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Feeding dairy ewes with a diet containing agri-food co-products: Implications on rumen metabolism

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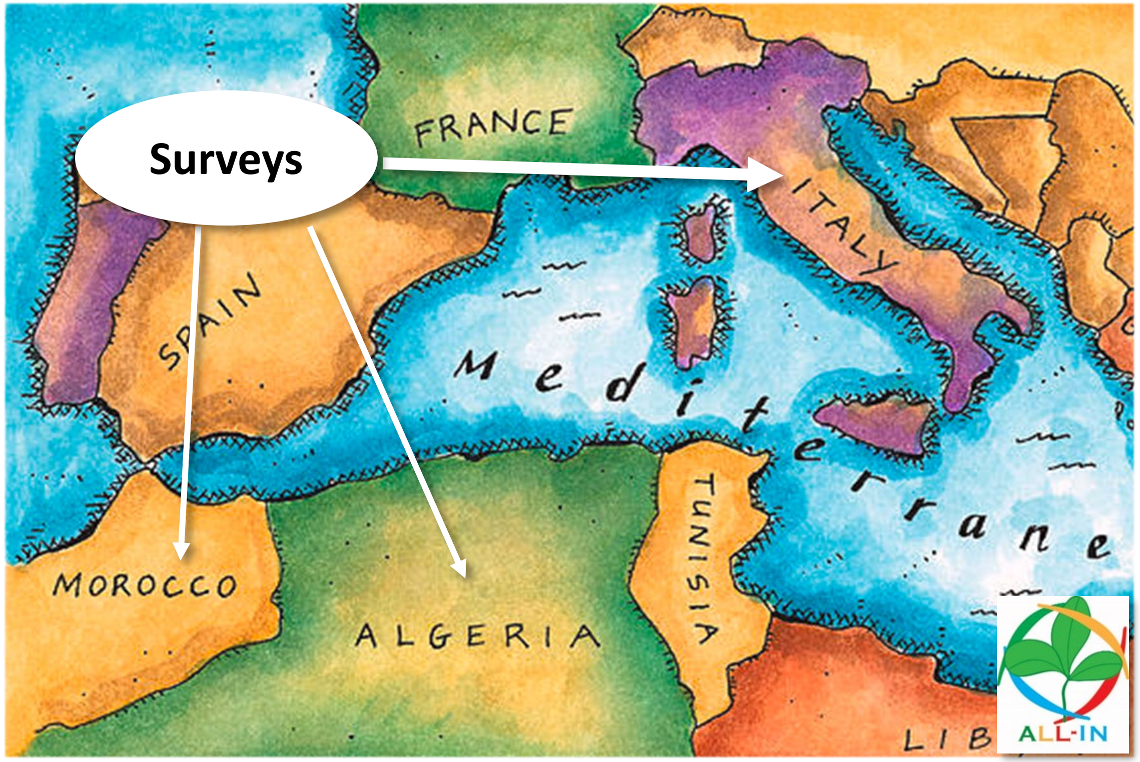
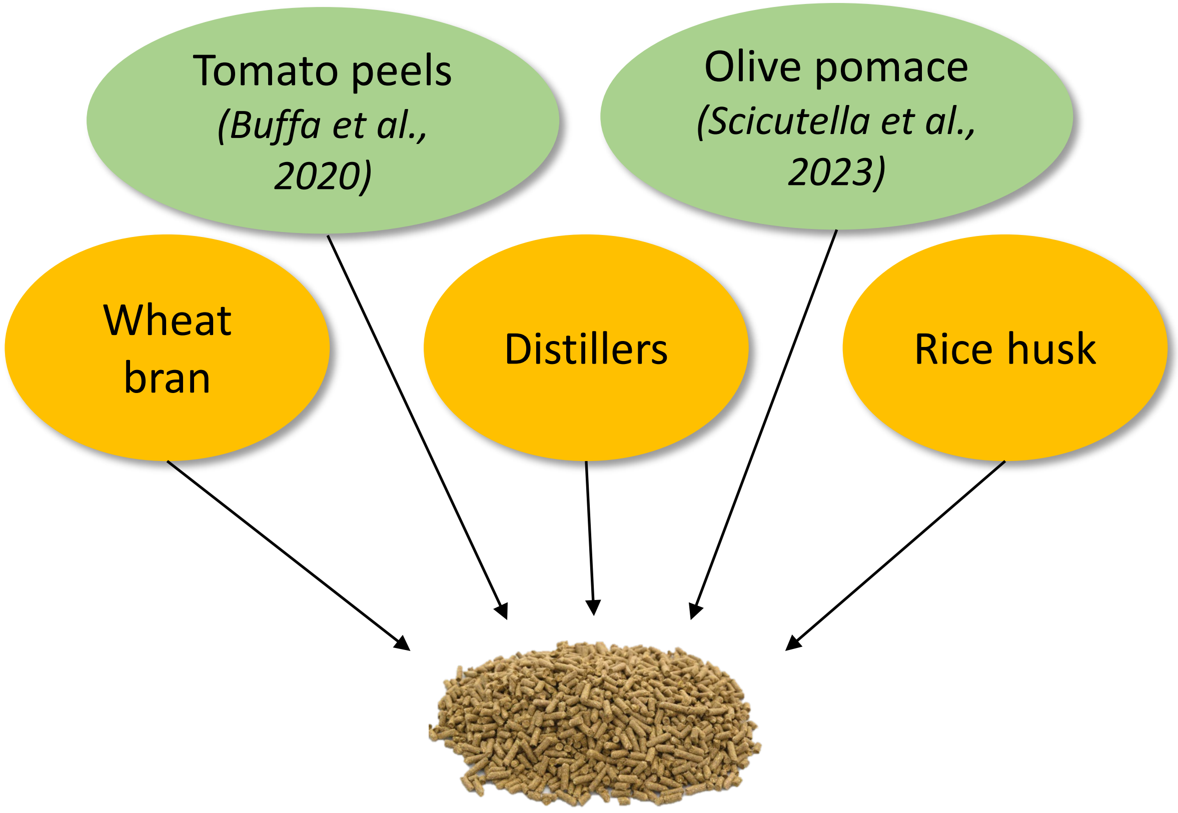
Pisa Livestock farming, Animal food quality, and Sustainability

Introduction

Can selected by- and co-products replace conventional feedstuffs?





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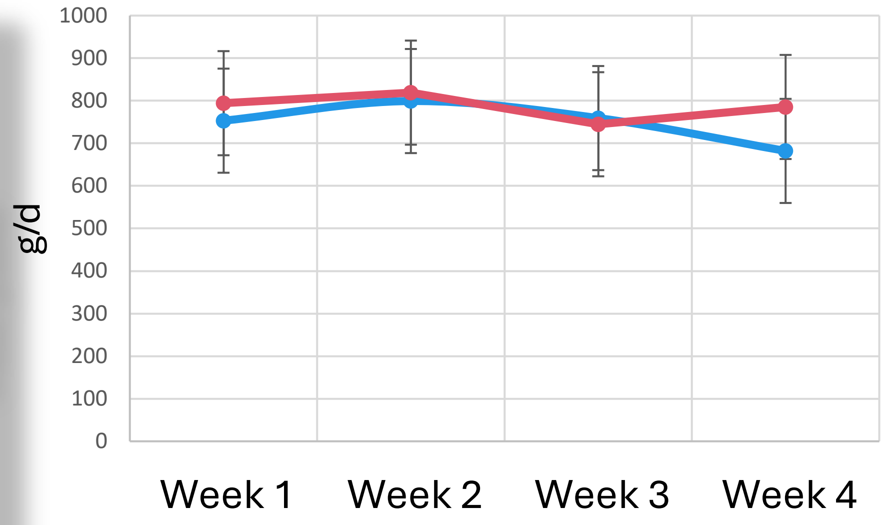
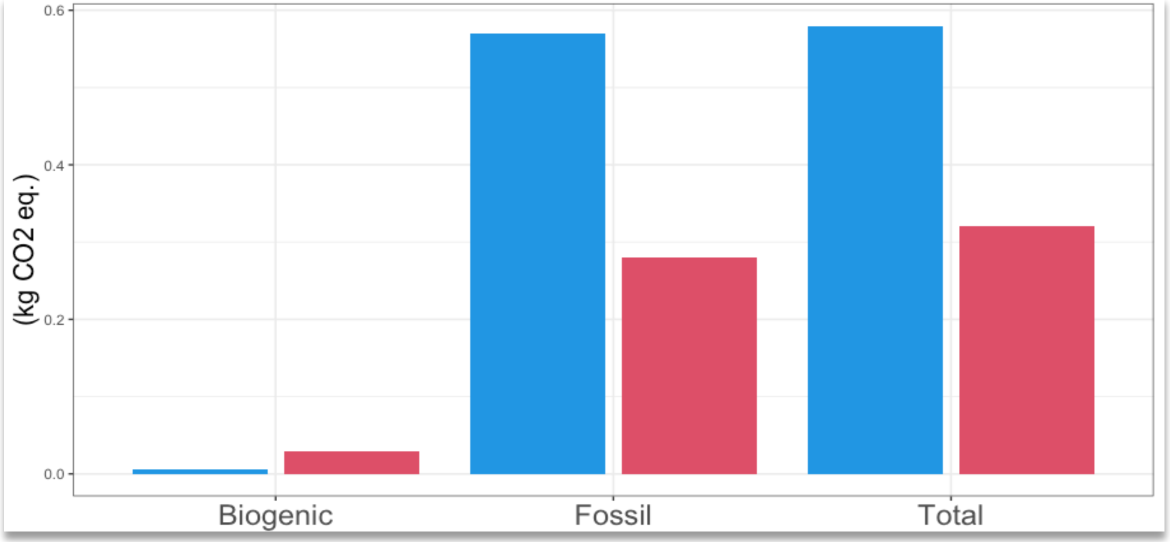
Background

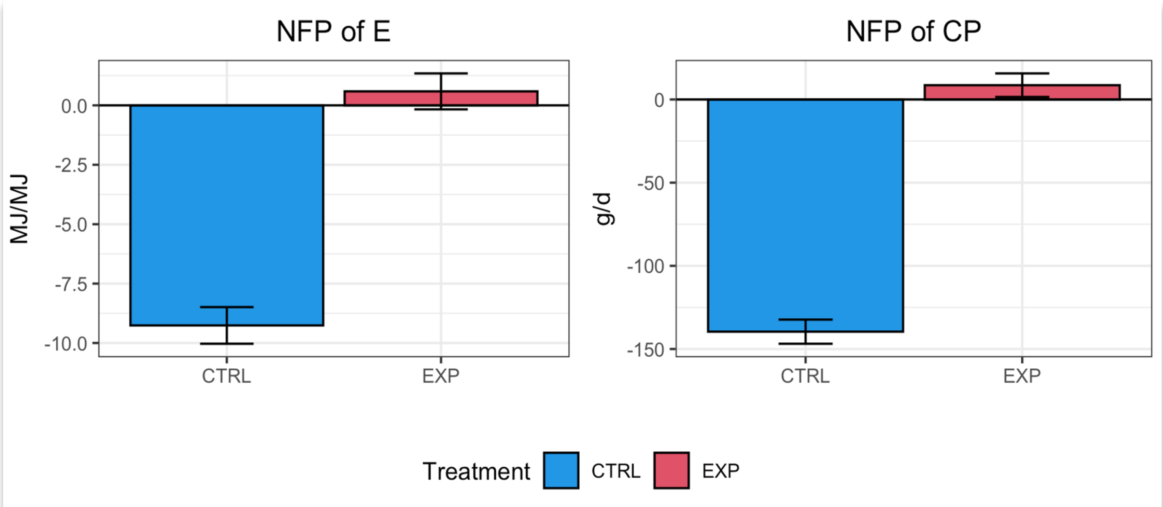
Milk yield



LCA

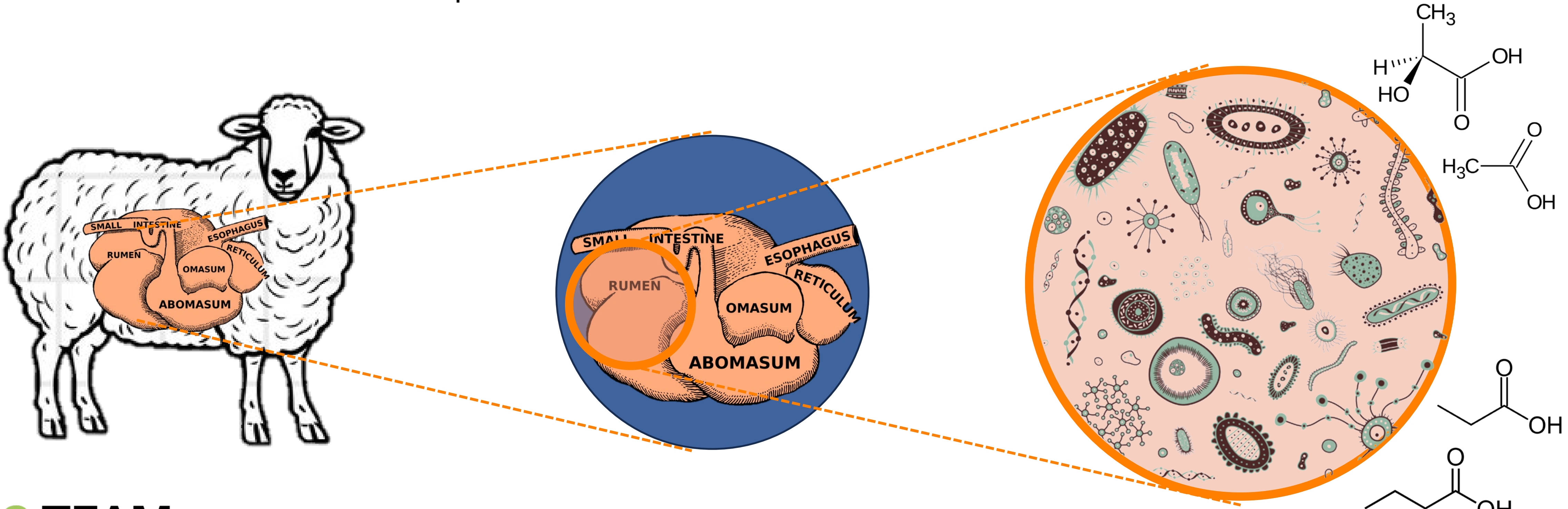


Food / feed competition

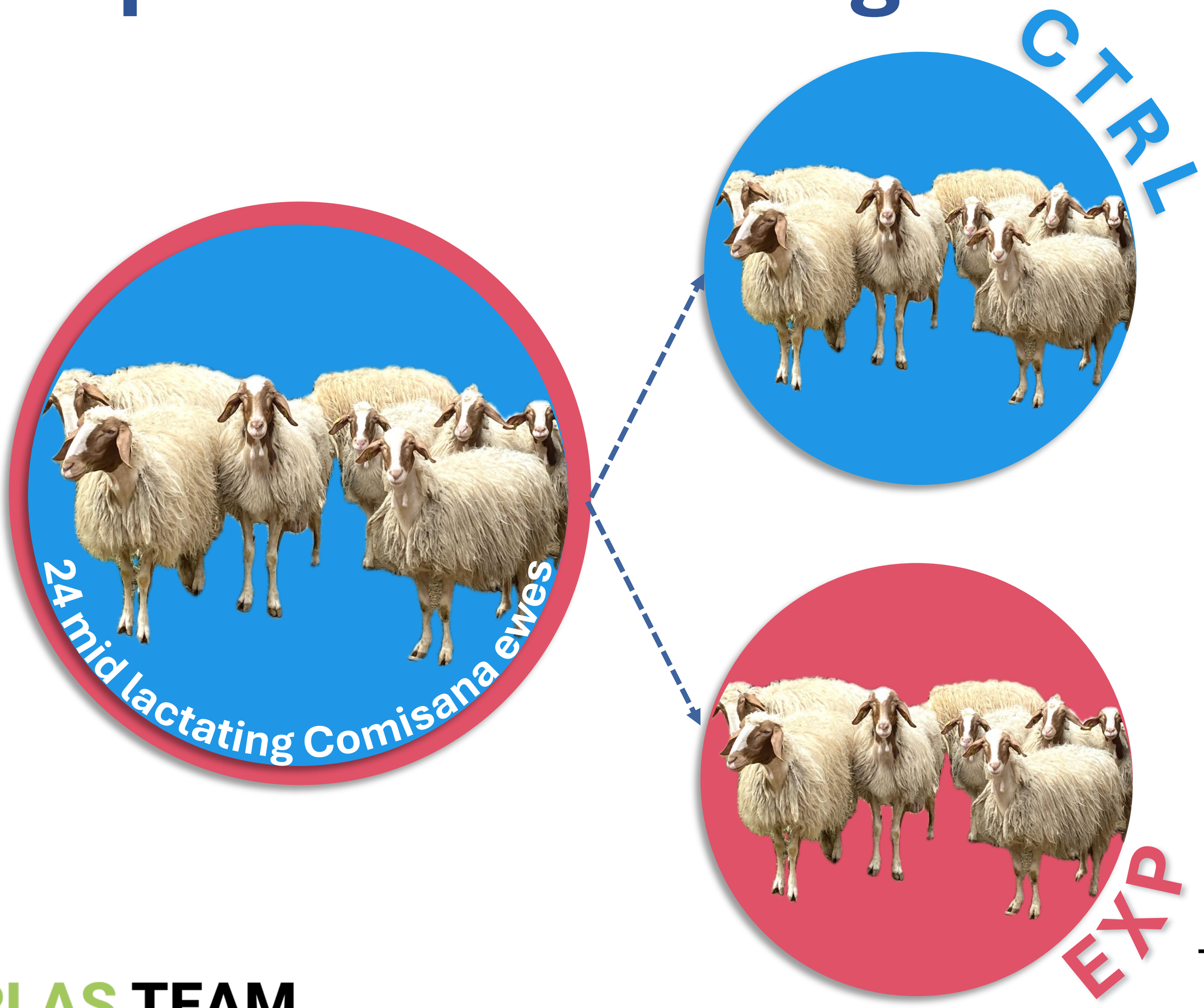


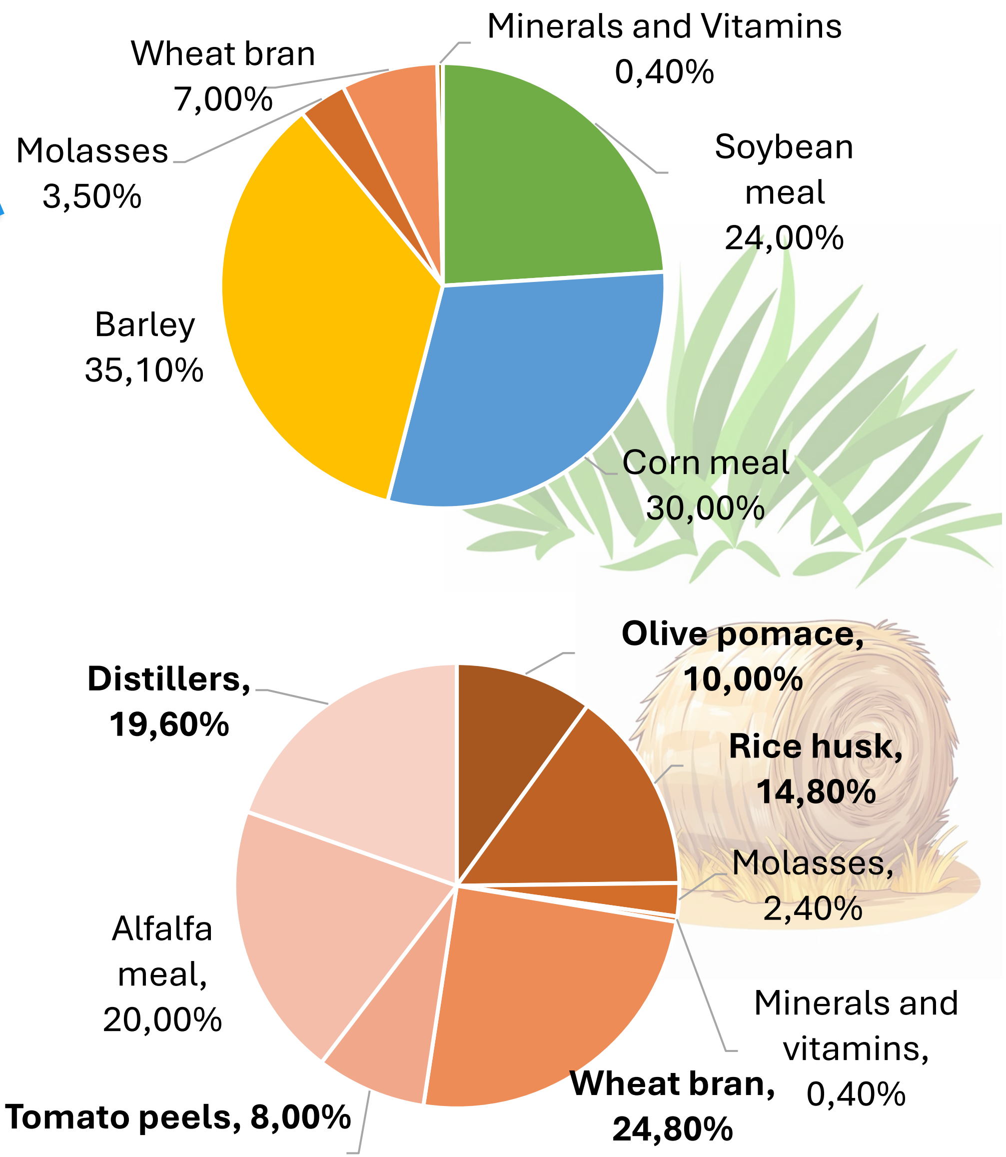
Aim of the study

Assessing the effect of the diet based on **by- and co-products** on volatile fatty acids (VFA), fatty acids (FA) concentrations, microbiota composition, and CH_4 from the rumen fluid of grazing dairy ewes



Experimental design





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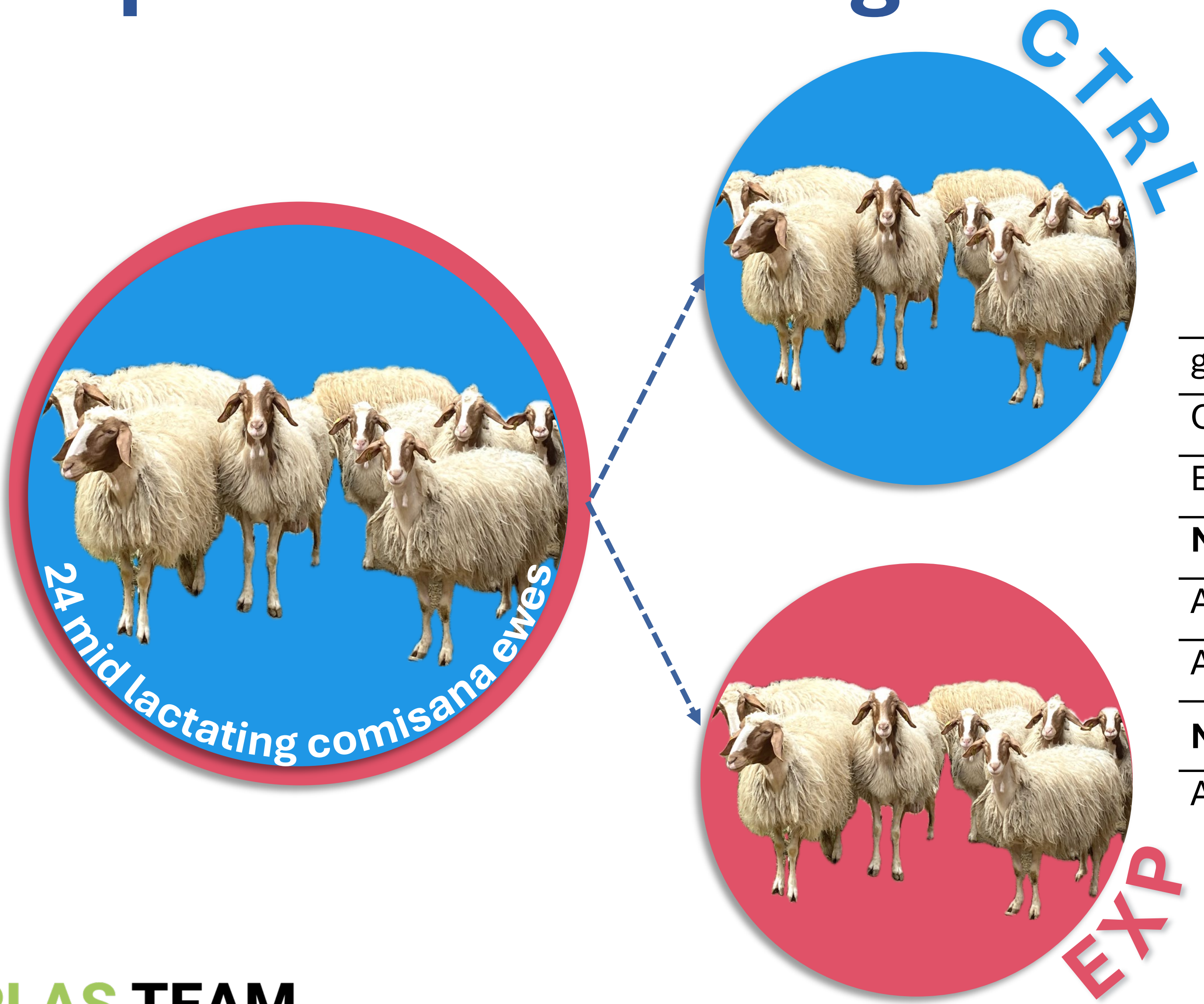
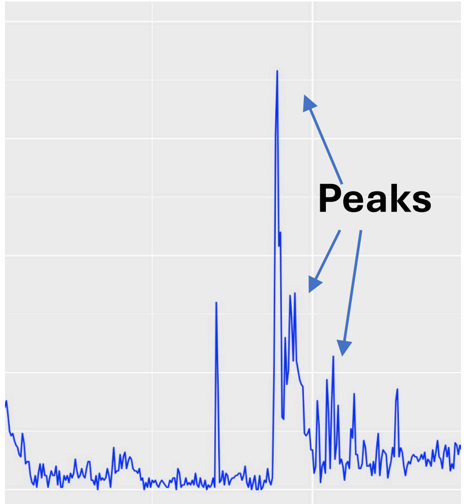
Experimental design



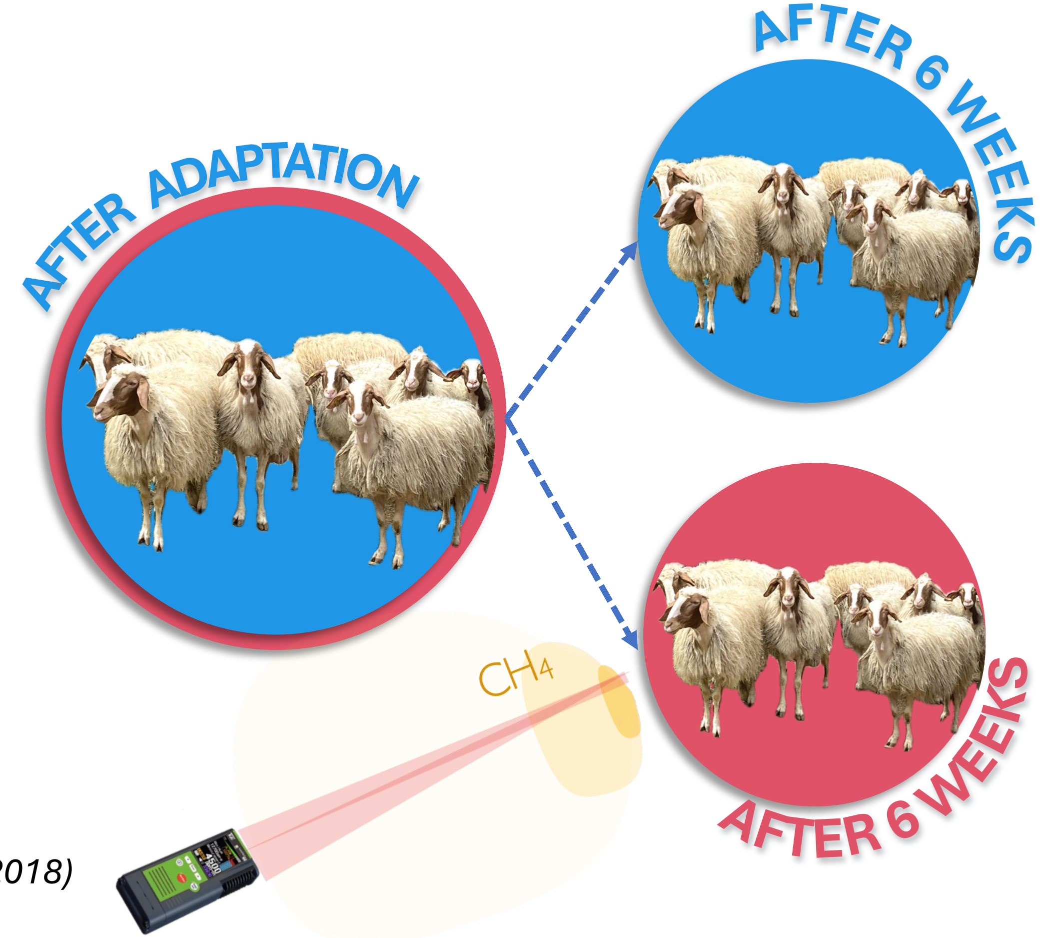
1 kg day^{-1} head^{-1}

	EXP pellet	CTRL pellet	Pasture	Hay
g/kg DM				
CP	21.80	21.10	13.84	16.71
EE	1.36	0.62	2.43	1.24
NDFom	**44.83**	**6.94**	48.08	65.5
ADFom	25.33	4.02	33.99	39.39
ADL	8.61	-	7.56	5.12
NFC	**23.74**	**66.89**	9.61	24.51
Ashes	8.27	4.45	11.14	6.93

Sampling and analyses



CH$_4$ profile of dairy ewes, adapted from *Sorg et al. (2018)*



16s seq.
Miseq Illumina
DADA2 and (Callahan et al., 2016) and Vegan packages (Oksanen at al., 2019)

VFA
HPLC

FA
Direct transesterification (Alves et al., 2013)

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Data Handling and Analysis

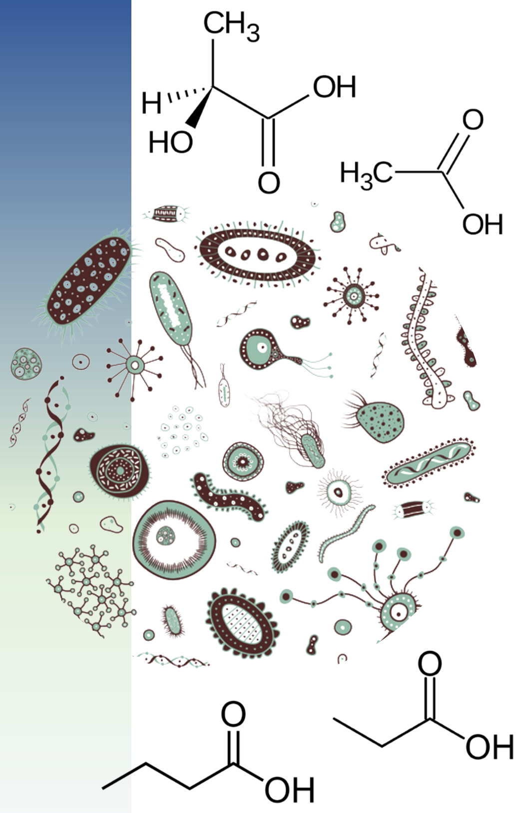
- Methanogenic profiles were elaborated as proposed by Sorg et al. (2018). The mean of methane peaks (ppmxm) was considered estimating the absolute CH_4.

- The Chao1 index, the ACE index, the Shannon diversity index, and the Simpson index were calculated to estimate the α-diversity. A non-metric multidimensional scaling (NMDS) and a permutational multivariate analysis of variance (PERMANOVA) were used to detect differences in β-diversity.

- All the ruminal data were analyzed using a linear mixed-effect model (R version 4.2.0) considering the fixed effects of treatment and the relative covariate for each response variable.

- For the microbiota data, a Kruskal-Wallis test was performed.

Results – VFA



	CTRL	EXP	SEM	*P-value*
pH	7.44	7.47	0.07	0.706
Lactate (mM)	9.09	4.83	1.48	0.055
Tot VFA (mM)	87.41	76.38	7.33	0.306
Acetate (%)	64.98	66.73	1.70	0.626
Propionate (%)	22.23	22.49	1.70	0.504
iso-butyrate (%)	1.85	1.71	0.14	0.518
Butyrate (%)	8.78	7.11	0.35	<0.001
iso-valerate (%)	2.27	1.60	0.18	0.014
Valerate (%)	0.43	0.35	0.06	0.351
Acetate:propionate	3.14	3.33	0.31	0.593

Both related to reactions incorporating H_2 *(Ungerfeld, 2020)*; however, no significant reductions of **acetate produced** (lower NDFom diet) or **methanogenesis** were detected.

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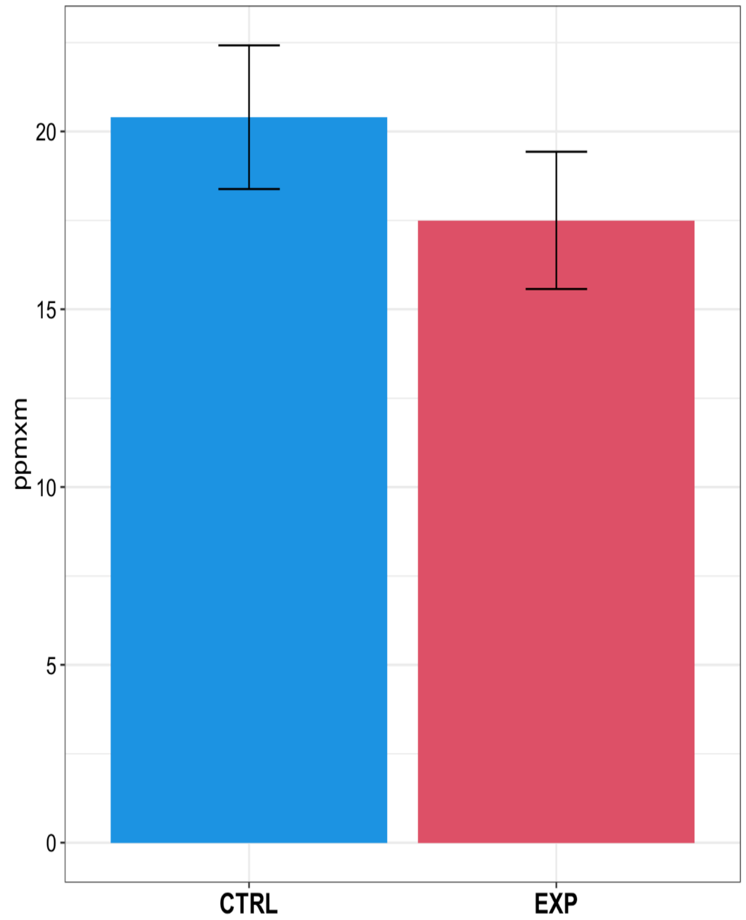
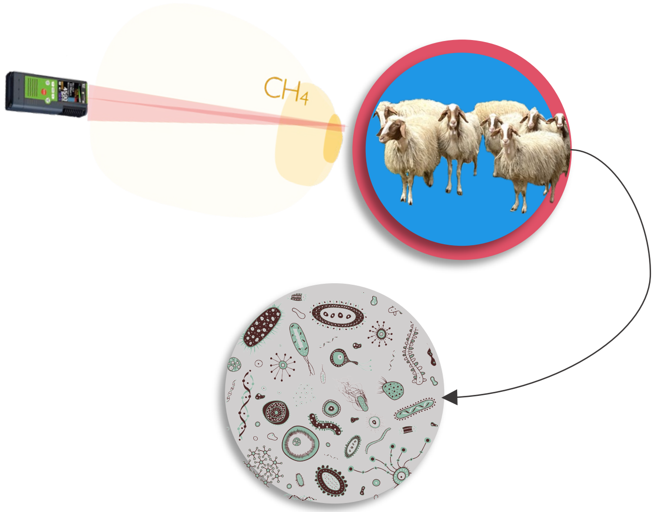
Results – enteric CH_4 emission

CH_4 peaks average *



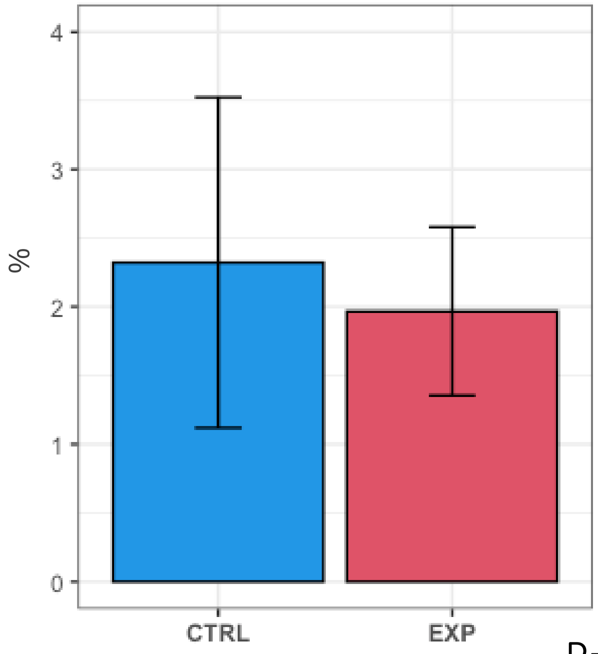
P=0.32

No differences despite NDFom content was EXP>>CTRL



No differences of Archaea at Domain level

Archaea relative abundance

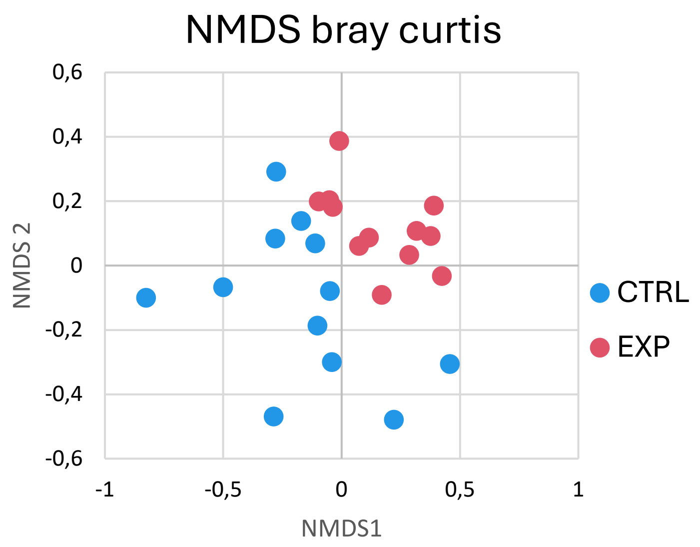


P=0.49

*parameter highly correlated with absolute methane emission in cattle *(Sorg et al., 2018)*

Results – bacterial community structure

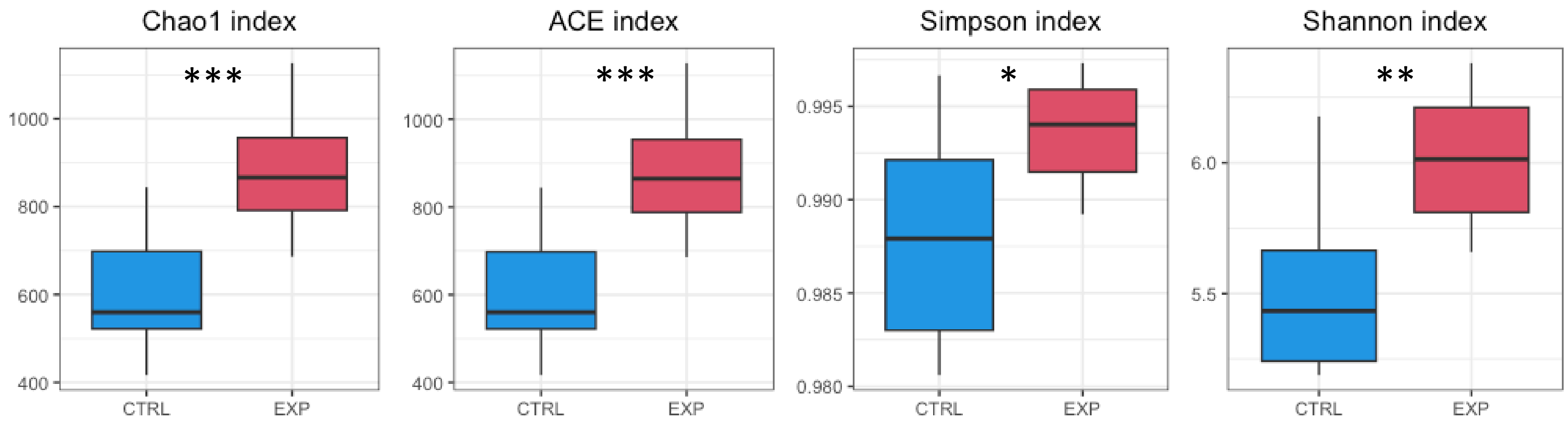
β-diversity



Permanova:

- CTRL vs. EXP – *p*= 0.002

Significant higher α-diversity in EXP



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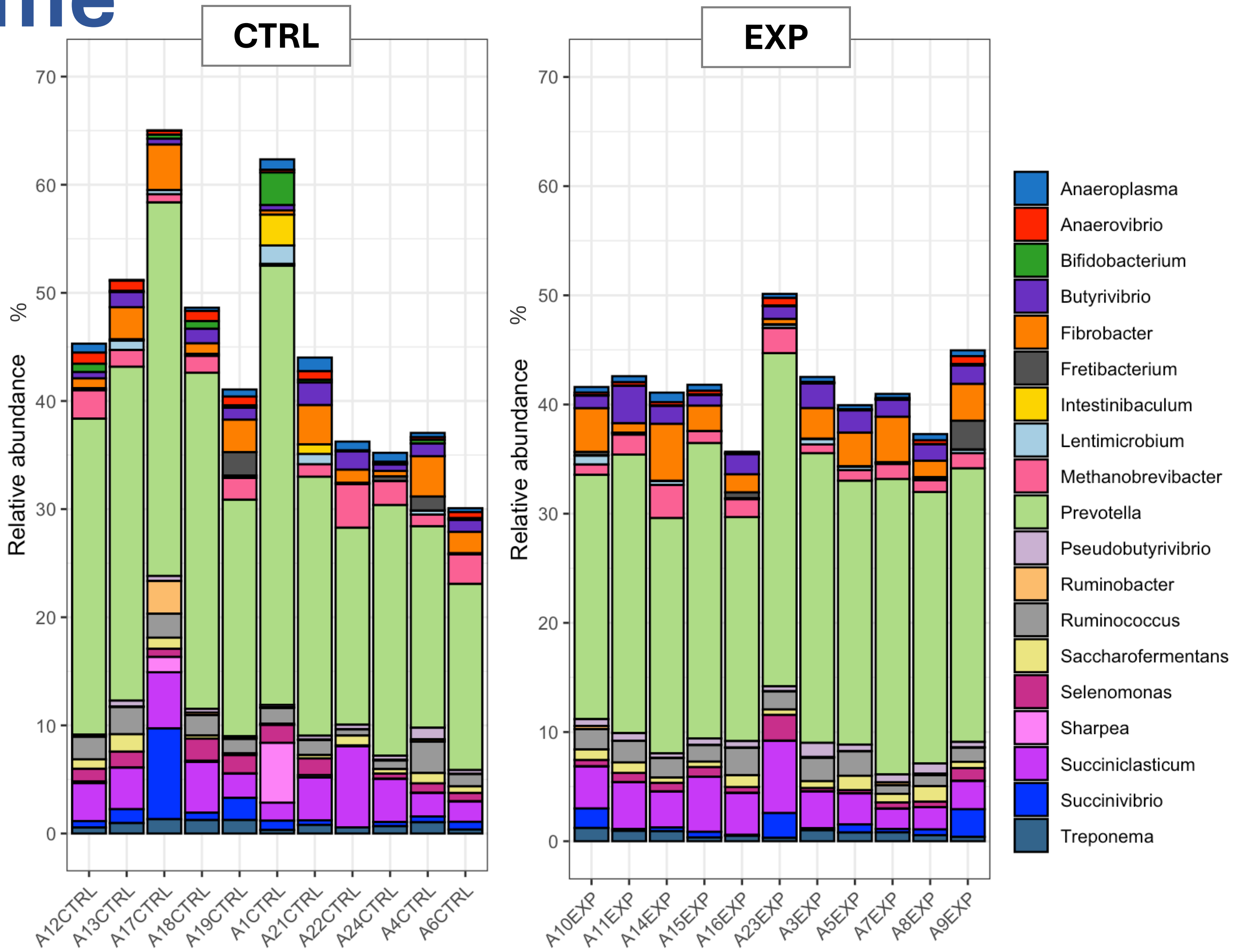
Core bacteriome

Prevotella spp.

Succinuclasticum spp.

Fibrobacter spp.



(Henderson et al., 2015; Manneli et al., 2018)

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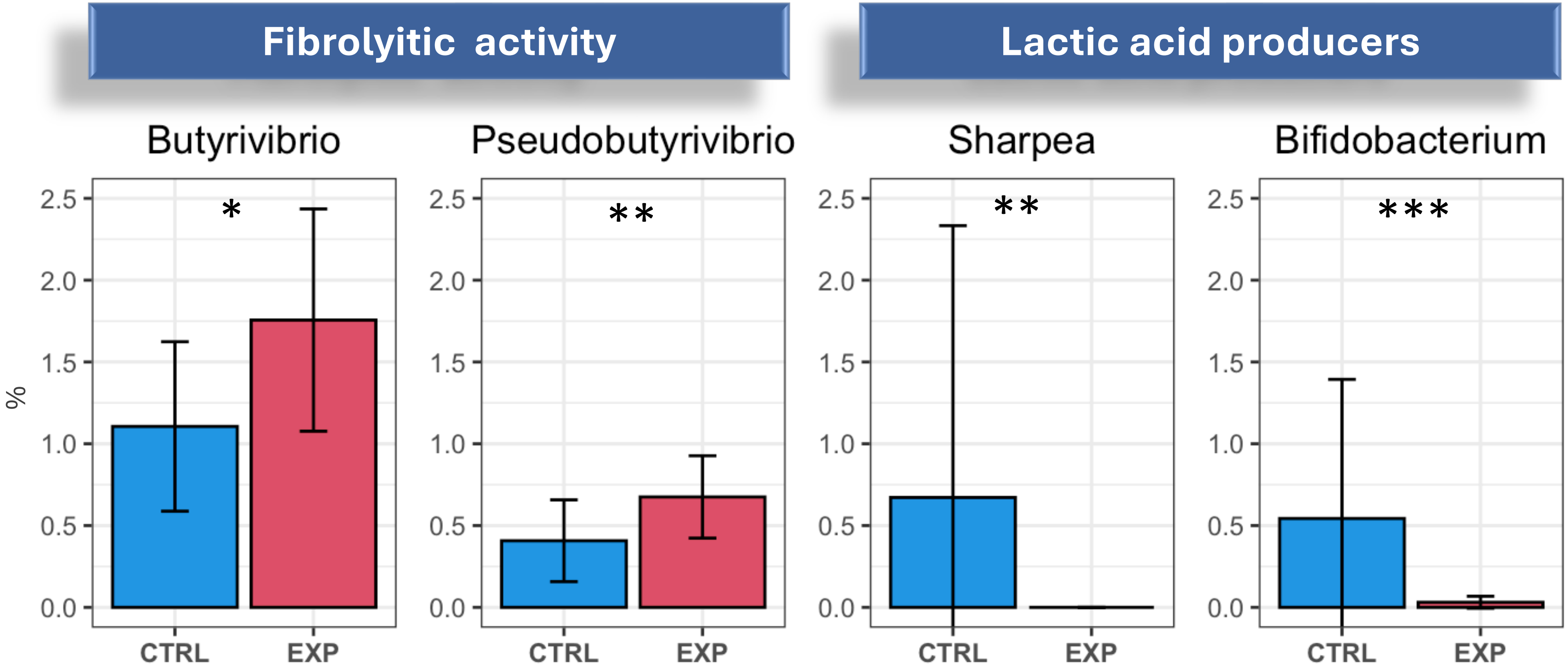
Differences at genus level



They occupy similar niches but apply different degradation strategies *(Palevich et al., 2020).*

More active when simple sugars are available (*Pokusaeva et al., 2011, Kumar et al., 2018*). Higher abundances supported by the higher lactic acid conc.

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Results – Diets FAs

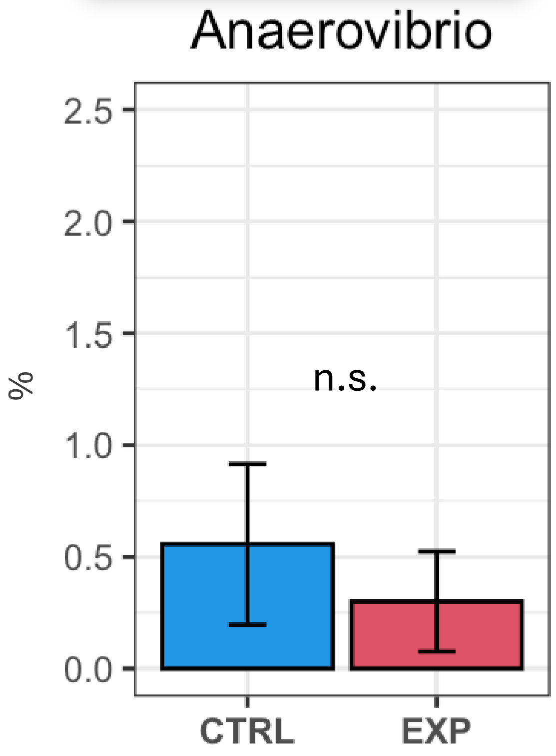
(Buccioni et al., 2012)

DIETS

	CTRL pellet	EXP pellet	Pasture
FA (g/100 g FAs)			
C14:0	0.19	0.29	0.71
C16:0	14.97	15.47	17.34
C16:1 cis-9	0.13	0.22	
C17:0	0.25	0.48	0.41
C18:0	2.89	2.59	2.01
C18:1 n-9	26.01	**36.36**	4.38
C18:1 cis-11	0.76	0.95	0.23
C18:2 n-6	**48.43**	34.61	20.72
C18:3 n-3	3.32	3.08	**46.57**
C20:0	0.39	0.59	1.03
C20:1 cis-11	0.37	0.47	
C22:0	0.47	0.59	0.73
C24:0	0.51	0.79	0.23
C22:5 n-3	0.29	0.28	
Others	1.02	3.21	5.65

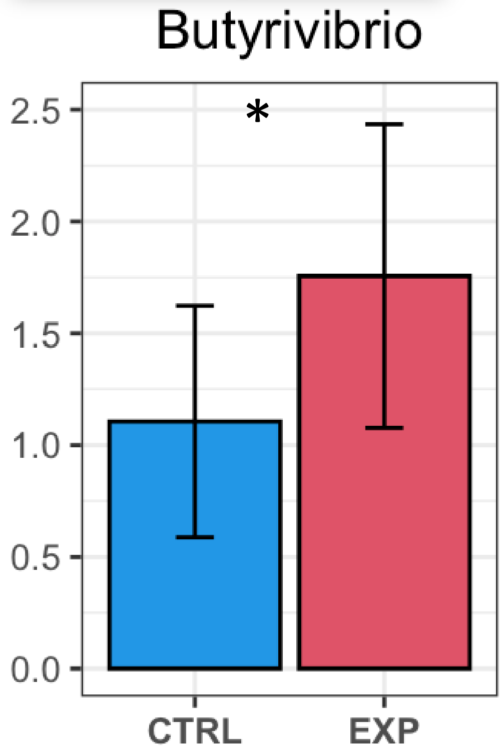
X

Lipolysis



✓

Biohydrogenation



In contrast with previous results obtained feeding olive pomace *(Mannelli et al., 2018)*

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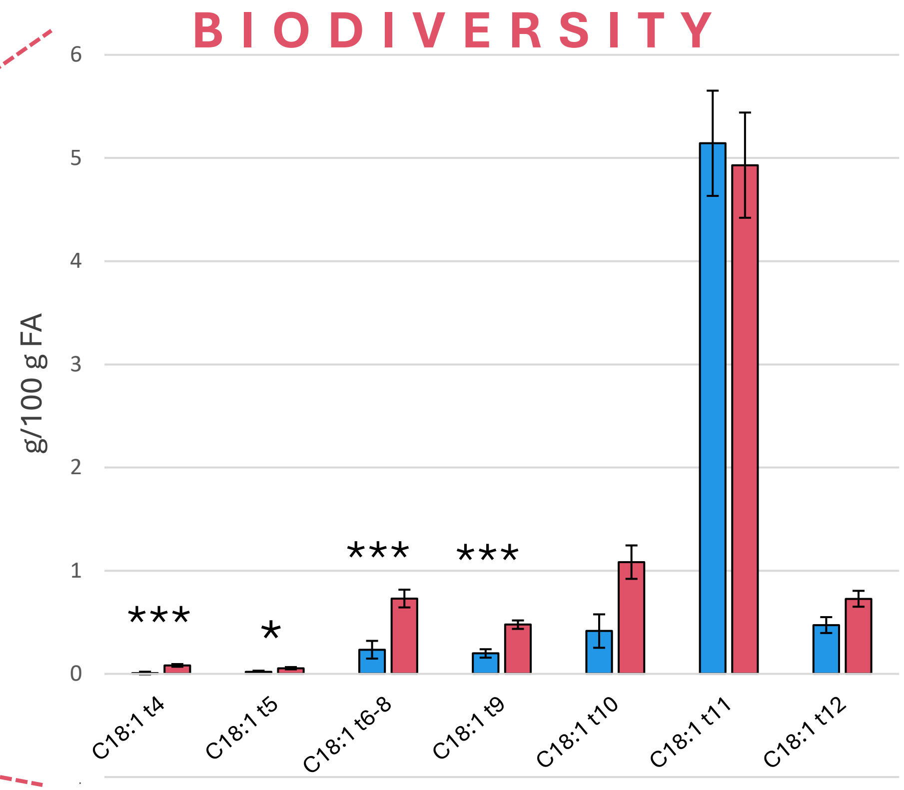
Results – Ruminal FAs

Diet **C18:2 cis-9,12** CTRL > EXP as in rumen liquor (10.5 vs. 6.3 ± 1.3 %, *p*=0.04)



- C18:1 c9 did not statistically differed (8.5 CTRL vs. 7.7 EXP ± 1.1 %).
- C18:0 (26.2 CTRL vs. 35.3 EXP ± 5.0 %)

Conclusions

- The study provides new evidence on the potential effect of by-products on the ruminal microbiome, which has been little studied *(Marcos et al., 2022)*.
- Relative abundances at genus, despite the fact they cannot reflect the ruminal activities, had a good correspondence with the measured fermentative traits.
- Our previous research showed that feeding EXP did not reduce milk yield in ewes; instead, it improved their environmental efficiency.
- In the present study, the EXP diet notably enhanced the α-diversity, suggesting that when simple sugars are less available, the **rumen environment** effectively **adapts** by supporting microorganisms capable of exploiting structural carbohydrates.
- Further research should investigate rumen metabolism and microbiota across different lactation phases and with varying mixtures of by-products.

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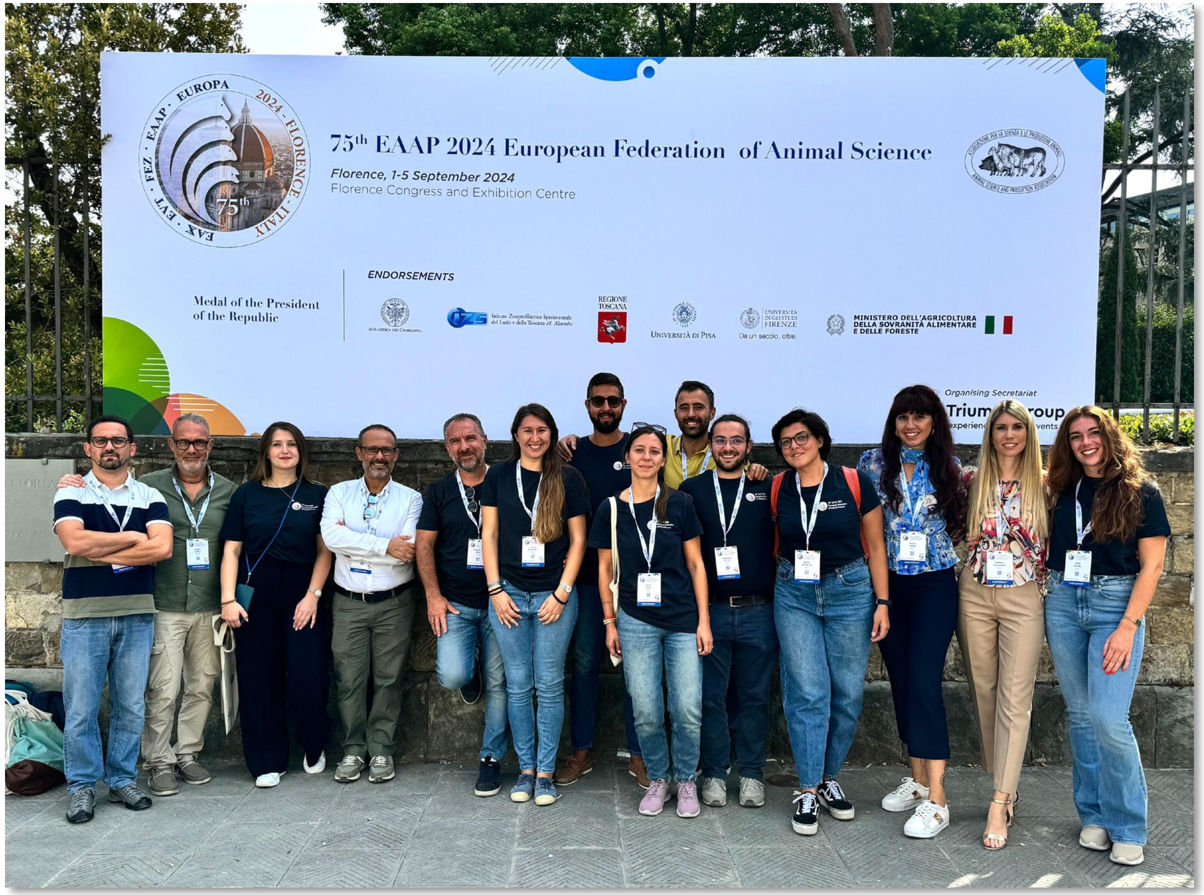

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Thank you for your kind attention!

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ALL-IN

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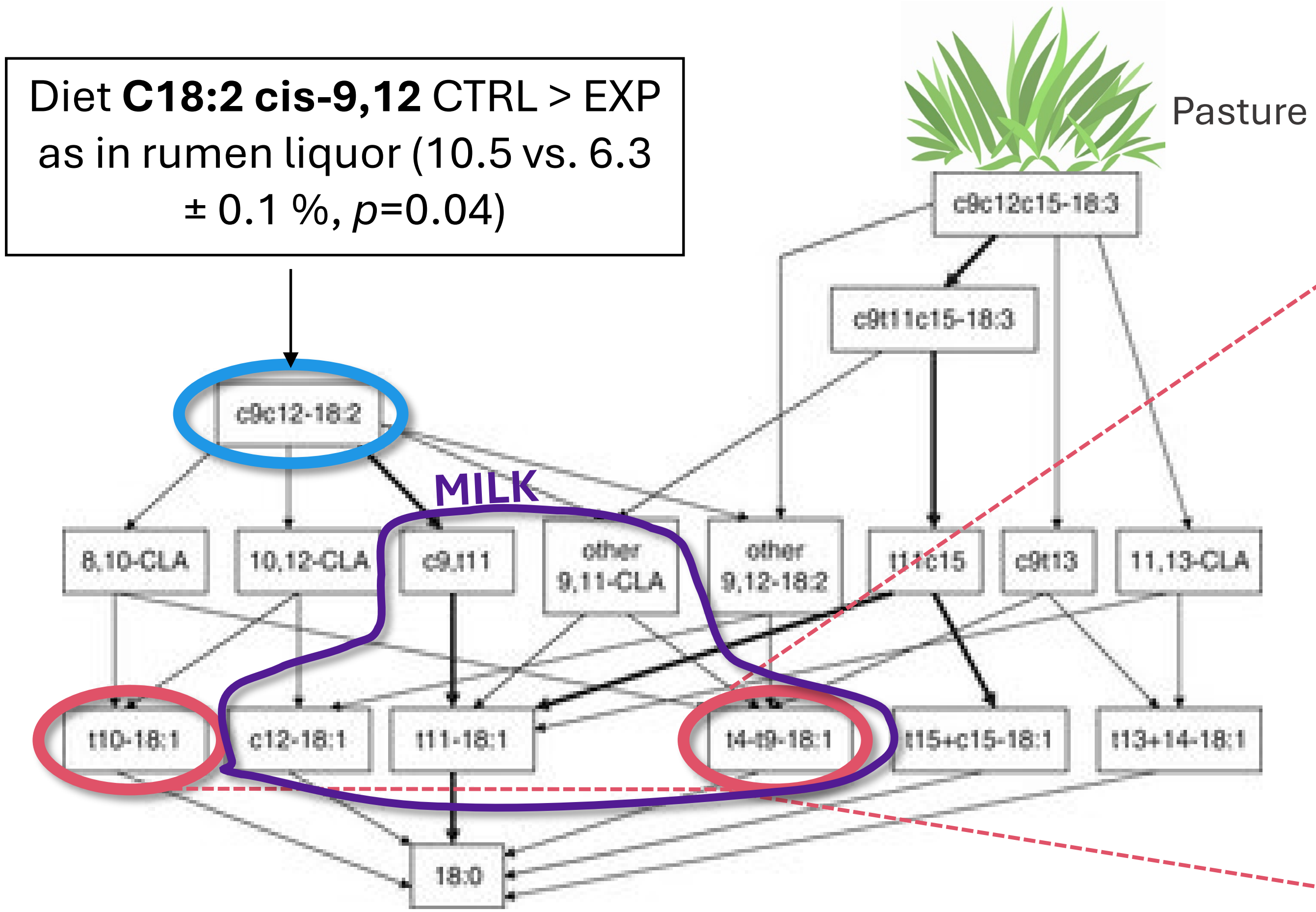
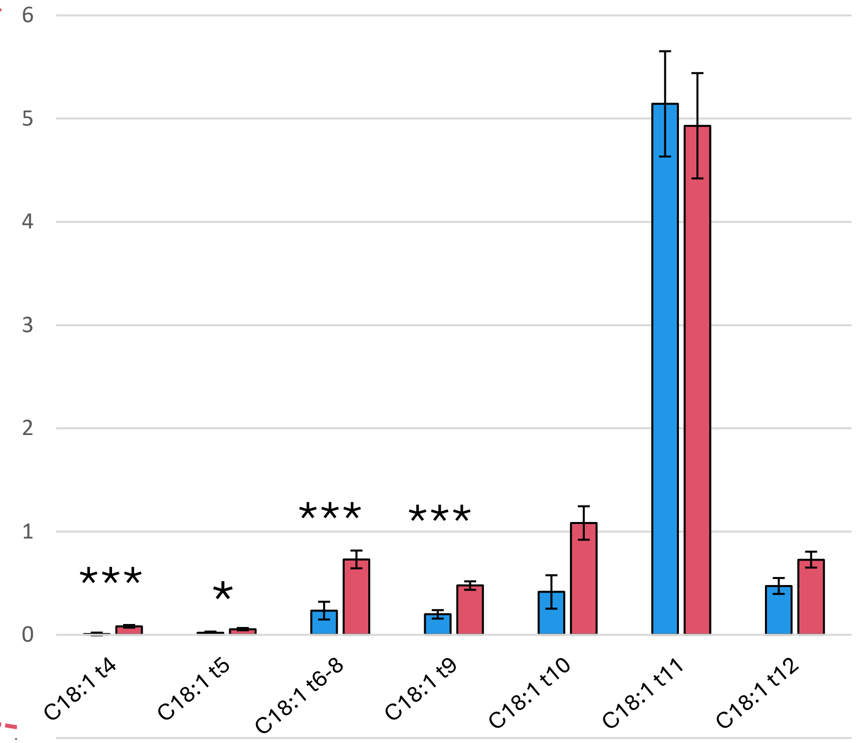
Supplementary – Ruminal FAs

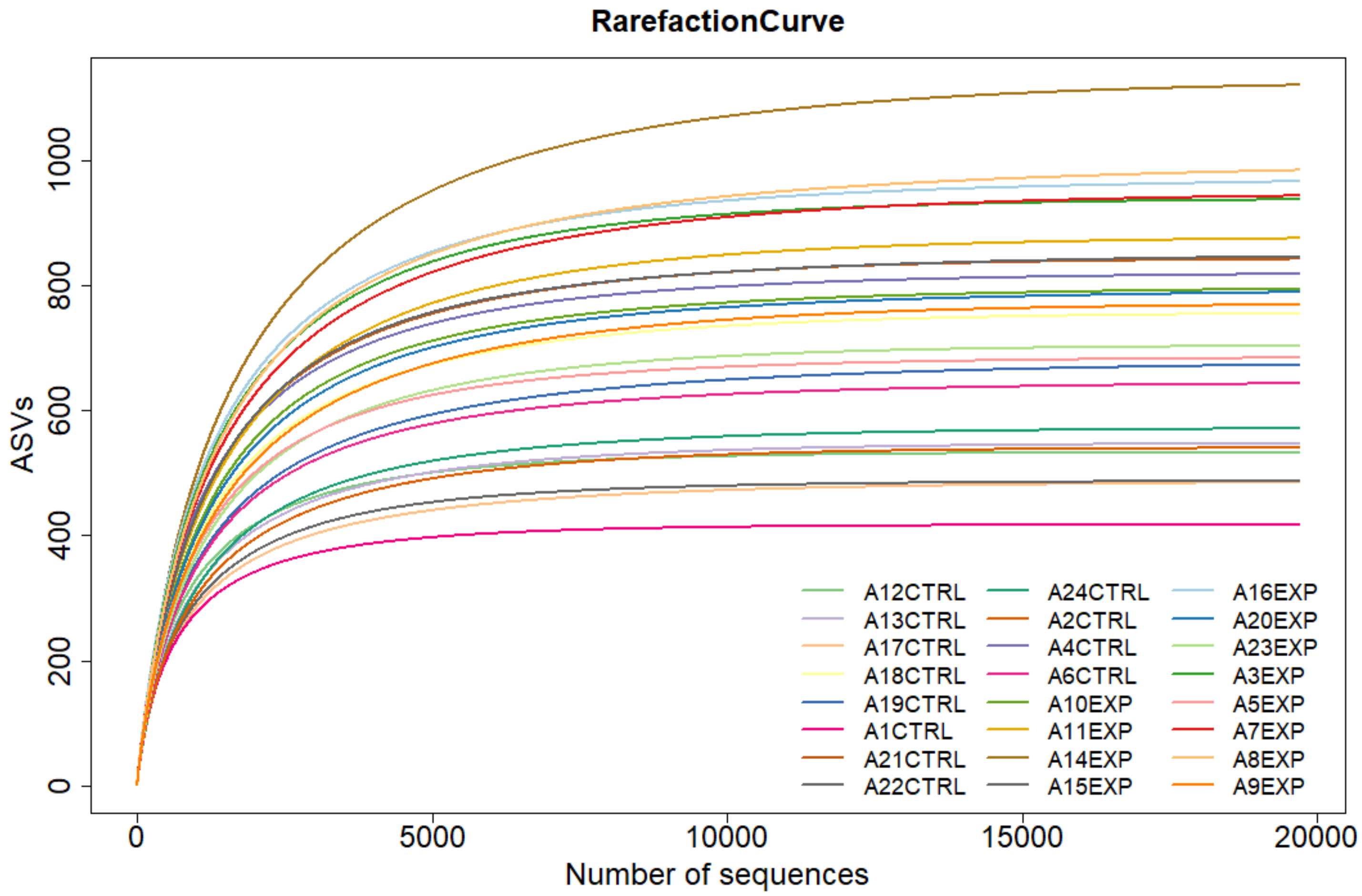
Diet **C18:2 cis-9,12** CTRL > EXP as in rumen liquor (10.5 vs. 6.3 ± 0.1 %, *p*=0.04)





C18:1 c9 did not statistically differed (8.5 CTRL vs. 7.7 EXP ± 1.1 %).

Supplementary material



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