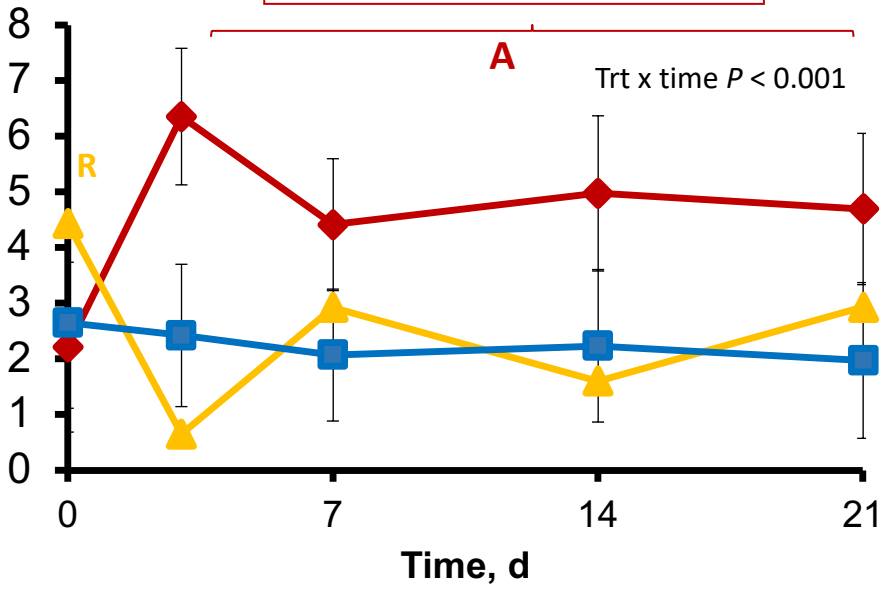
Ecow, UK

SARA Recovery Control

Mean rumen pH



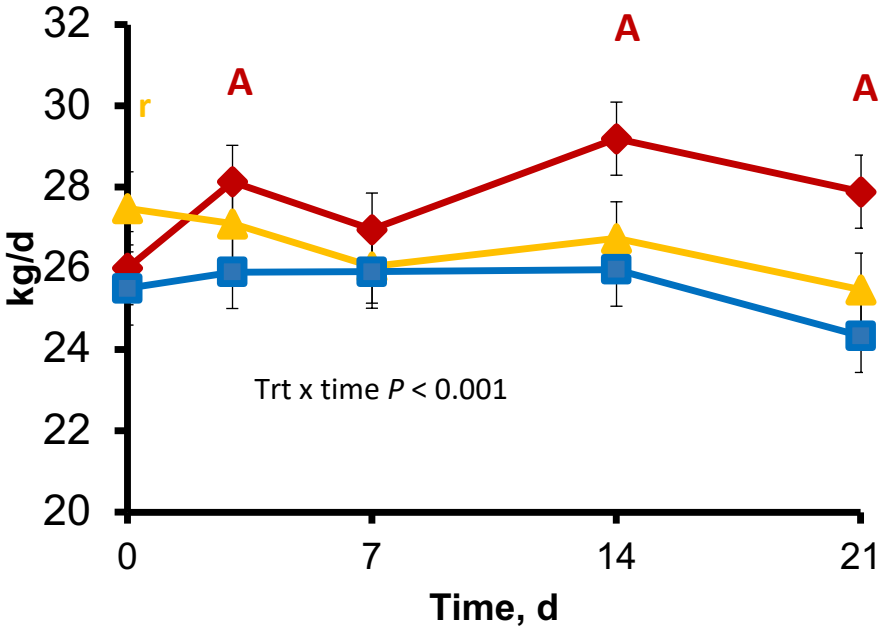
Time below 5.6, h/d



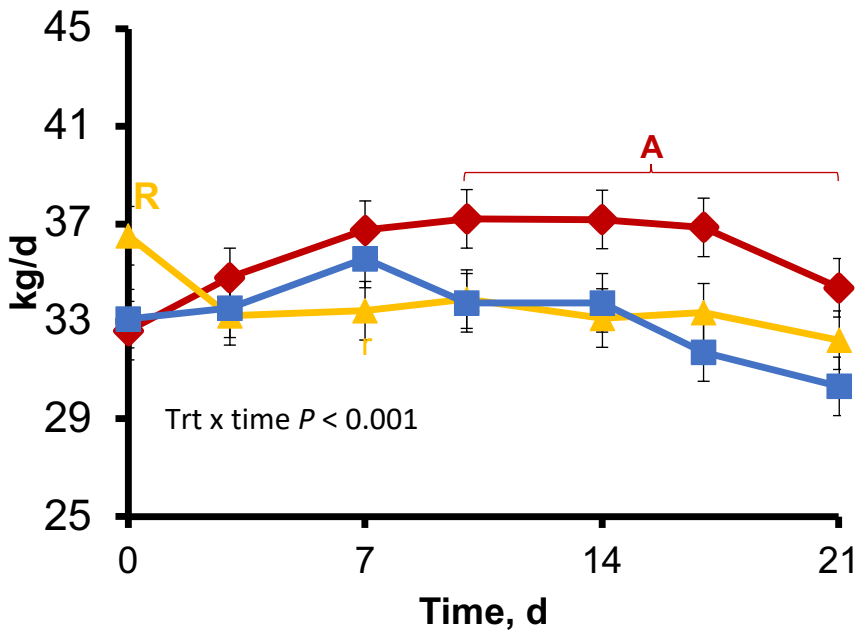
Dry matter intake and milk yield

SARA Recovery Control

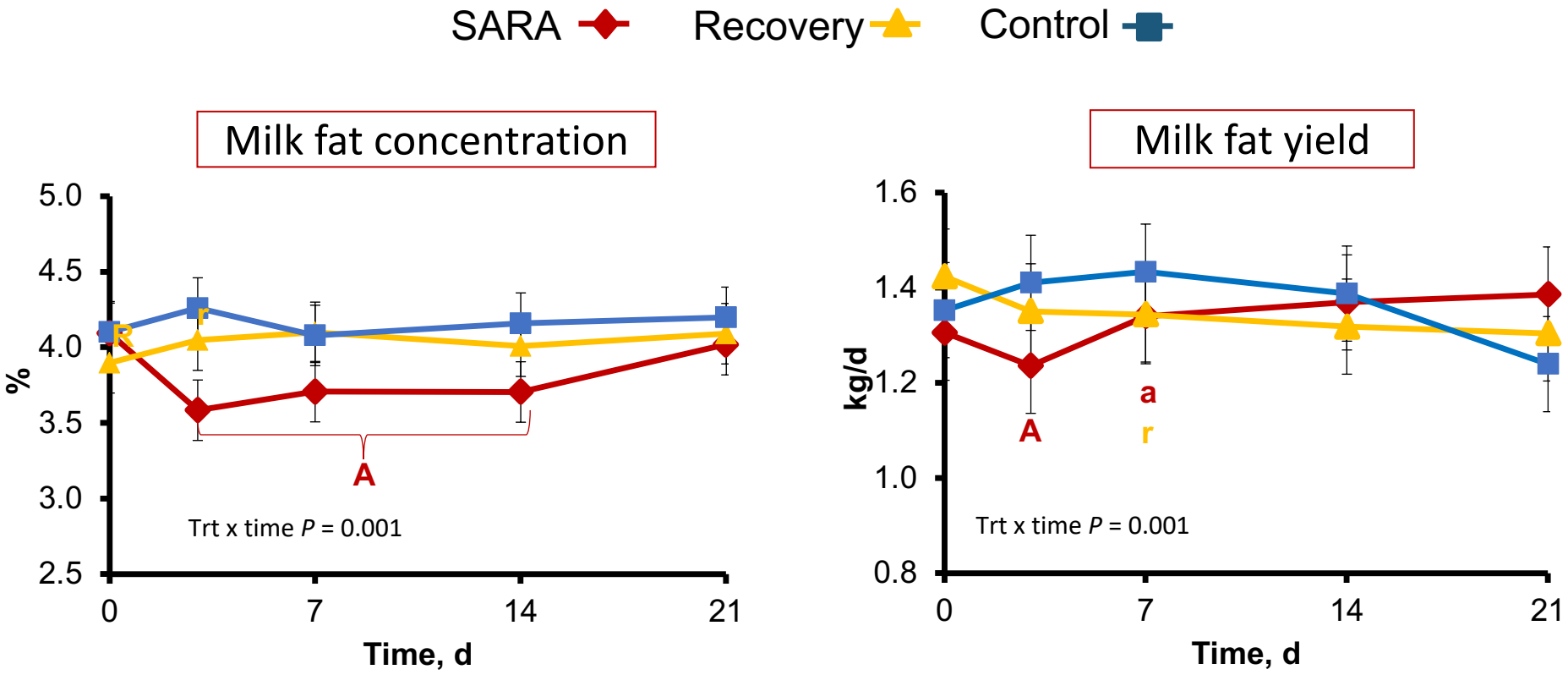
Dry matter intake



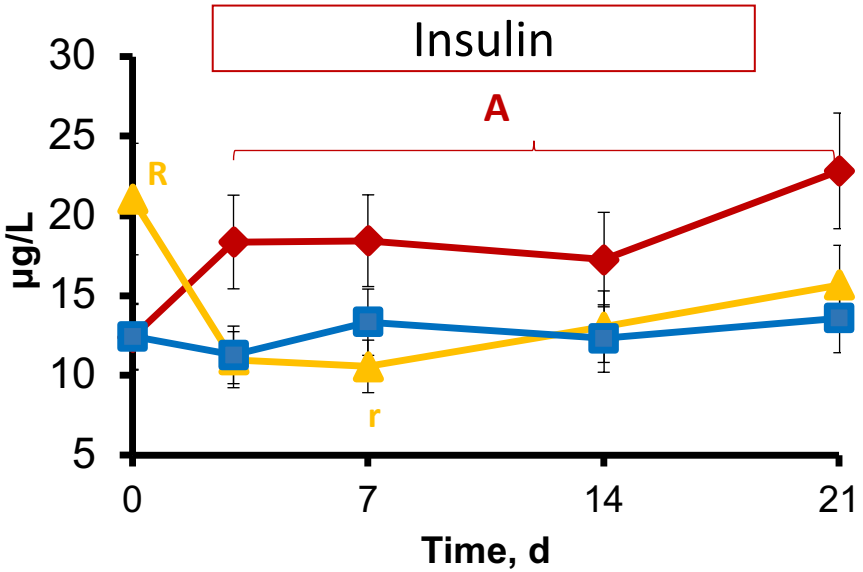
Milk yield



Milk fat synthesis

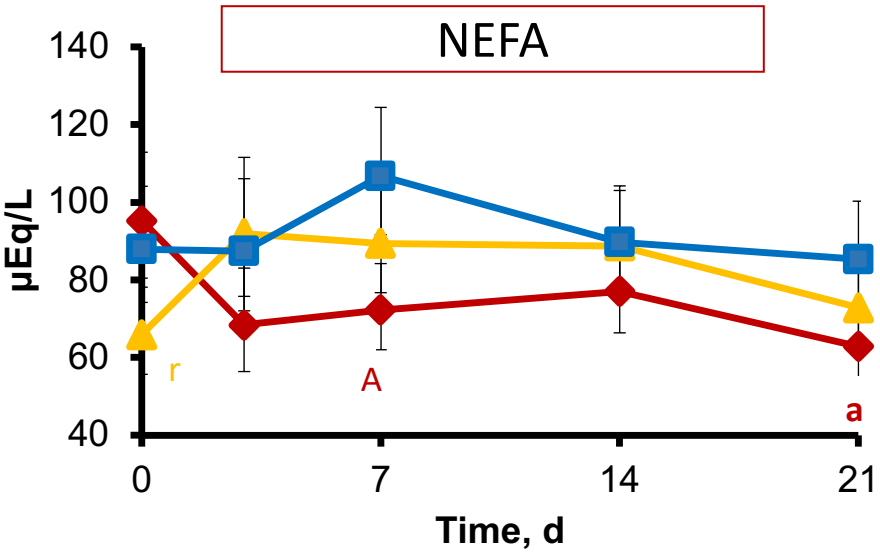


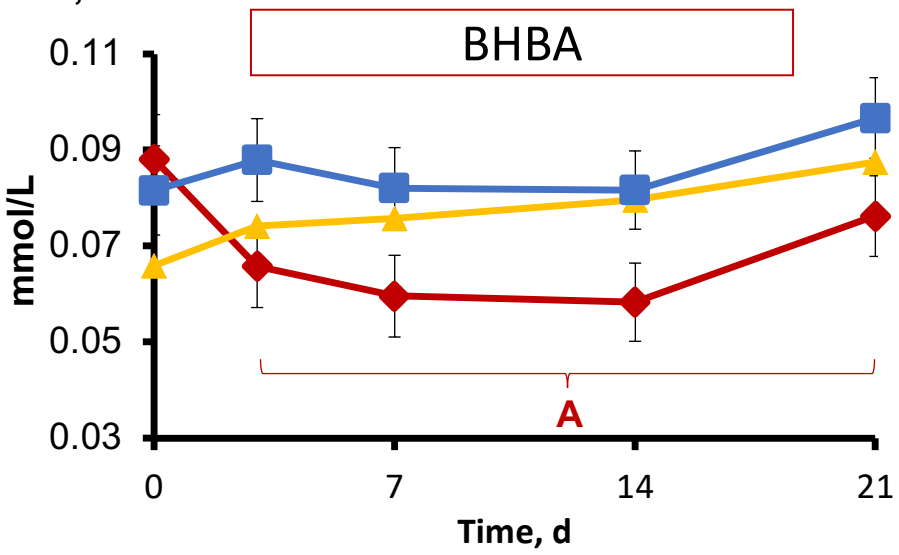
Plasma insulin, NEFA and milk BHBA



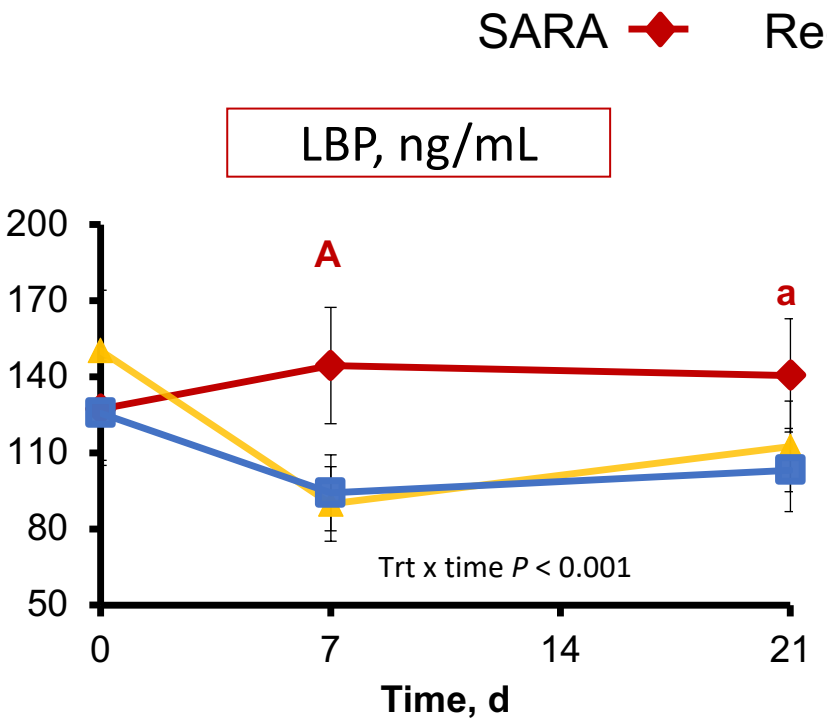
SARA
Recovery
Control

All Trt x time *P* = 0.001





Immune response



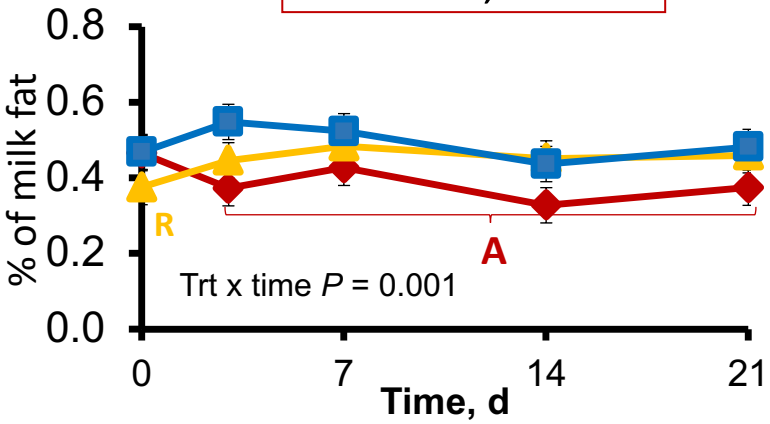
No effects detected on plasma cytokines:

IFNα, IFNγ, IL-13, IL-1α, IL-1 F5, IL-21, IP-10, MIG, MIP-1β, and TNFα

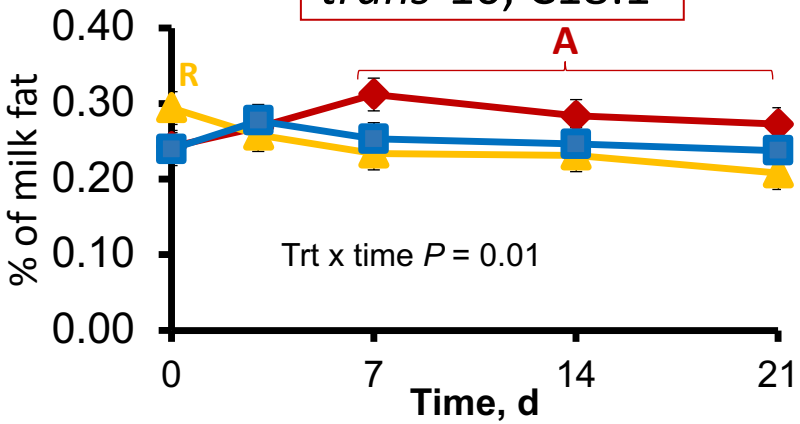
Biohydrogenation pathways

SARA Recovery Control

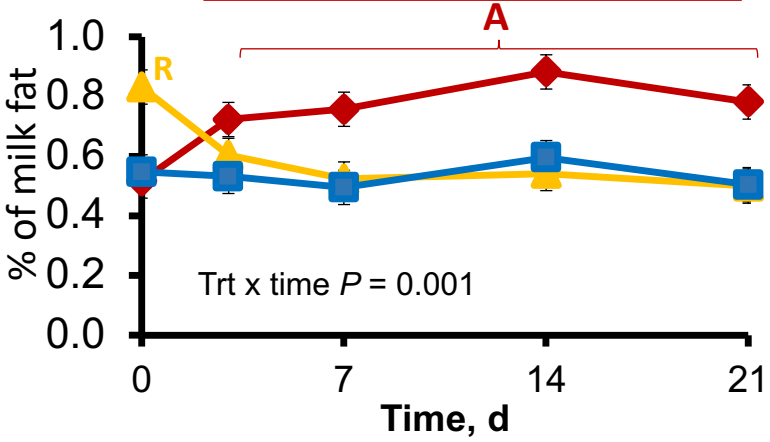
trans-11, C18:1



trans-10, C18:1



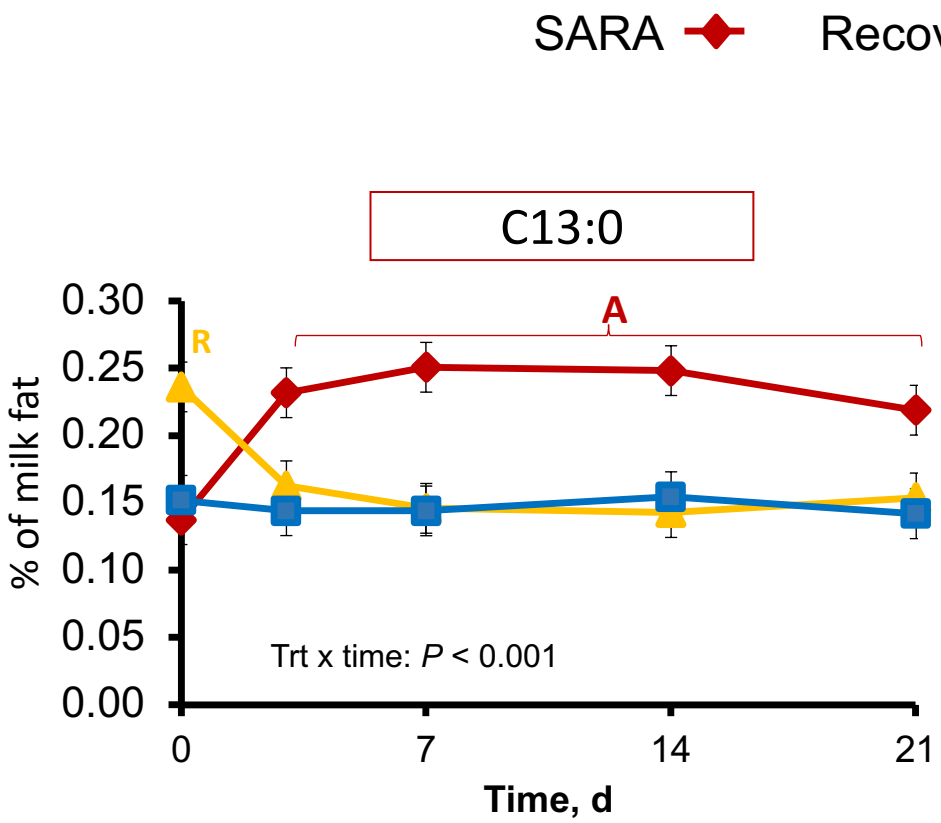
trans-10/trans-11 ratio

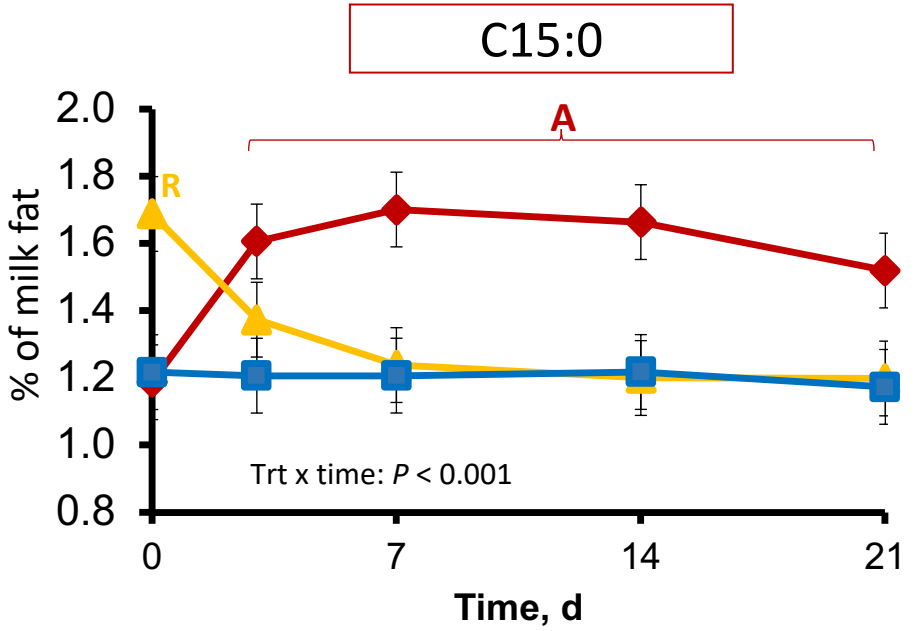


trans-10, *cis*-12 CLA not detected

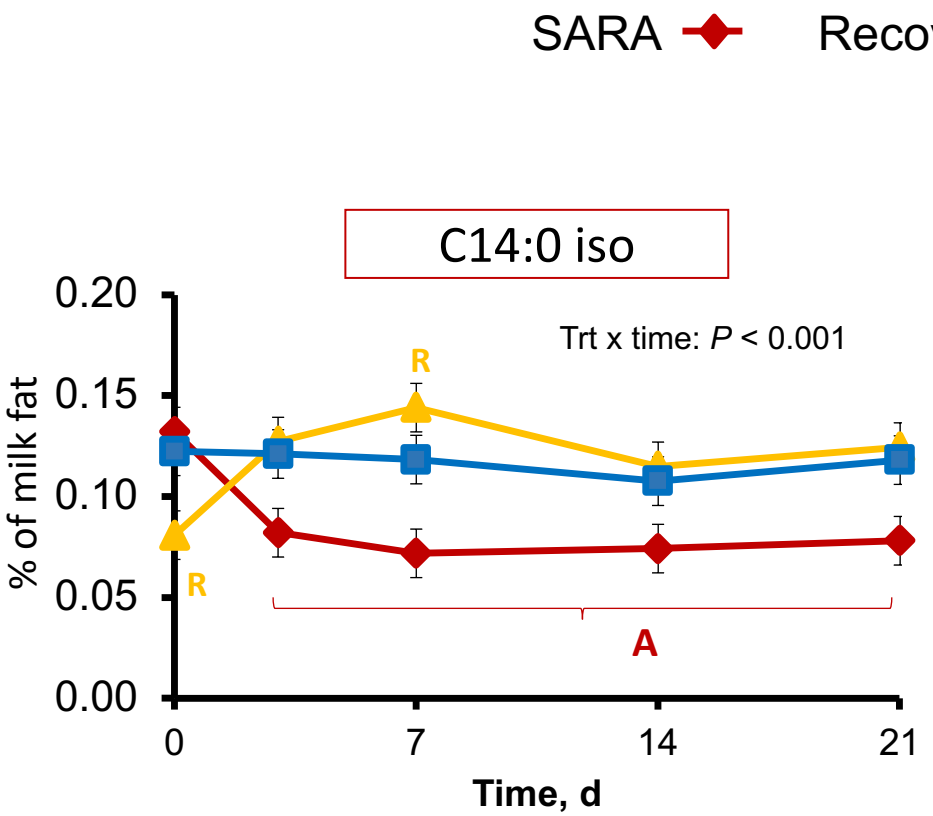
Gama-proteobacteria were associated with the *trans*-10/*trans*-11 ratio (r=0.70)

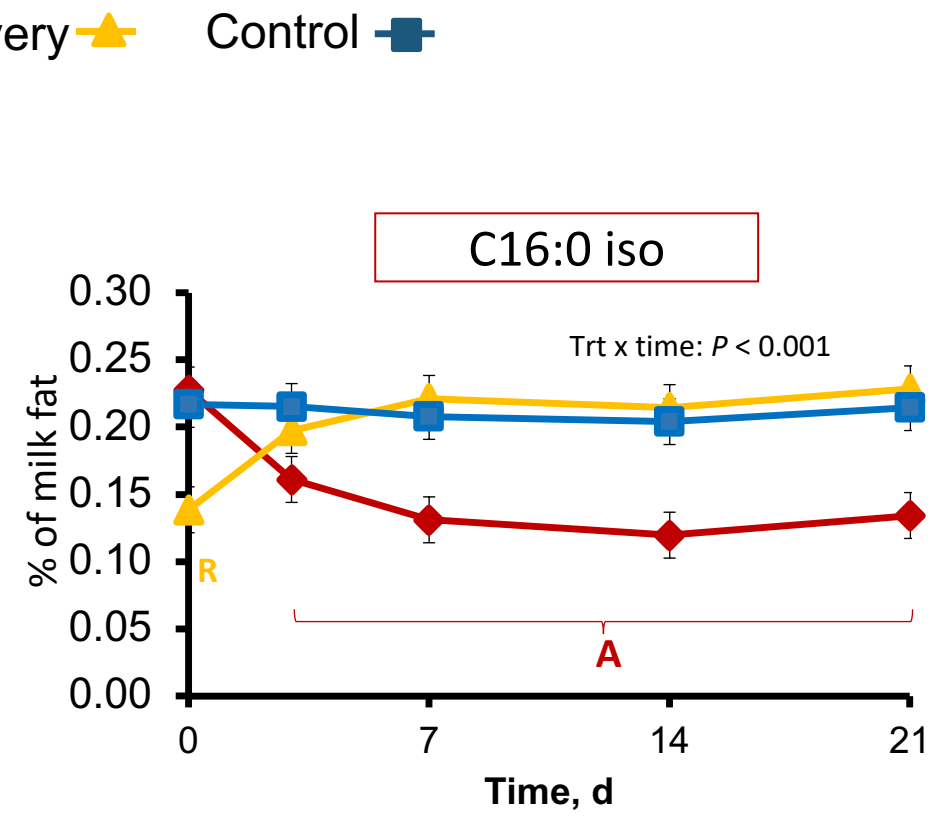
Odd chain fatty acids



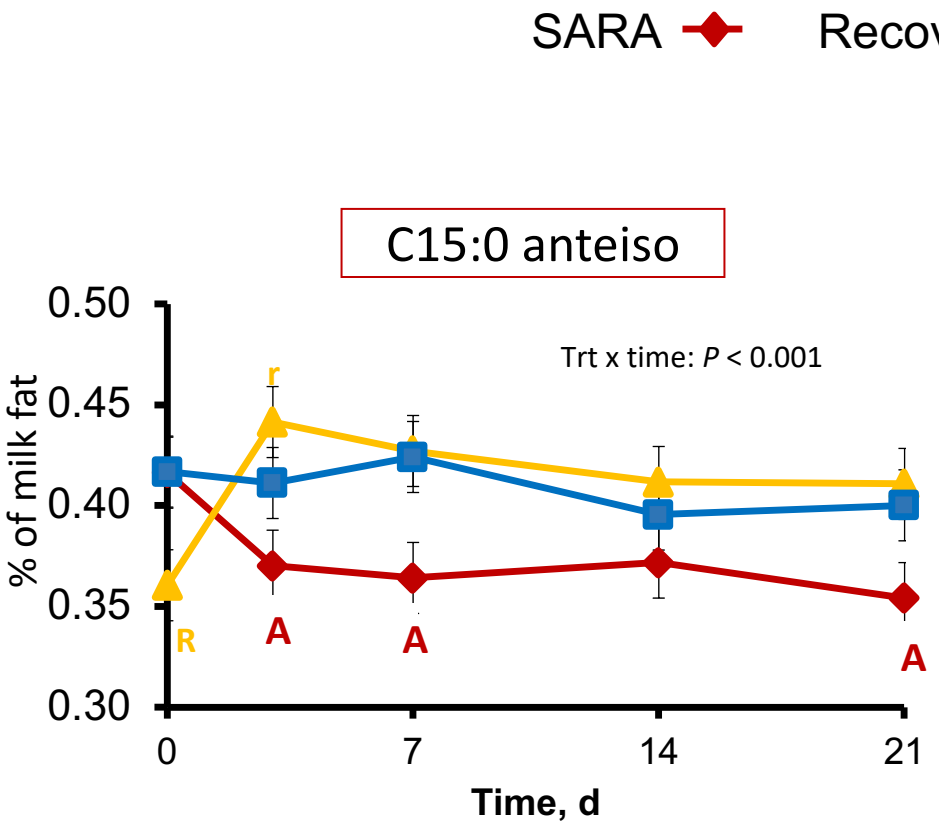


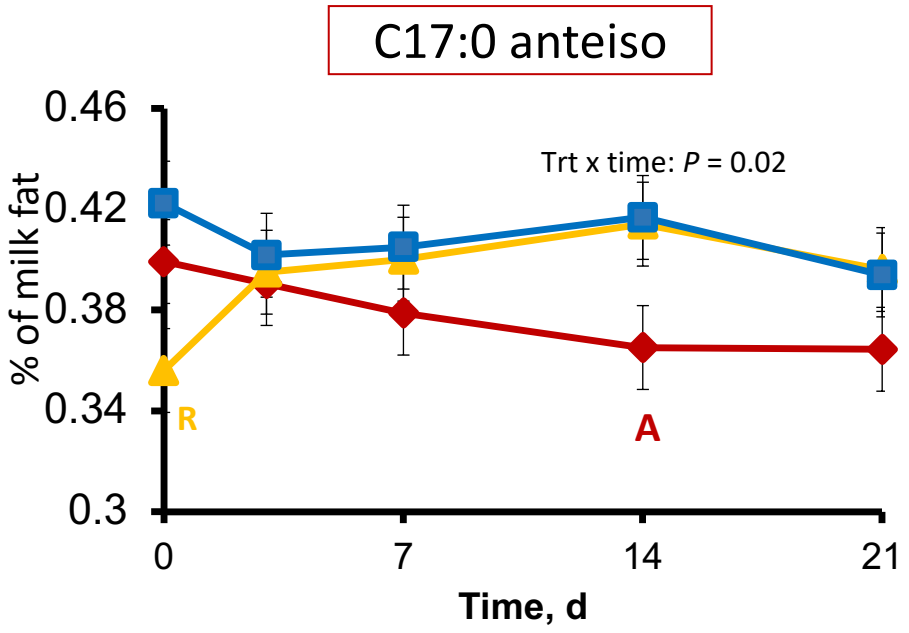
Branched chain fatty acids (iso)



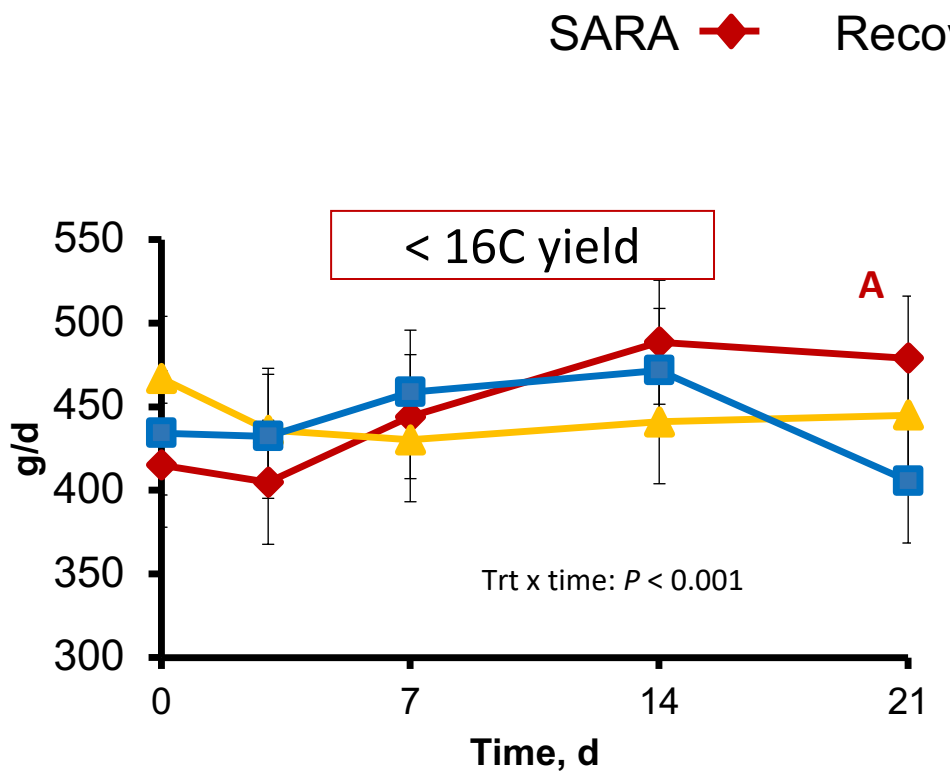


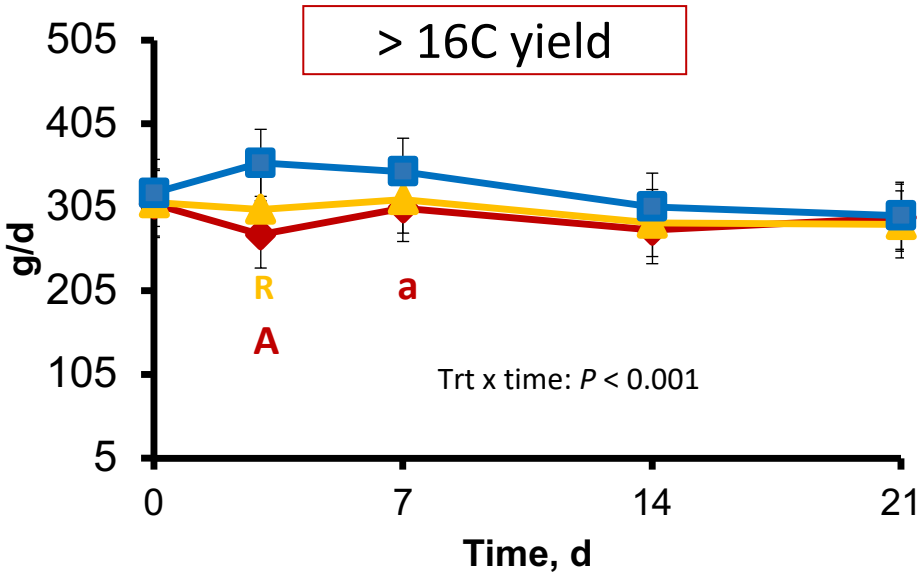
Branched chain fatty acids (anteiso)





Branched chain fatty acids (anteiso)





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. Changes detected in *iso* and *anteiso* fatty acids by d 3 of diet switch.
- Potential to develop models for early prediction of SARA by indirect methods.


Thanks!
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