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Using odd and branched-chain fatty acids to investigate dietary induced changes in the caecum of rabbits

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Introduction

- Odd-numbered (ONFA) and branched-chain (BCFA) fatty acids (OBCFA) are major components of bacterial membrane lipids and vary among microbial species.
- Changes in rumen OBCFA pattern have been used to describe dietary effects on ruminal bacteria.
- Data on caecal OBCFA is scarce in rabbits

Objective

To investigate the interactions between nutrition and potential changes in caecal bacteria populations using OBCFA, in rabbits.

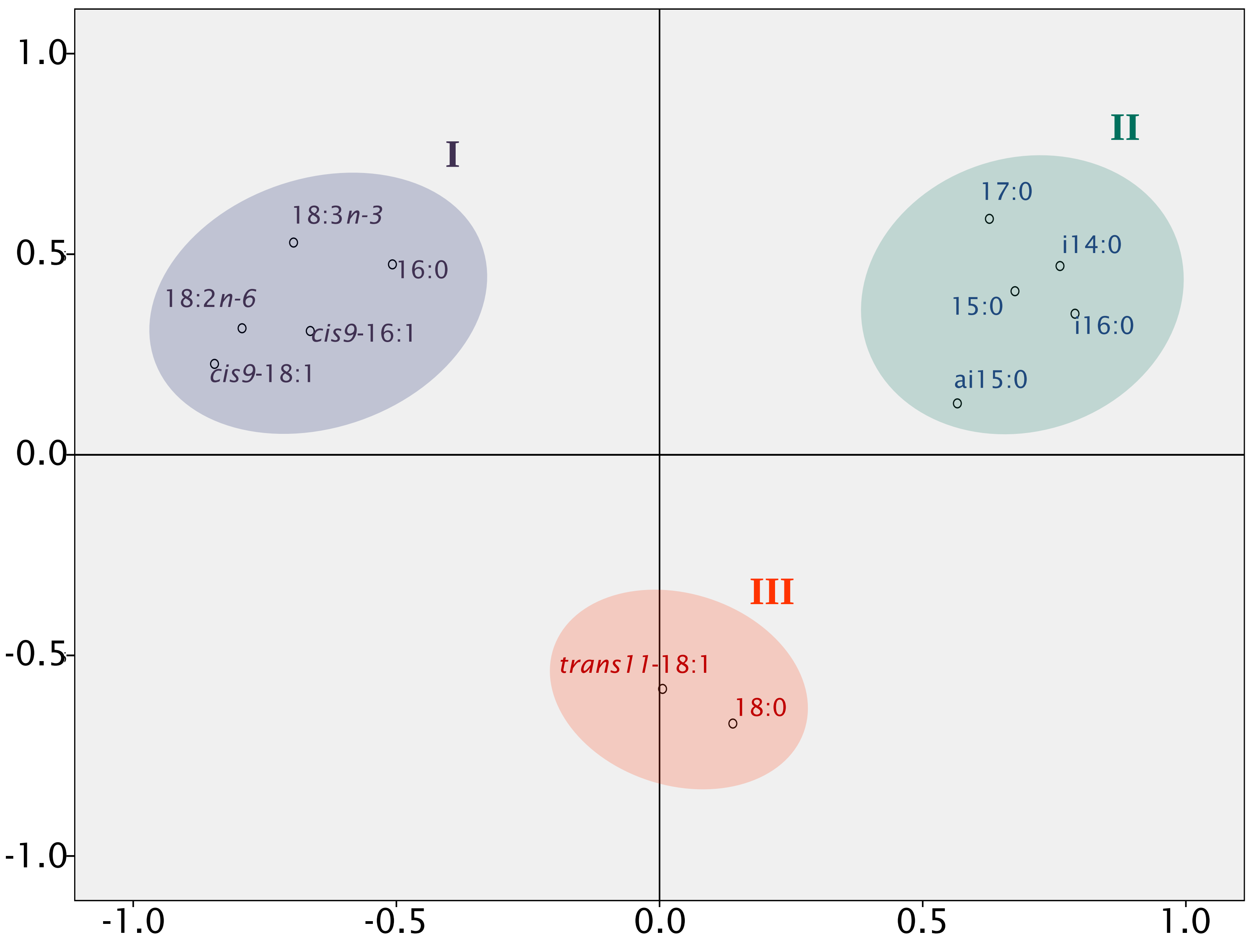
Materials and Methods

- 4 Diets: Low (165 g/kg) vs. High (240 g/kg) digestible fibre (DF) content, with soybean oil (SO) addition (20 g/kg) or not (2x2 design); **LDF0**$_{n=11}$, **LDF20**$_{n=12}$, **HDF0**$_{n=12}$, **HDF20**$_{n=12}$.
- Fatty acid (FA) determination in freeze-dried caecal contents (at 77 days of age), and feed samples.
- Data analysis: GLM procedures (two-way ANOVA) and principal component analysis (PCA).
- Evaluation of the results by comparison to literature data.

Results

- Traces of ONFA and no BCFA in diets. PCA suggested the origin of dietary derived vs. microbial FA (Fig. 1).
- HDF increased the contribution of ONFA and reduced that of BCFA in OBCFA pattern (Table 1).
- SO decreased the importance of OBCFA in total microbial FA (Table 1), but its effects depended on the readily available substrate (Fig. 2).

Figure 1
PCA loading plot and clustering of caecal FA (% of total FA)



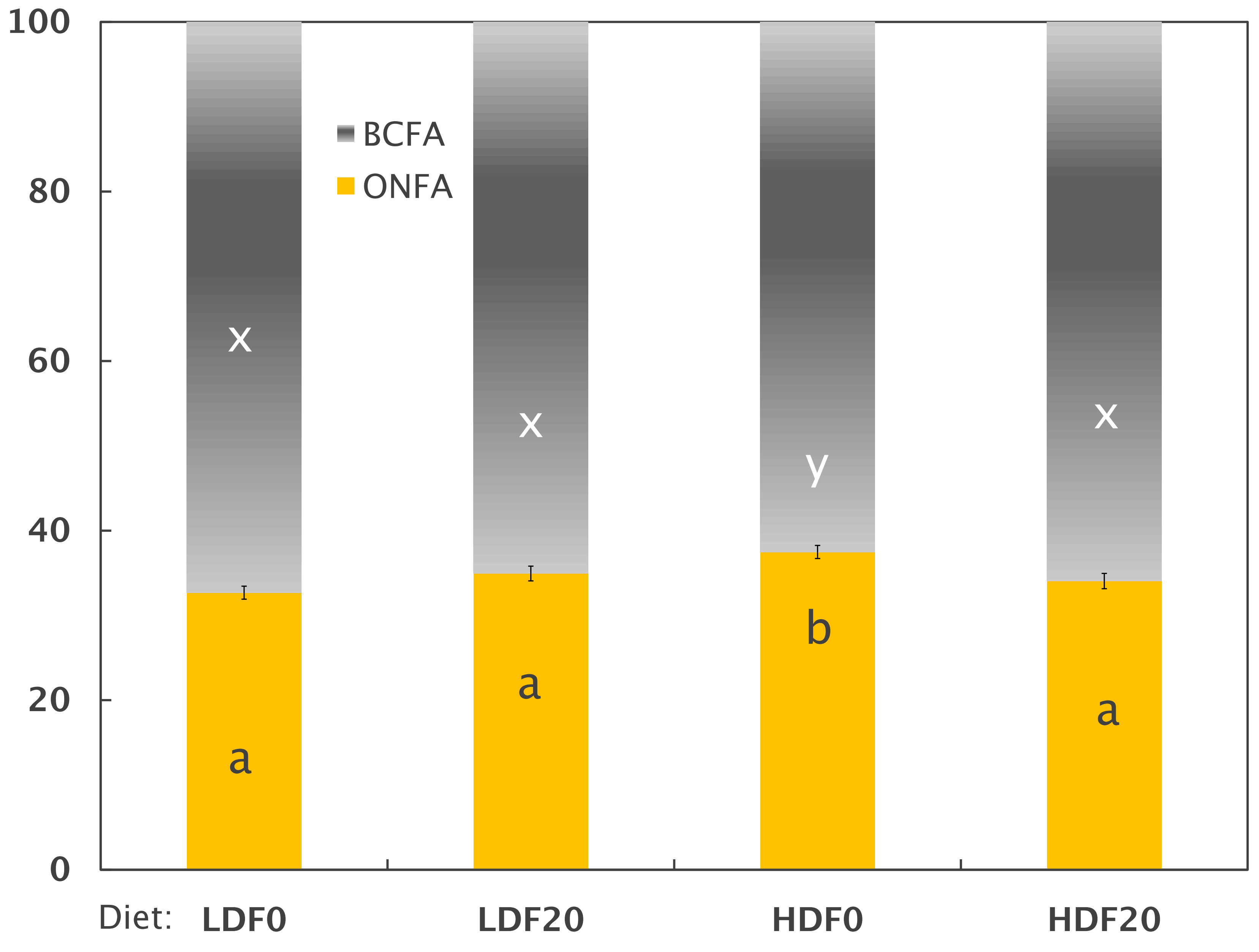
Cluster I: dietary FA; **Cluster II:** microbial origin (*de novo* synthesized) FA; **Cluster III:** FA derived from the activity of caecal bacteria mainly; (*n*=47).

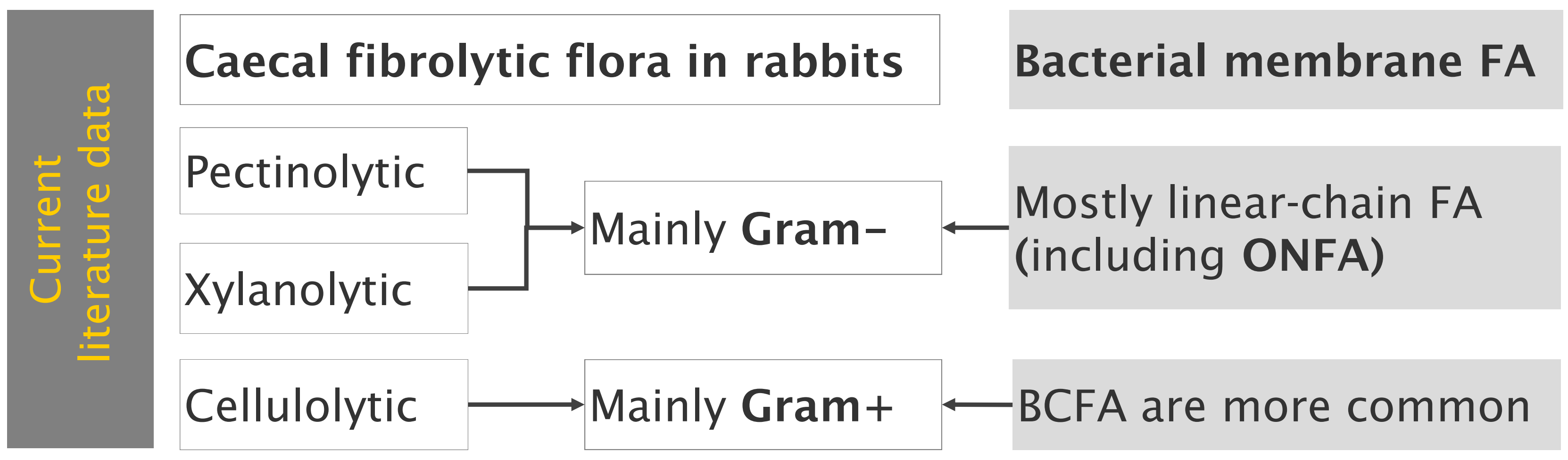
Table 1
Contribution of individual odd (ONFA) and branched-chain (BCFA) FA (as % OBCFA) in the OBCFA pattern and total OBCFA (% of total FA)

	DF		SO		RMSE	Significance[4]		
	LDF	HDF	0	20		DF	SO	DFxSO
i14:0	13.5	13.0	13.6	12.9	0.53	ns	ns	ns
ai15:0	27.7	27.1	26.2	28.5	1.10	ns	*	*
15:0	25.8	28.8	27.2	27.5	0.83	***	ns	**
i16:0	22.6	21.9	22.8	21.7	0.83	ns	ns	ns
ai17:0	2.4	2.3	2.3	2.4	0.22	ns	ns	ns
17:0	8.0	7.0	7.9	7.0	0.26	**	**	ns
ONFA[1]	33.8	35.8	35.1	34.5	0.83	*	ns	***
BCFA[2]	66.2	64.2	64.9	65.5	0.83	*	ns	***
OBCFA[3]	12.8	12.2	13.3	11.7	0.47	ns	***	ns

*[1] ONFA, sum of 15:0+17:0 (% OBCFA); [2] BCFA, sum of i14:0+ai15:0+i16:0+ai17:0 (%OBCFA); [3] OBCFA, sum of odd and branched-chain FA (% of total FA); [4] ns, P>0.05; *, P<0.05; **P<0.01; ***, P<0.001*

Figure 2
DFxSO interactions on OBCFA pattern (ONFA and BCFA, as %OBCFA)
a, b and x, y= differences (P<0.05) between diets for ONFA and BCFA, respectively





Caecal fibrolytic flora in rabbits

Bacterial membrane FA

Pectinolytic
Xylanolytic
→ Mainly **Gram−** ← Mostly linear-chain FA (including **ONFA**)

Cellulolytic → Mainly **Gram+** ← BCFA are more common

Conclusions

- HDF effects on OBCFA pattern likely indicate potential shifts in the relative proportions of fibrolytic bacteria.
- The reduced OBCFA in response to SO addition suggested a decreased *de novo* FA synthesis by caecal bacteria.
- Further investigation is necessary to establish the potential of OBCFA to describe interactions between nutrition and caecal bacteria in rabbits.