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Structure-dependent degradation of milk oligosaccharides by newly isolated intestinal commensal bacterial strains from suckling piglets and rabbits

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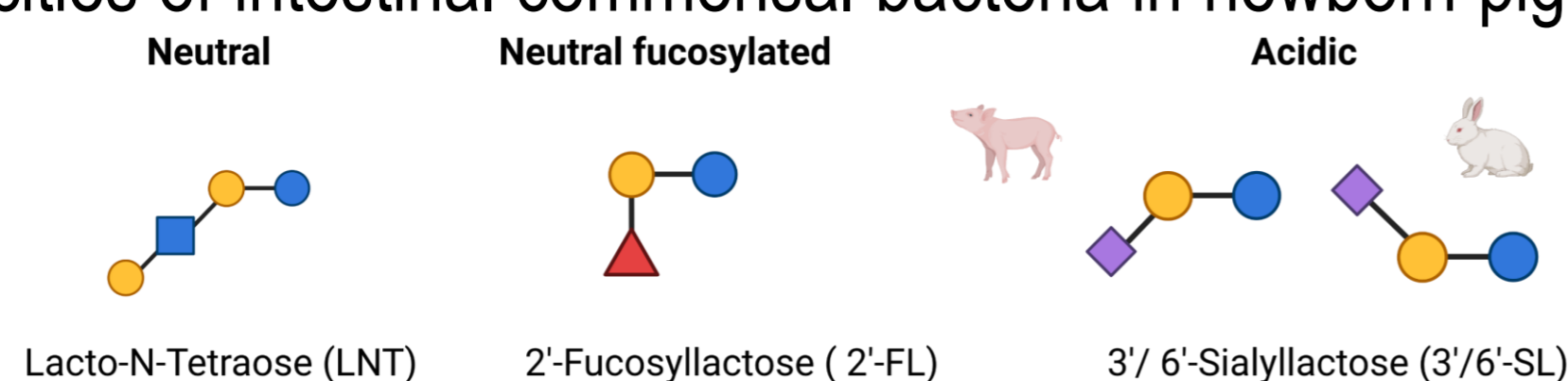
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Introduction

Milk oligosaccharides (MOs) are bioactive component with multiple benefits for neonatal and long term health. Interestingly milk oligosaccharides composition varies widely among mammalian species. The influence of this high structural diversity of MOs on the holobiont development remains to be explored.

Objectives

Analyze functional links between MO structural diversity and metabolic capacities of intestinal commensal bacteria in newborn pigs and rabbits.



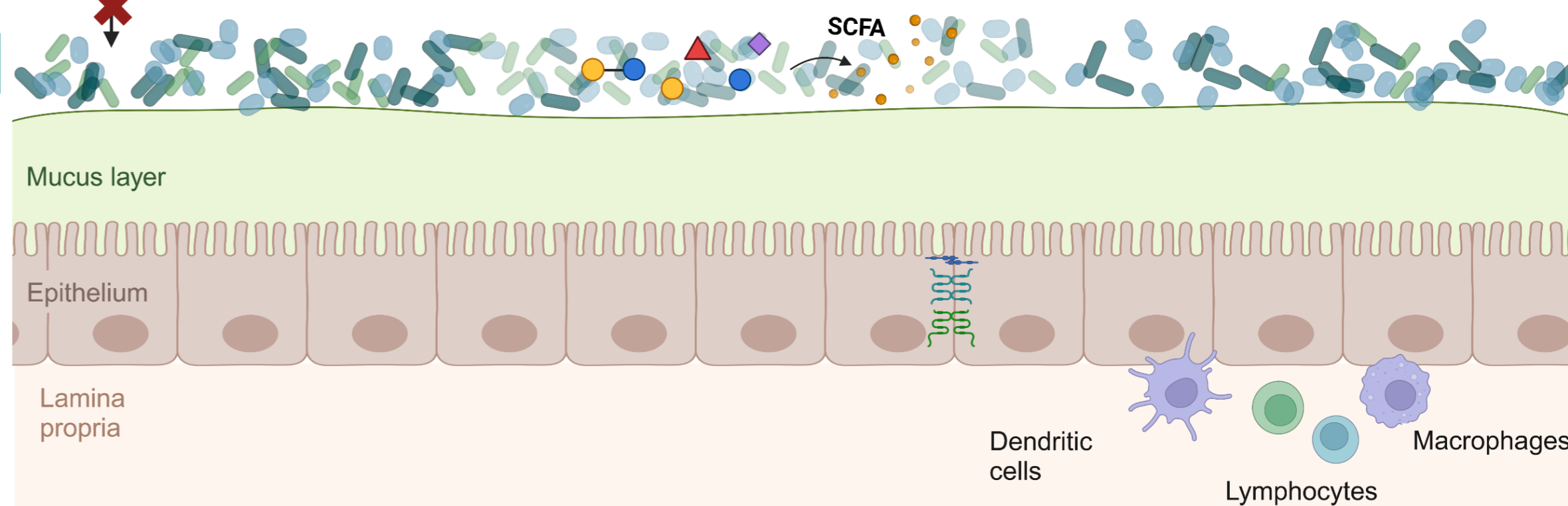
Gut health benefits of MO

Prevents adhesion
Campylobacter jejuni
(Coppa et al. 2006, Manthey et al. 2014)

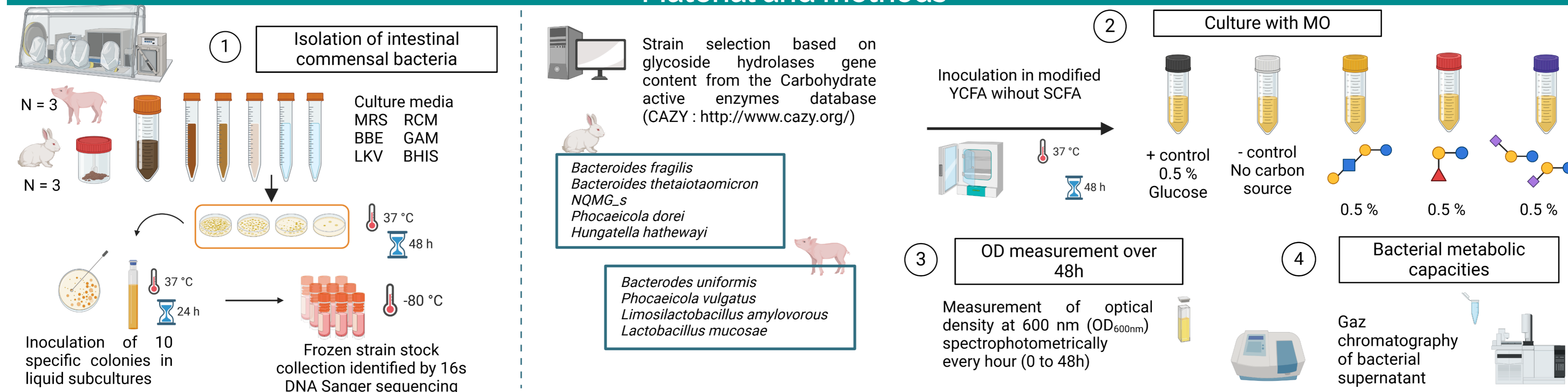
Prebiotic action
Bifidobacterium, bacteroides
(Marcobal et al. 2011, Salli et al. 2021, Kijner et al. 2022)

Strengthens the epithelial barrier
Butyrate by *Bifidobacterium*
(Suligoj et al. 2020)

Immunomodulation
(Kurakevich et al. 2013, Noll et al. 2016, Xiao et al. 2019)

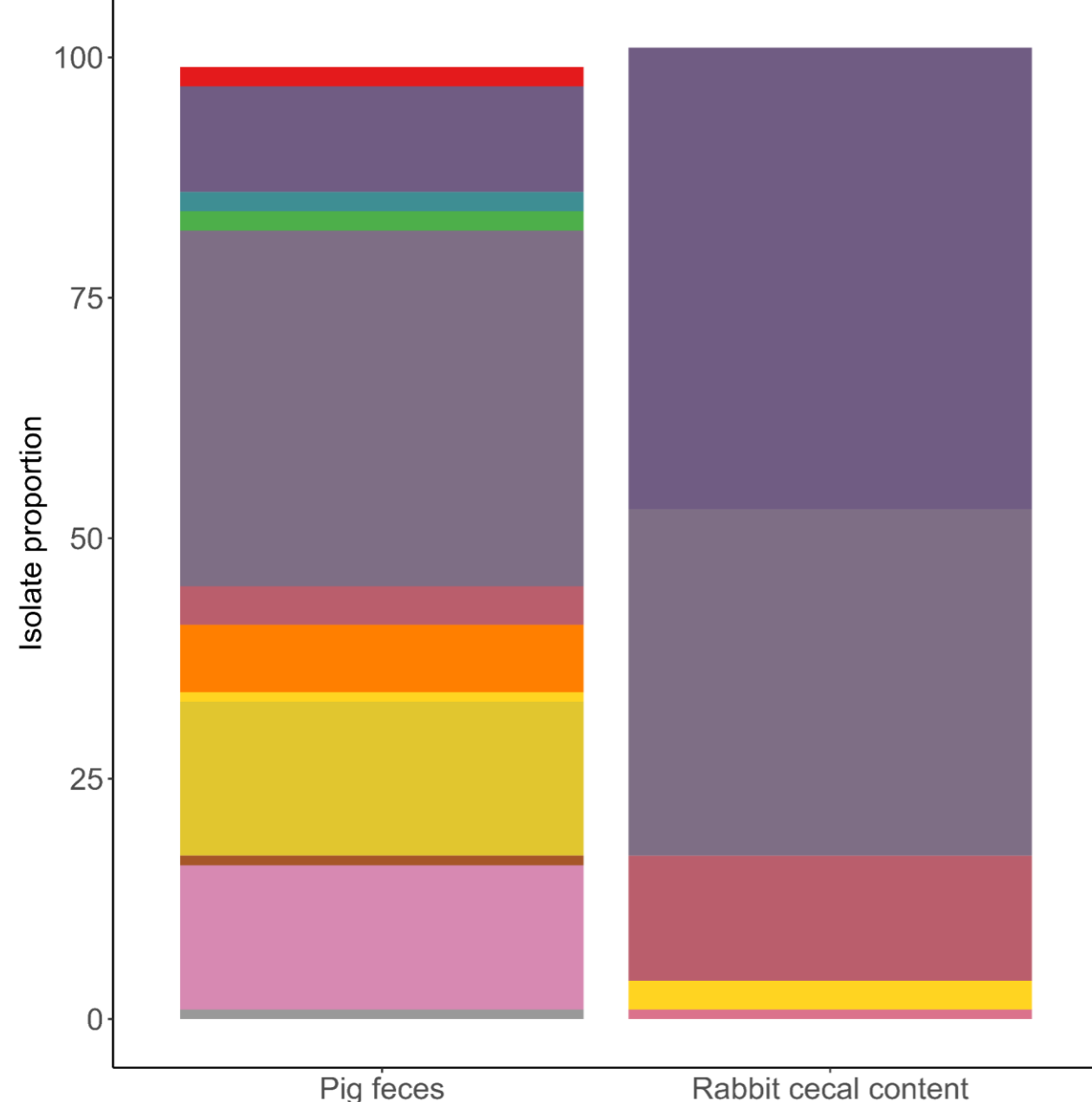


Material and methods



Results

Bacterial families isolated from pig and rabbit gut



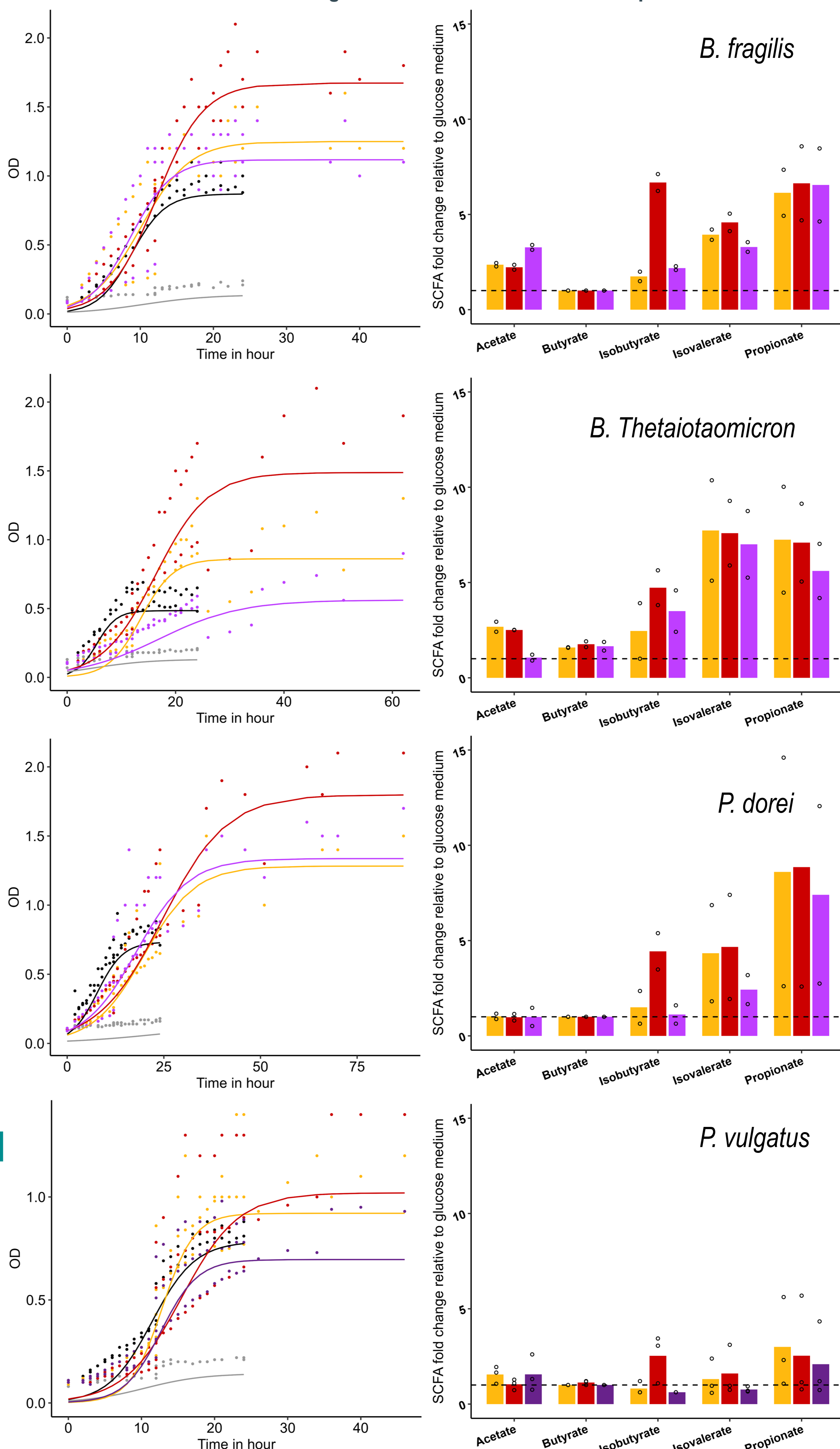
- | | | |
|-----------------------|-----------------------|--------------------|
| ■ Acidaminococcaceae | ■ Enterococcaceae | ■ Rikenellaceae |
| ■ Bacteroidaceae | ■ Erysipelotrichaceae | ■ Streptococcaceae |
| ■ Clostridiaceae | ■ Lachnospiraceae | ■ Veillonellaceae |
| ■ Desulfovibrionaceae | ■ Lactobacillaceae | |
| ■ Enterobacteriaceae | ■ Porphyromonadaceae | |

149 isolated colonies
17 identified strains

94 isolated colonies
26 identified strains

■ Positive control ■ Negative control ■ LNT ■ 2'-FL ■ 6'-SL ■ 3'-SL

Bacterial degradation of MOs is structure dependent



Conclusion and Perspectives

- Milk oligosaccharide metabolism depends on their structure and varied within a same genera
- Whole genome sequencing is ongoing to identify genes implicated in MO metabolism