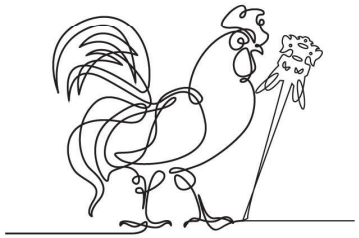

23rd European Symposium on Poultry Nutrition

ESPN 2023

RIMINI/ITALY JUNE 21 - 24

Feeding the microbiome

Richard Ducatelle, Evy Goossens, Venessa Eeckhout & Filip Van Immerseel
Ghent University, Belgium

GHENT UNIVERSITY

LIGHT

Livestock Gut Health Team Ghent

VETERINARY SCIENCES

SHANGHAI RANKING
Global Ranking of Academic Subjects
TOP 1
Veterinary Sciences
2022

No.1
2022
2021
2020
2019
2018
2017

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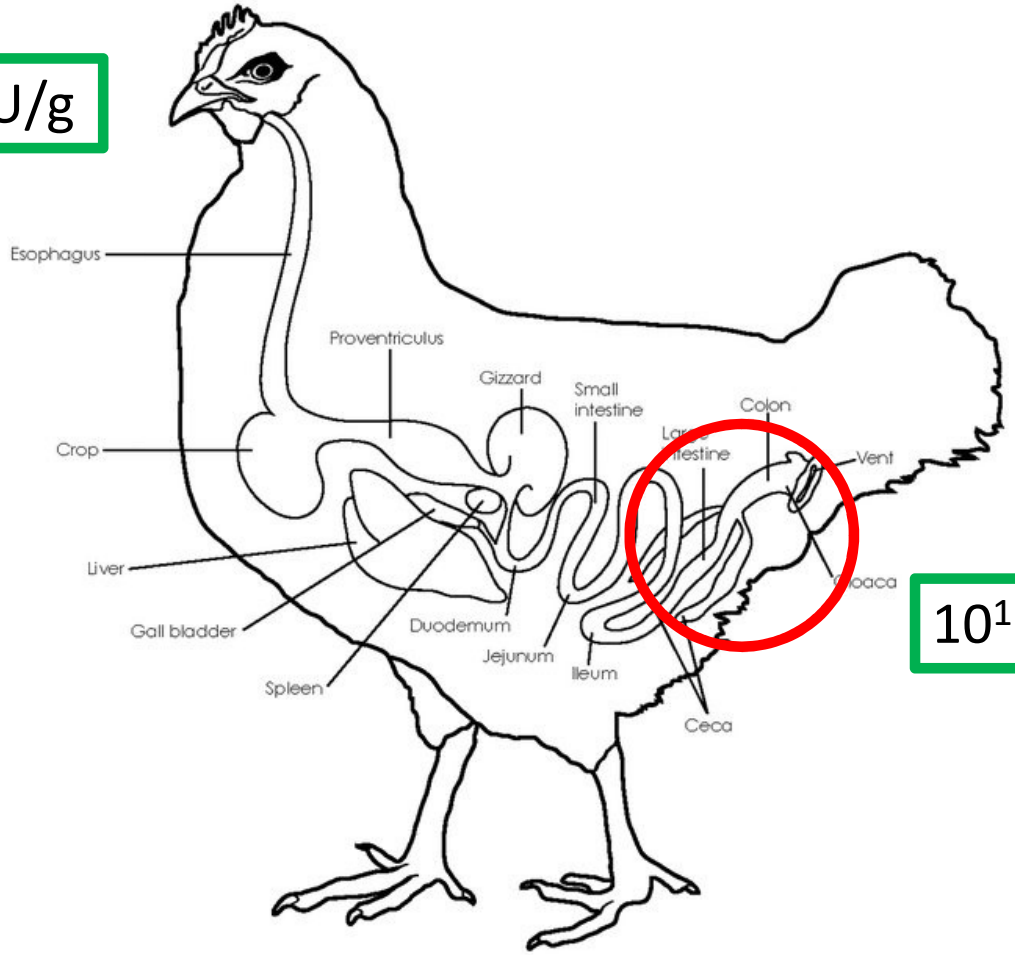
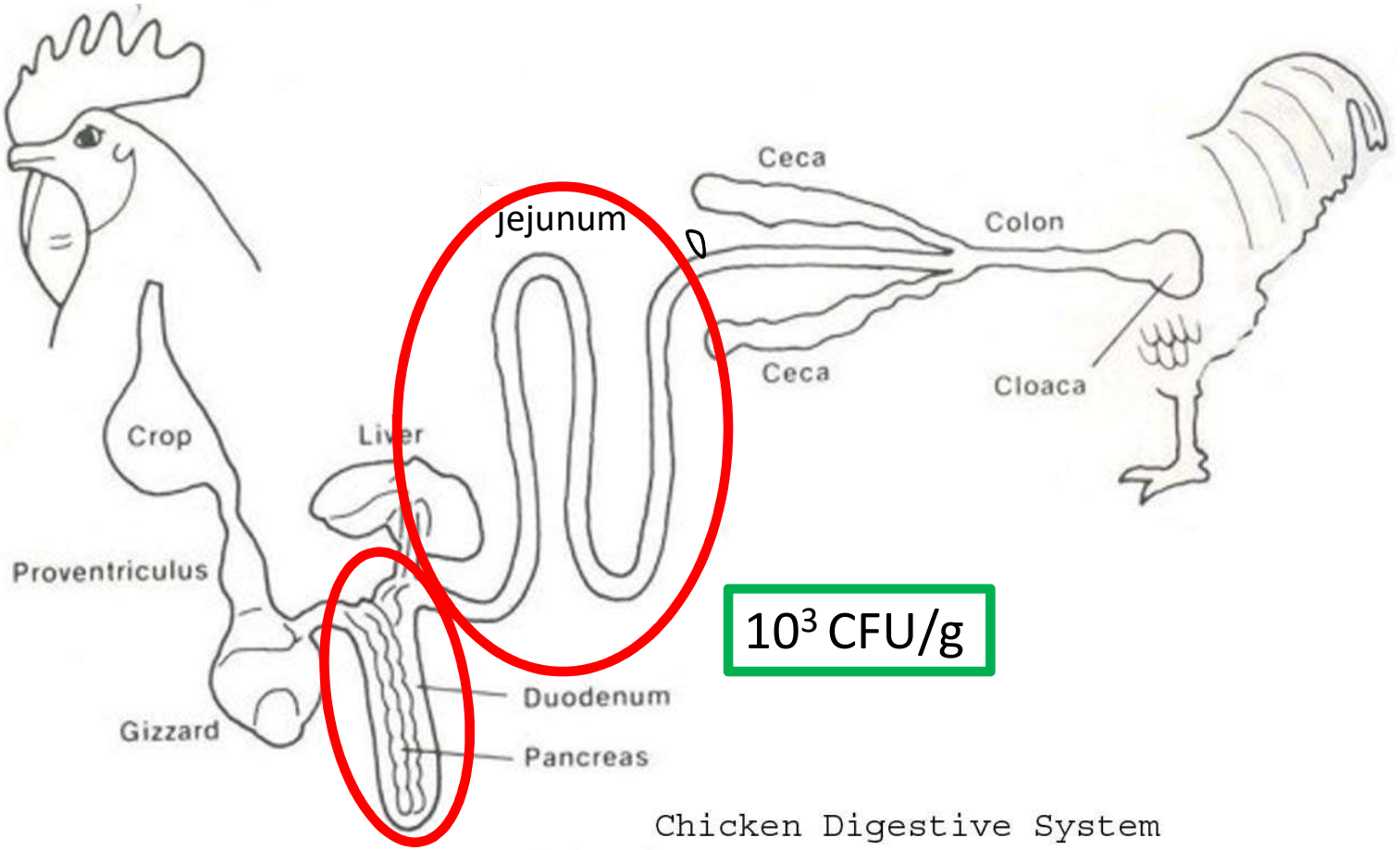
FACULTY OF VETERINARY MEDICINE
accredited by EAEVE

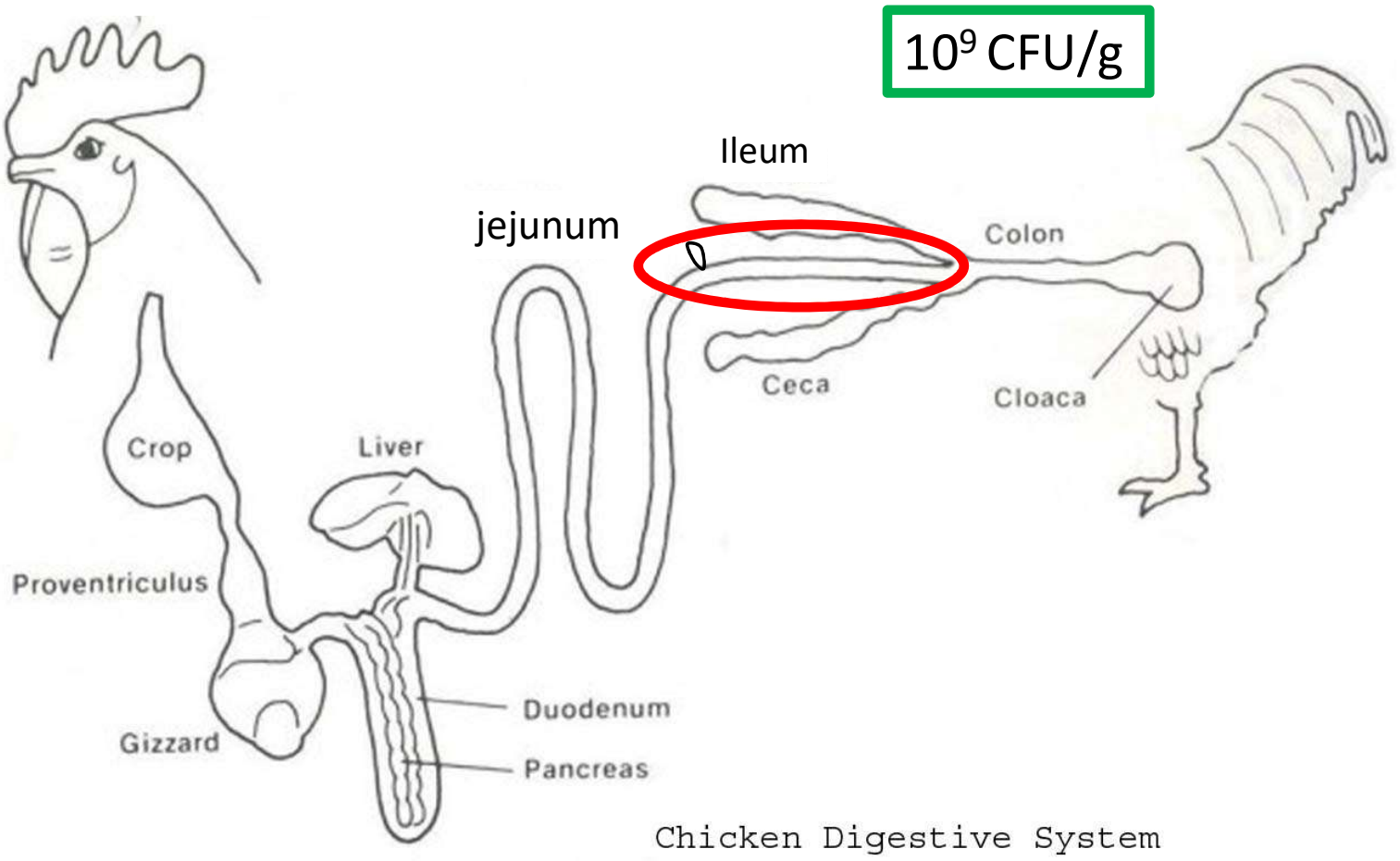
10^6 CFU/g

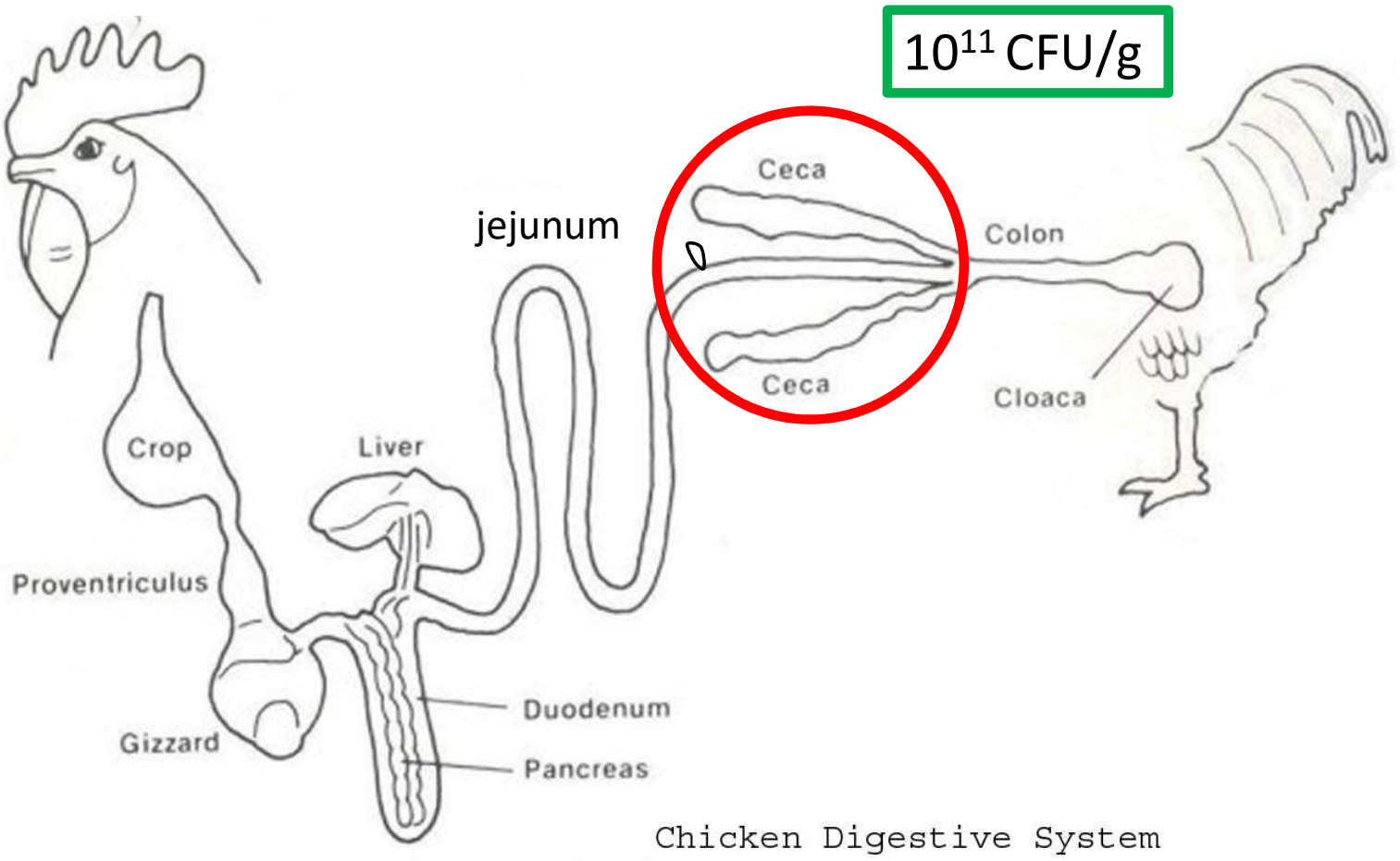


10^{11} CFU/g



Chicken Digestive System


10^9 CFU/g
Ileum
jejunum
Colon
Ceca
Cloaca
Crop
Liver
Proventriculus
Duodenum
Gizzard
Pancreas
Chicken Digestive System



Chicken Digestive System

The microbiota of the human colon

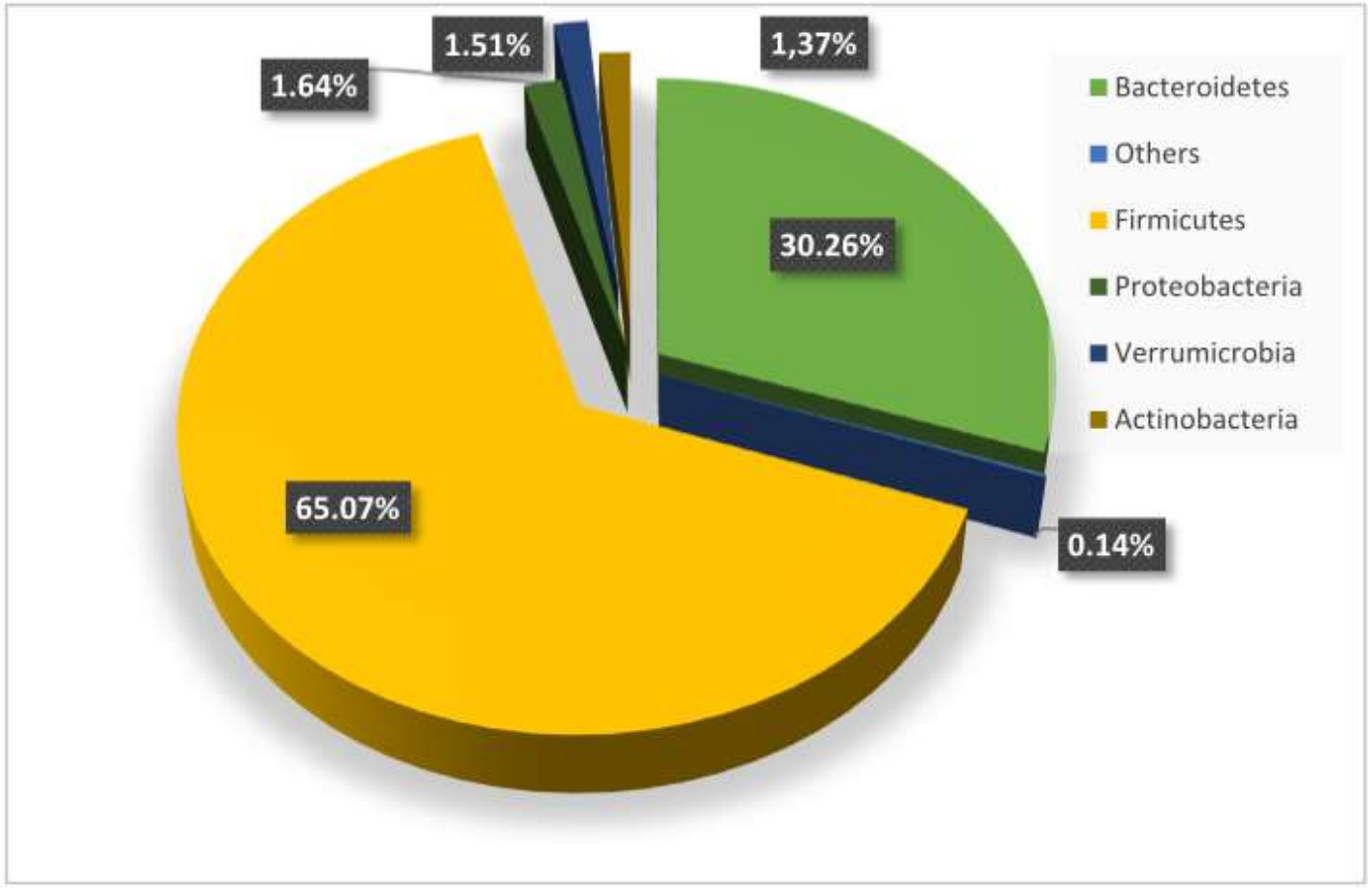
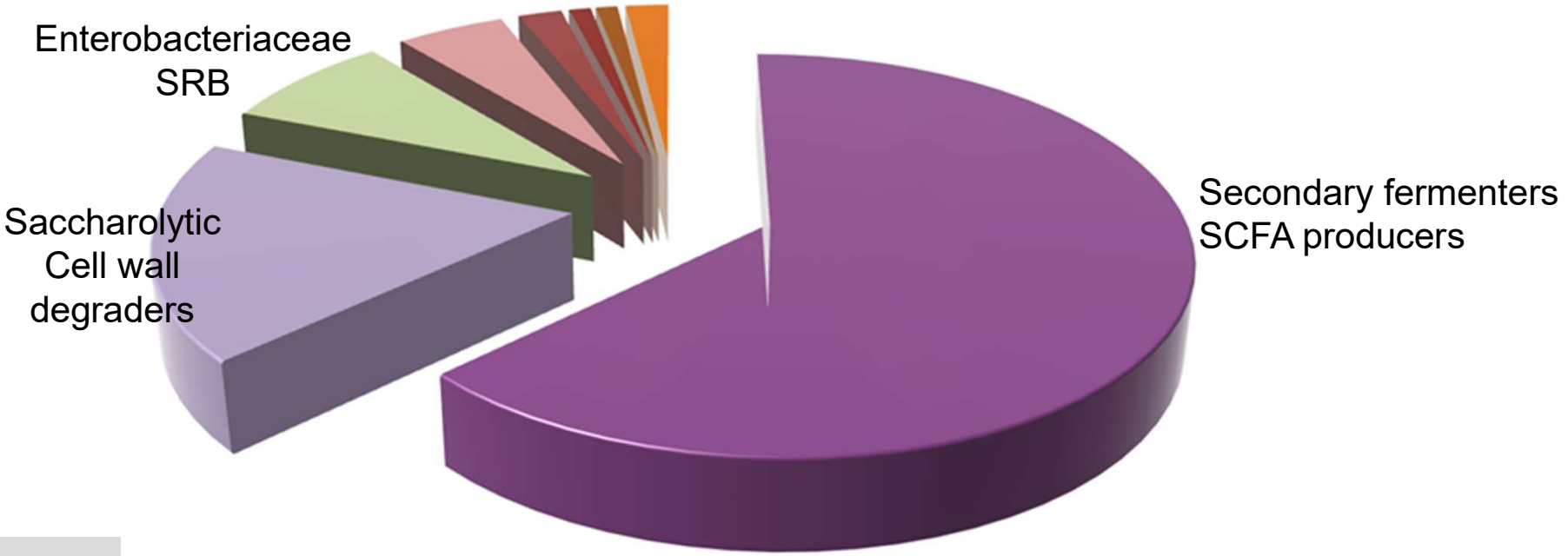


Fig. 2. Distribution of major bacterial phyla population according to their relative abundance in the human gut [28].

The mature microbiota of the chicken caeca



Dominant phyla:

Firmicutes	*Bacteroidetes*	*Proteobacteria*	*Actinobacteria*
Verrucomicrobia	*Spirochaetes*	*Fusobacteria*	other

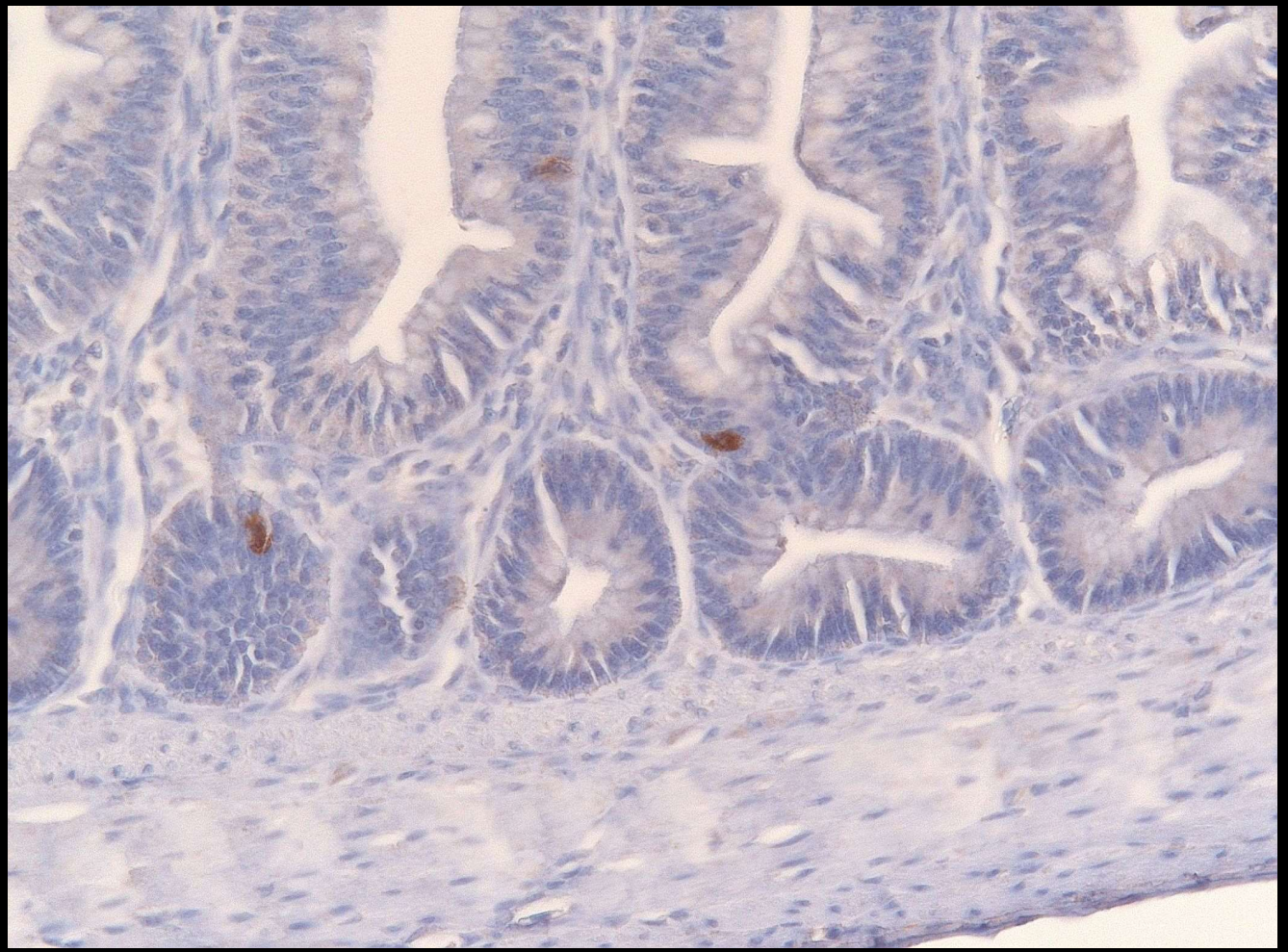
Short chain fatty acids, lactate, succinate, ….

Contribution to total energy harvest = 10%

Effects of butyrate

Interkingdom signaling

L-cells produce GLP2



Where does the microbiome come from?

Parent flock

Feed

Bacteria

Drinking water

Bacteria

Insects

Rodents

Bacteria

Bedding

Bacteria

Visitors

Farmer

Cats

Who is feeding the microbiome?

The host !

Gastroenterology Report, 7(1), 2019, 3–12

doi: 10.1093/gastro/goy052
Review

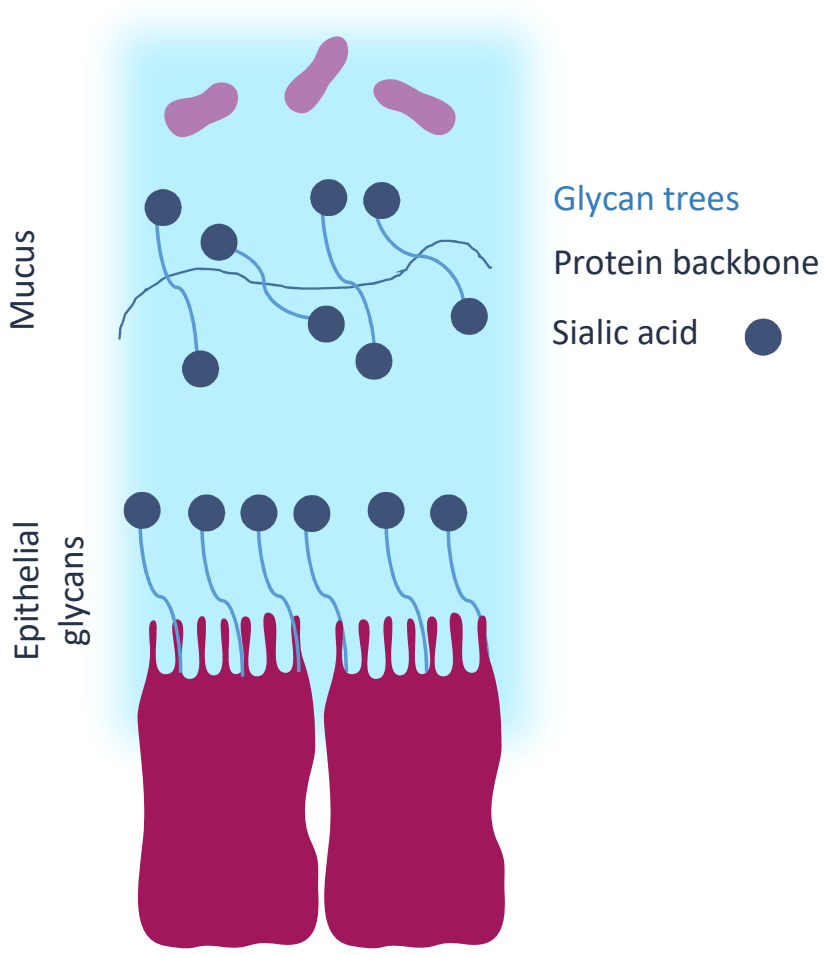
REVIEW

Fight them or feed them: how the intestinal mucus layer manages the gut microbiota

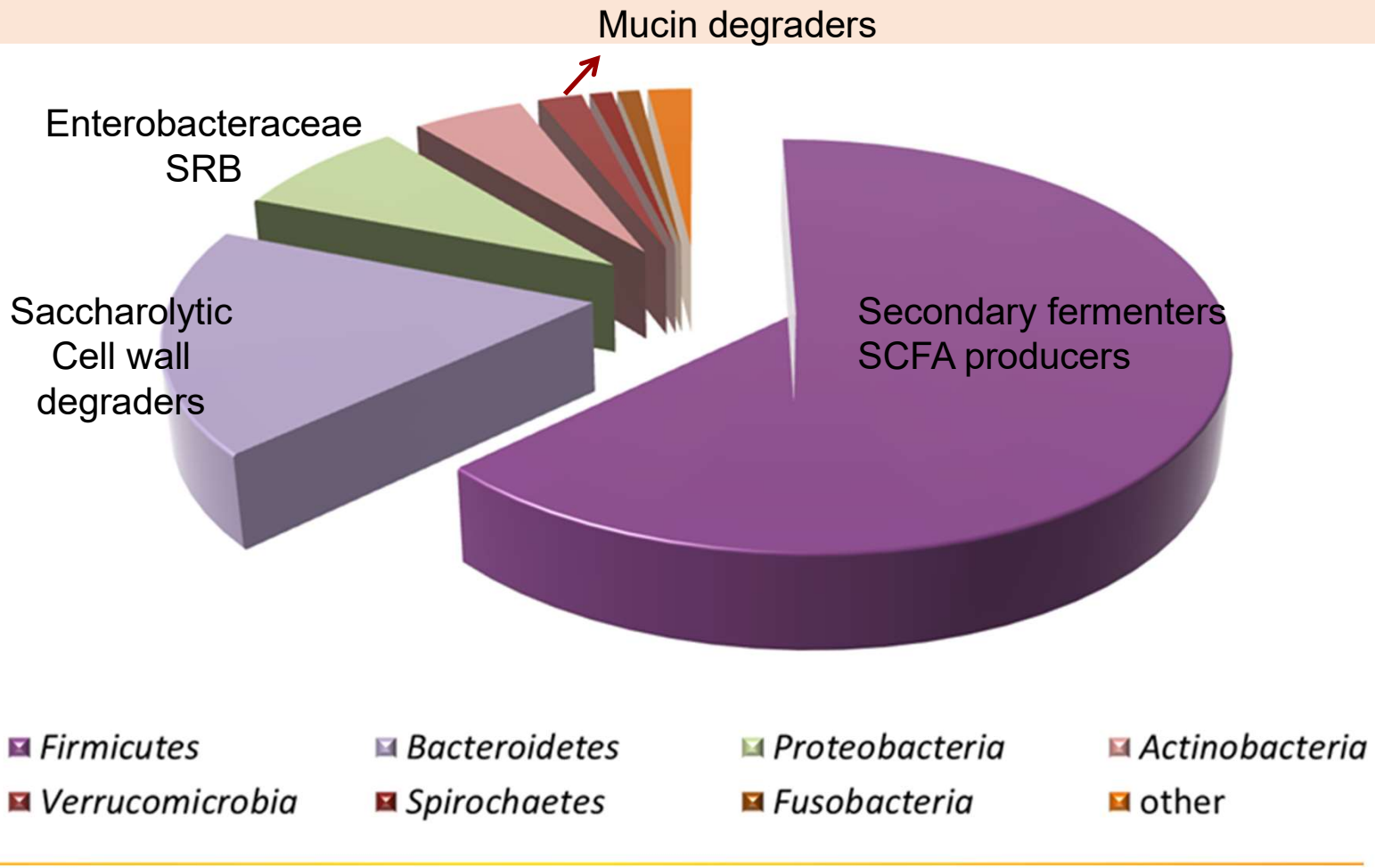
Bjoern O. Schroeder *

Wallenberg Laboratory and Sahlgrenska Center for Cardiovascular and Metabolic Research, Department of Molecular and Clinical Medicine, Institute of Medicine, Bruna Stråket 16, University of Gothenburg, SE 413 45 Gothenburg, Sweden

Intestinal mucus



The microbiota of the chicken gut



nature communications

Article

https://doi.org/10.1038/s41467-023-37533-6

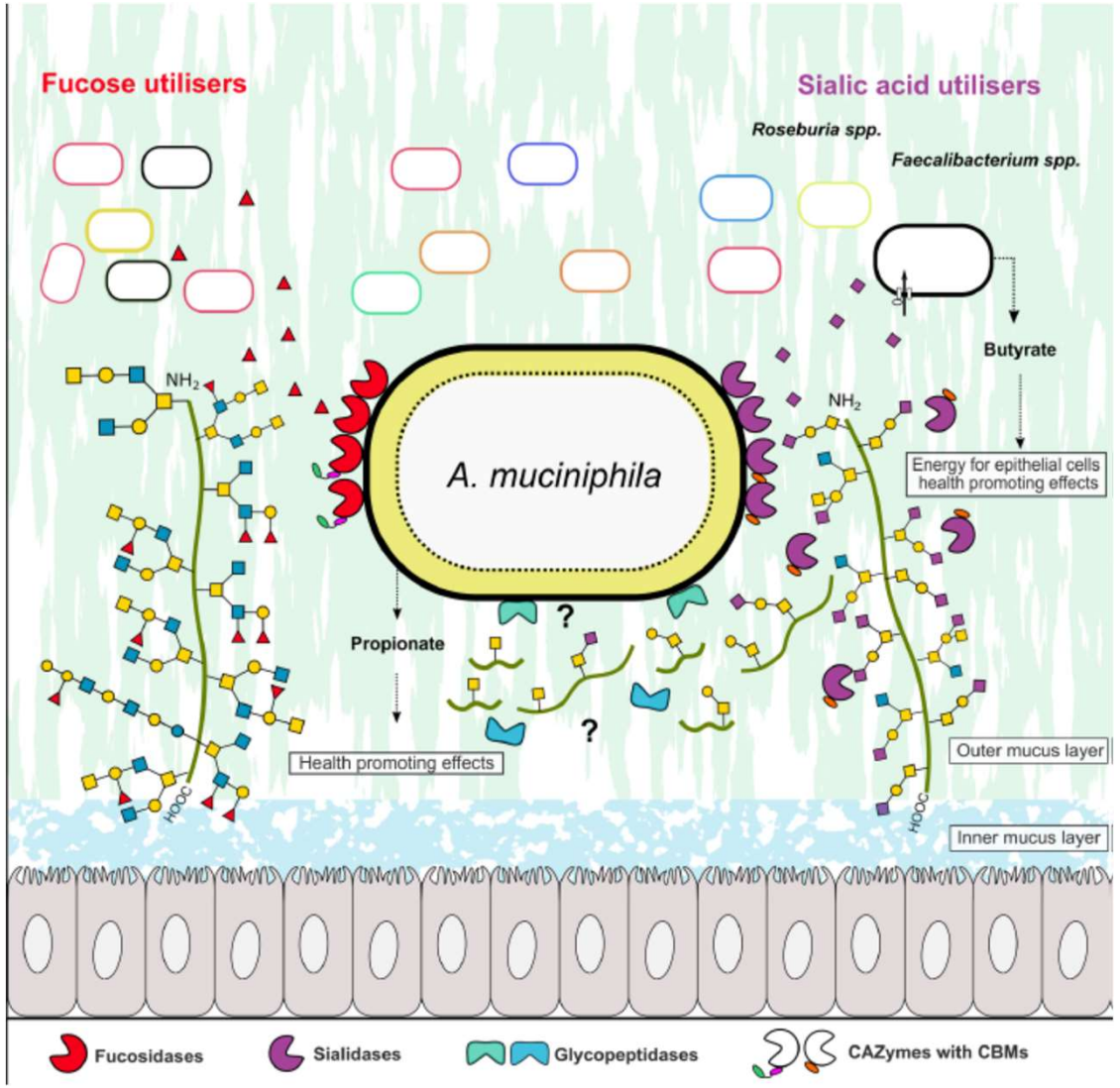
Sialidases and fucosidases of *Akkermansia muciniphila* are crucial for growth on mucin and nutrient sharing with mucus-associated gut bacteria

Received: 1 October 2022

Accepted: 21 March 2023

Published online: 01 April 2023

Bashar Shuoker[1,2,7], Michael J. Pichler[1,7], Chunsheng Jin[3], Hiroka Sakanaka[1], Haiyang Wu[4], Ana Martínez Gascueña[4], Jining Liu[5], Tine Sofie Nielsen[1], Jan Holgersson[5], Eva Nordberg Karlsson[2], Nathalie Juge[4], Sebastian Meier[6], Jens Preben Morth[1] ✉, Niclas G. Karlsson[3] & Maher Abou Hachem[1] ✉



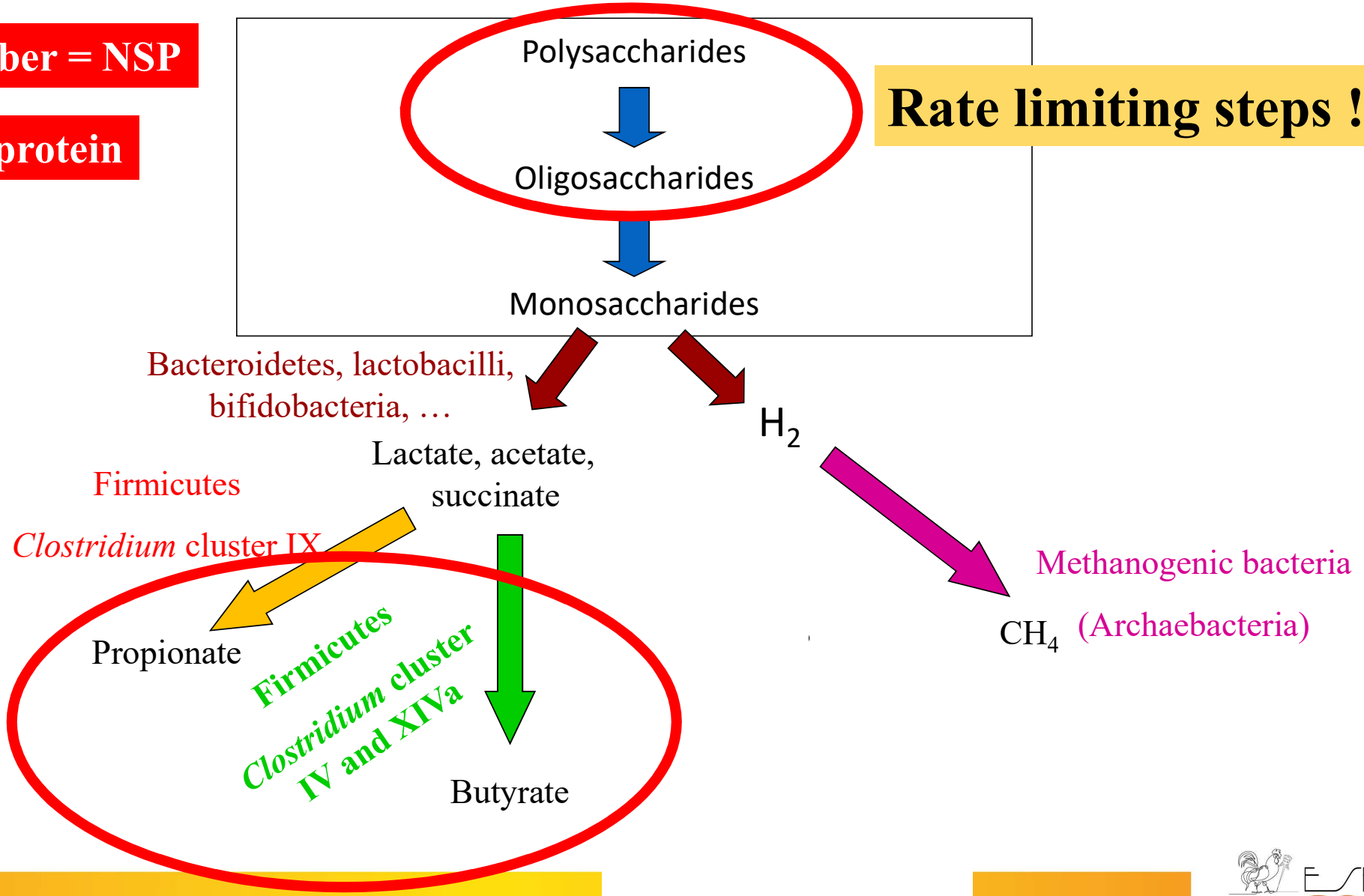
(Shuoker et al., 2023)

Feeding the microbiome?

The leftovers !

Dietary fiber = NSP

Residual protein



Rate limiting steps !

Dietary fiber

The portion of plant-derived food that cannot be completely broken down by digestive enzymes

Planta (2016) 243:281–296
DOI 10.1007/s00425-015-2450-x

REVIEW

The polyploidy and its key role in plant breeding

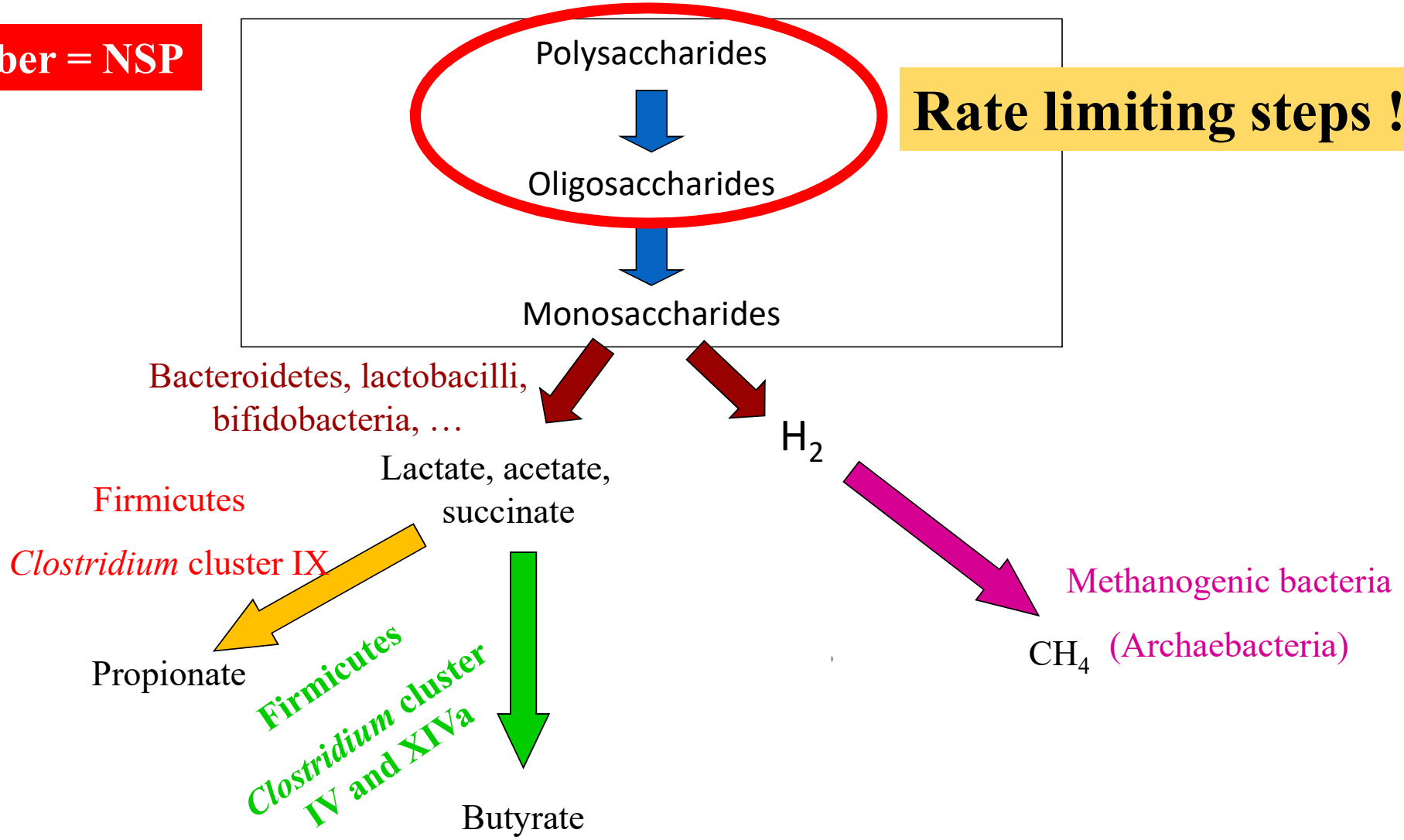
Mariana Cansian Sattler[1] · Carlos Roberto Carvalho[2] · Wellington Ronildo Clarindo[1]

Higher yields

Increased cell size

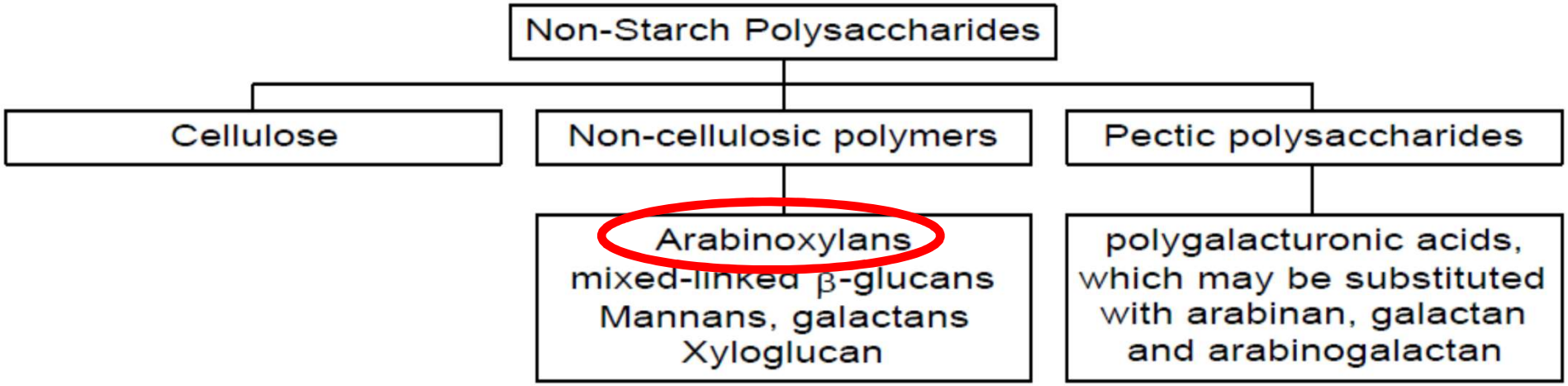
Less dietary fiber

Dietary fiber = NSP



Rate limiting steps !

Dietary fiber =

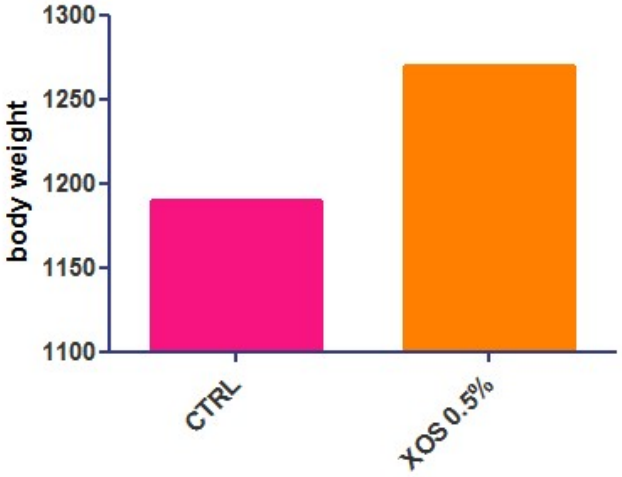


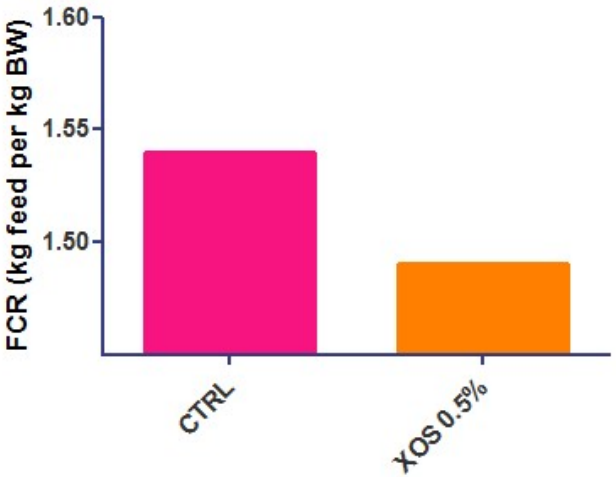
(Choct M., 1997)

Effects of oligosaccharide supplements: the case of XOS

Add 0.5% XOS to broiler feed

Day 26:



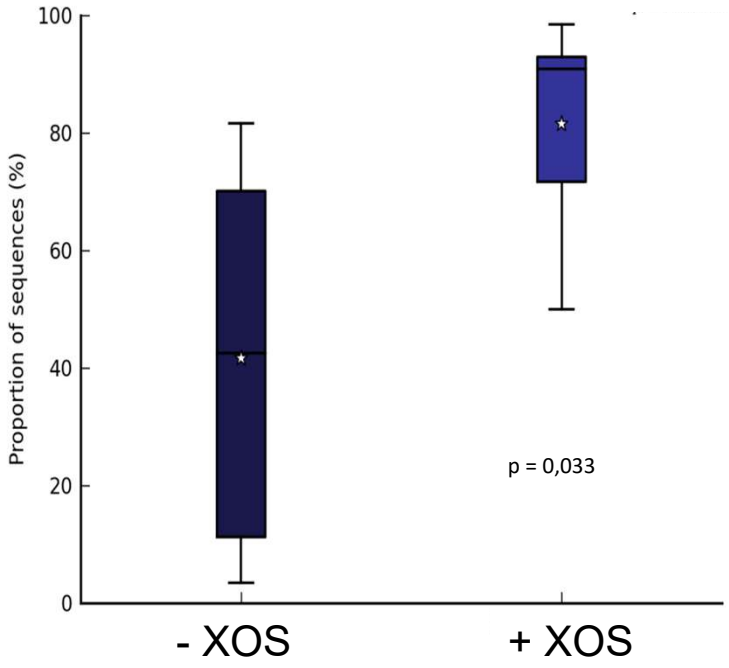


De Maesschalck et al., 2015

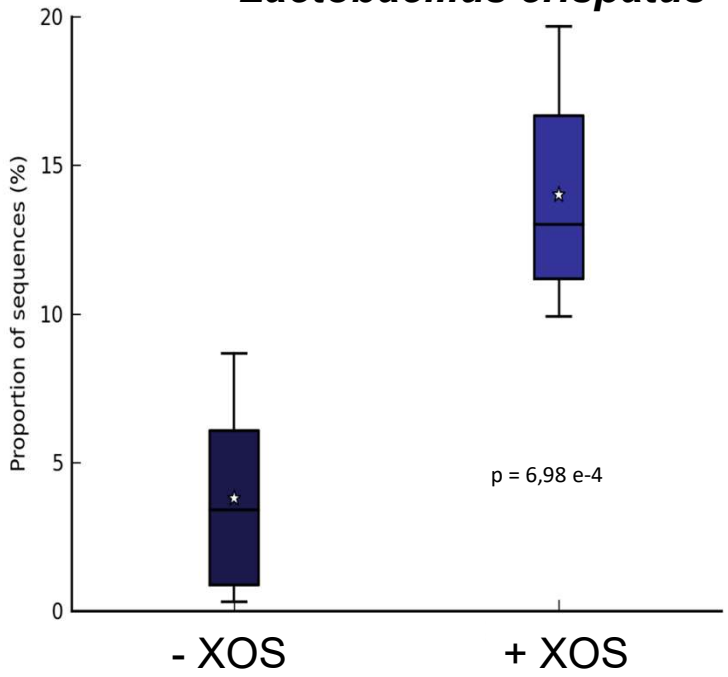
Microbiota

Colon

Lactobacillaceae



Lactobacillus crispatus

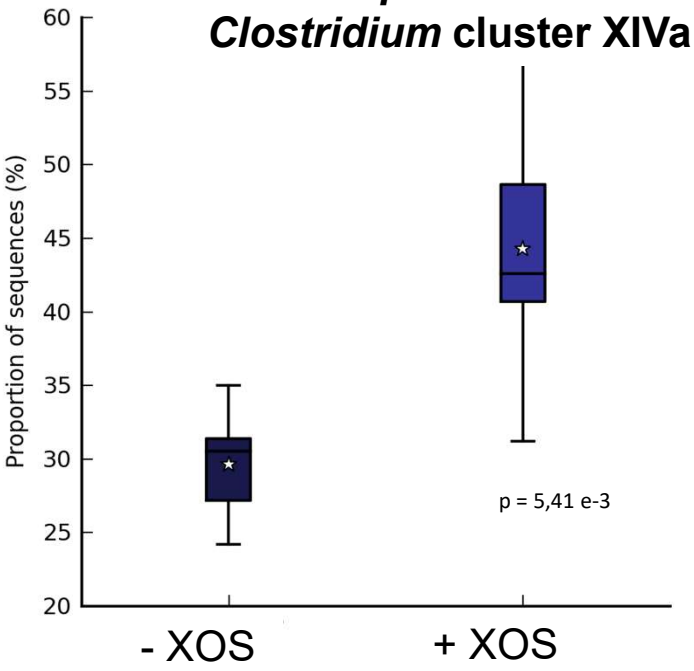


De Maesschalck et al., 2015

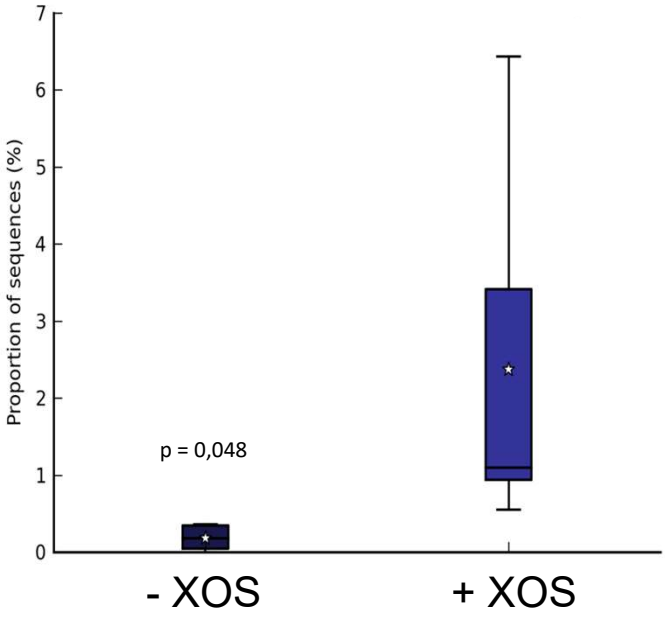
Microbiota

Caecum

***Lachnospiraceae* = *Clostridium* cluster XIVa**

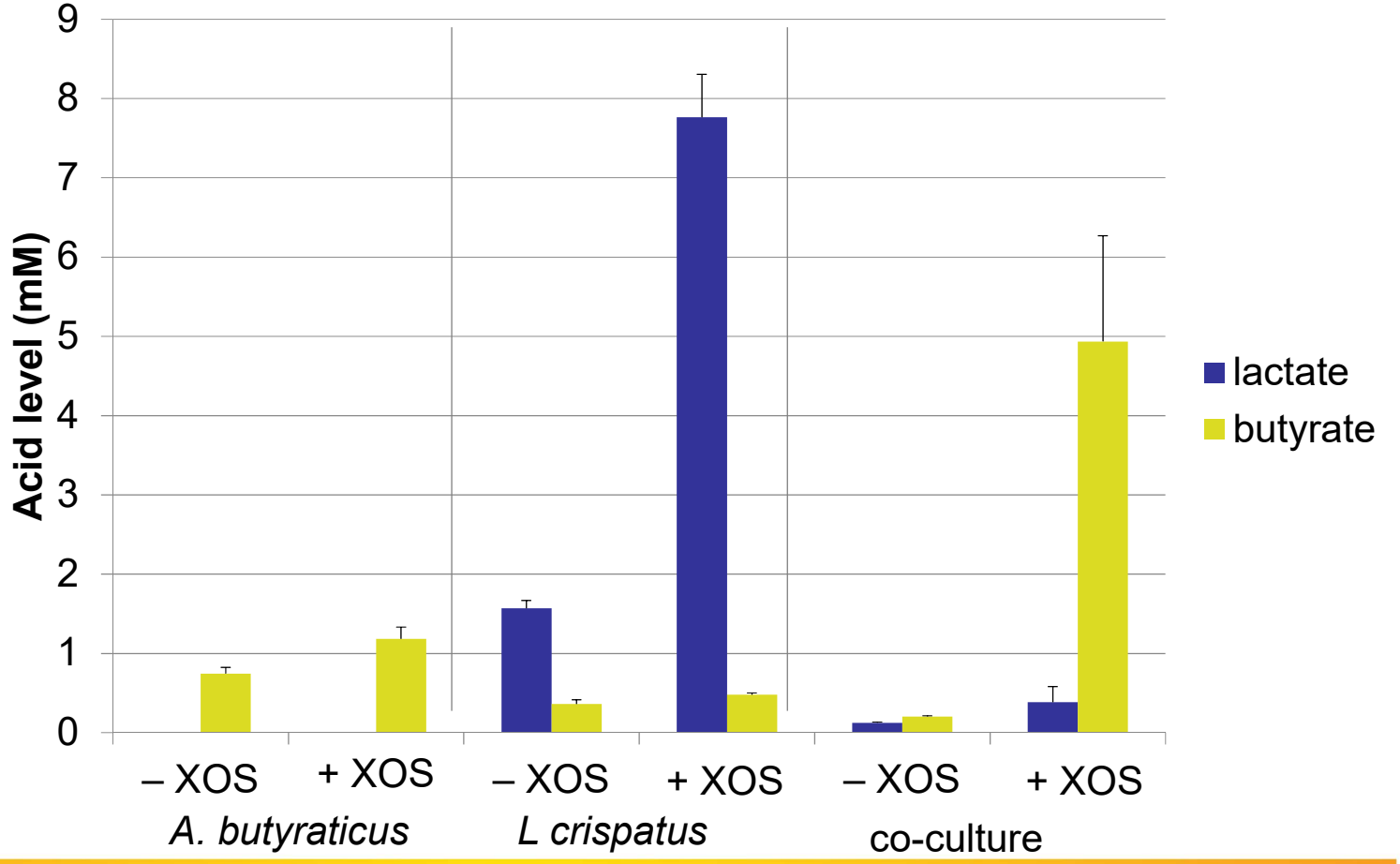


Anaerostipes butyraticus



De Maesschalck et al., 2015

Cross-feeding

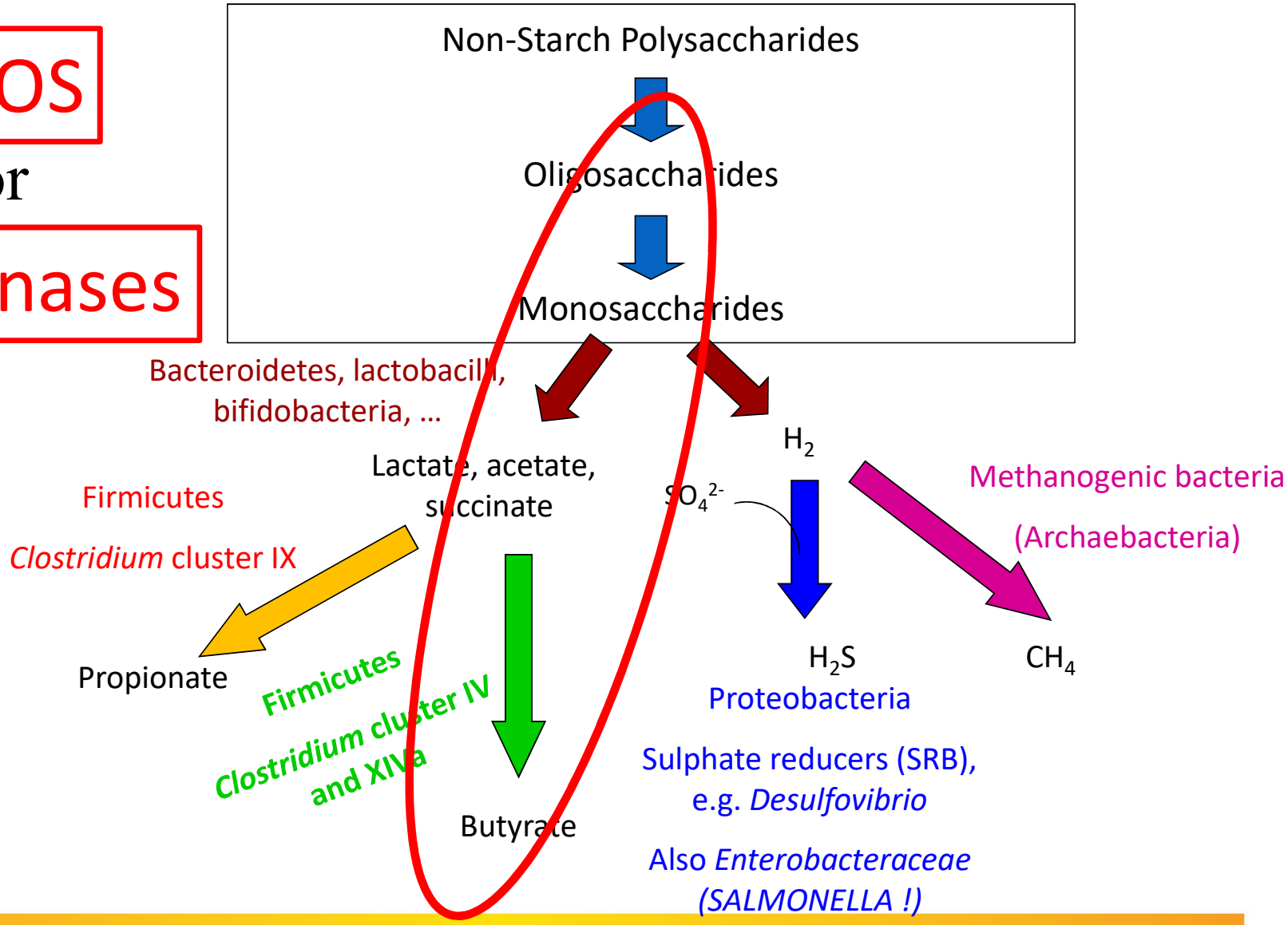


De Maesschalck et al., 2014

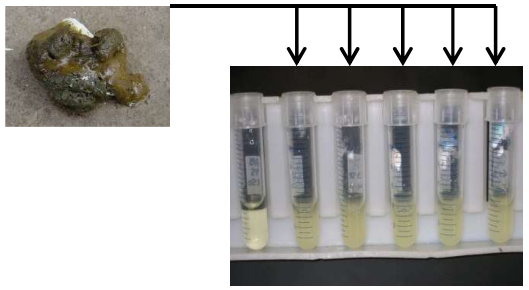
+ XOS

or

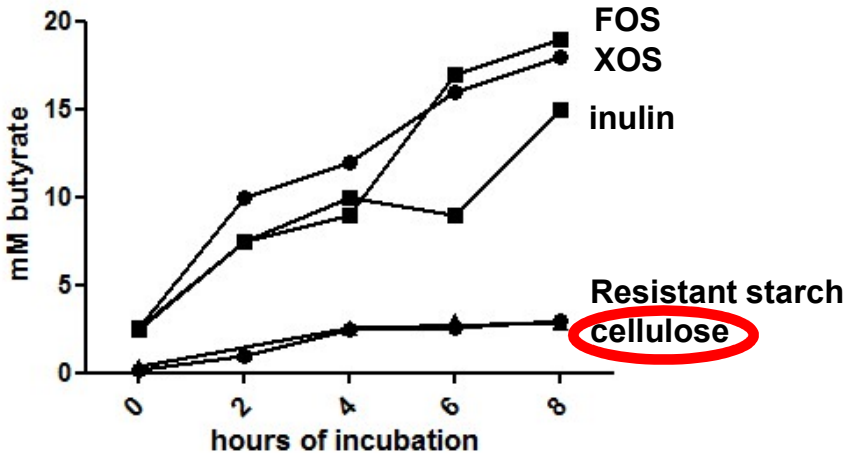
+ xylanases



Effects of different prebiotics on cecal butyrate producing microbiota

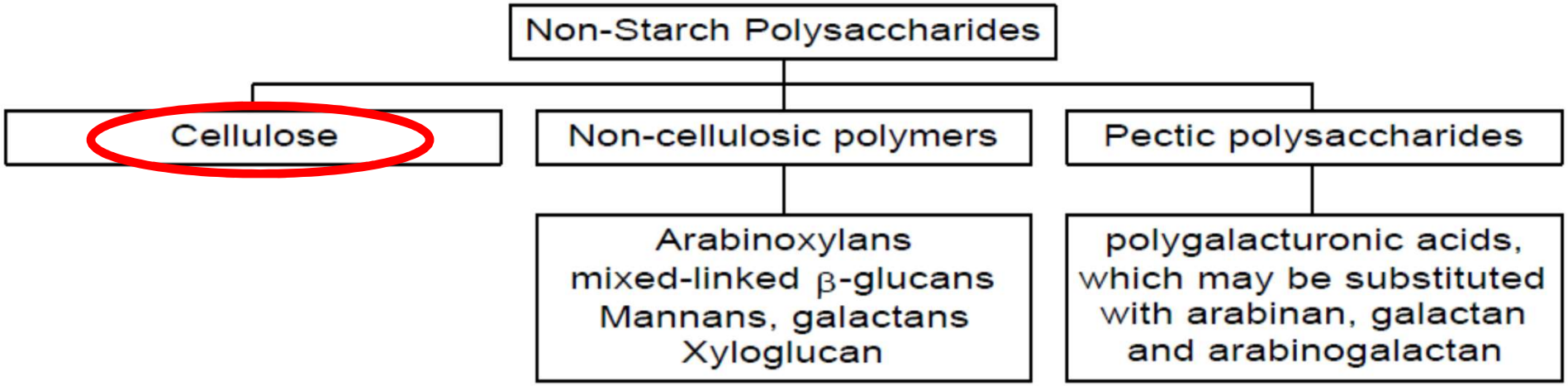


+ substrates
Measure SCFA during time



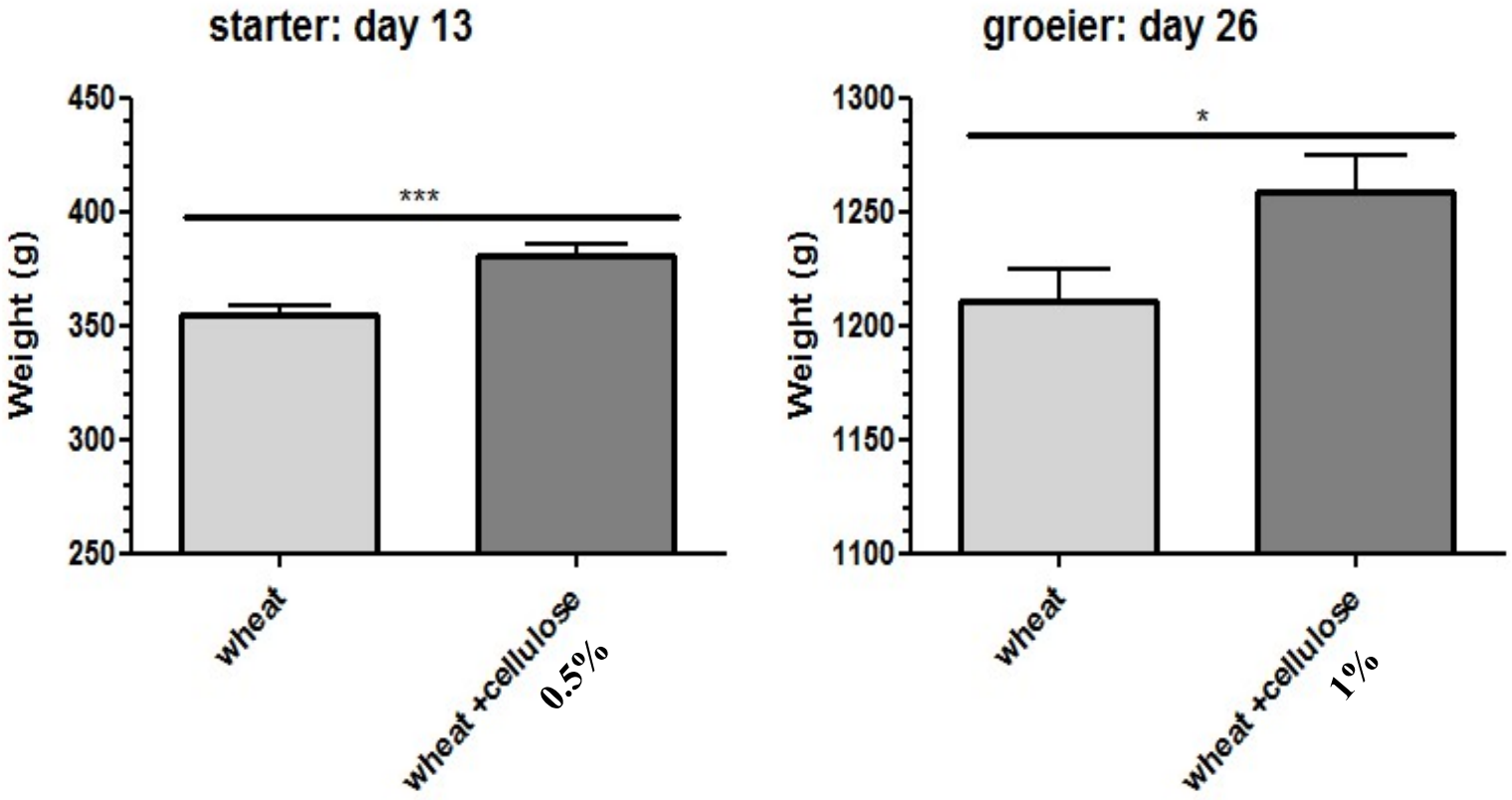
De Maesschalck et al., 2015

Dietary fiber =



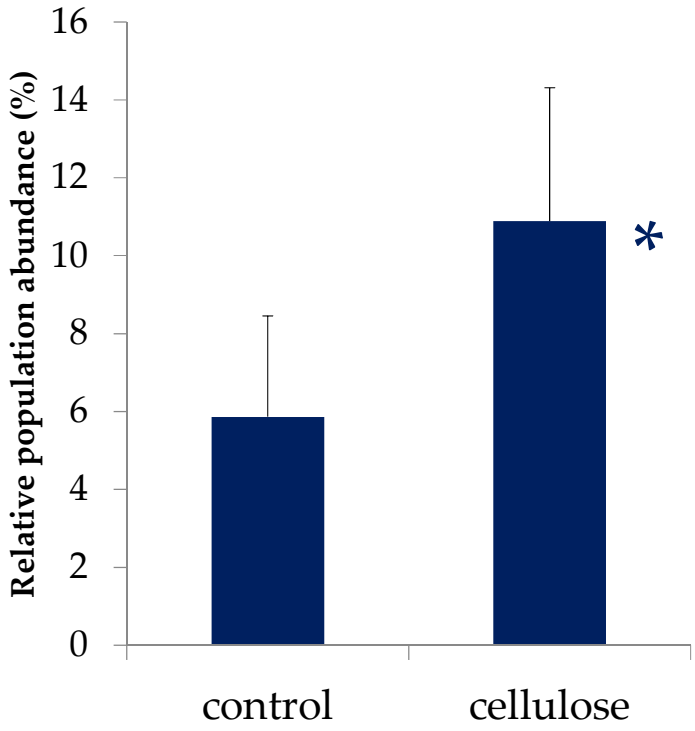
(Choct M., 1997)

in vivo effects of cellulose



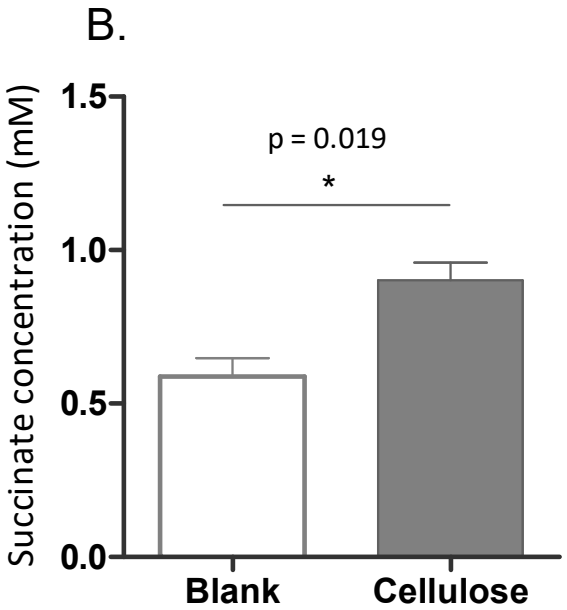
Microbiota composition: caeca

Alistipes

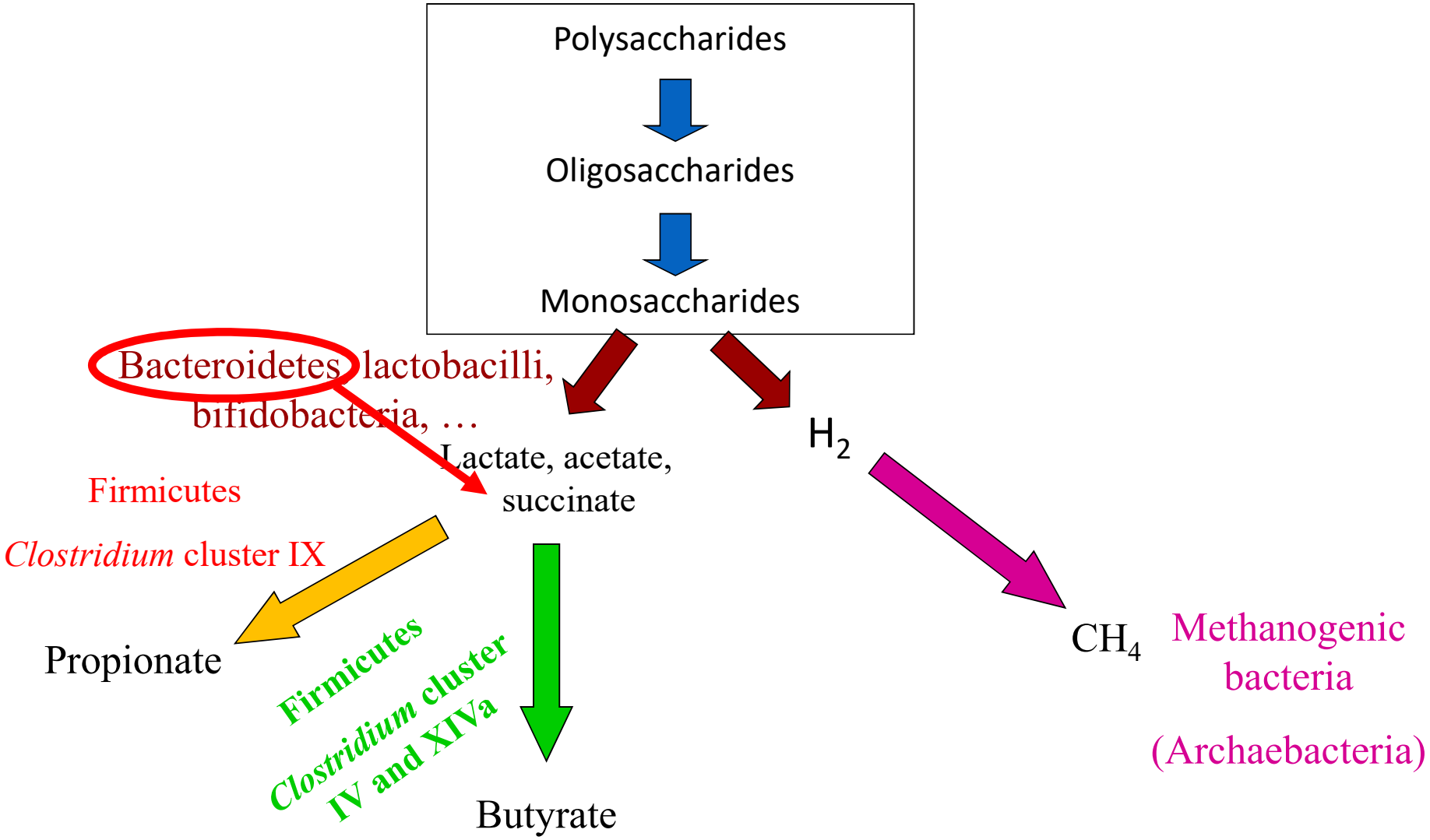


phylum: *Bacteroidetes*
class: *Bacteroidia*
order: *Bacteroidales*
family: *Rikenellaceae*
genus: *Alistipes*

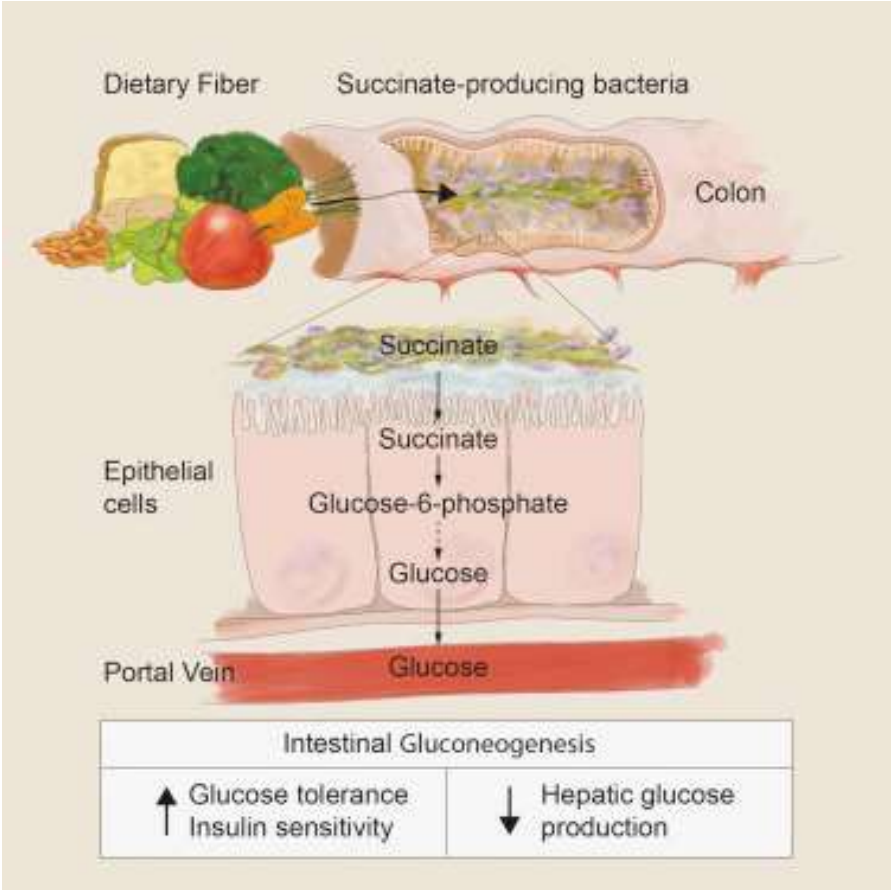
Succinate production by *Alistipes finegoldii* in the presence of cellulose



Cellulose breakdown in the intestinal lumen does not require a microbial network


Polysaccharides
Oligosaccharides
Monosaccharides
Bacteroidetes, lactobacilli, bifidobacteria, …
Lactate, acetate, succinate
H_2
Firmicutes
Clostridium cluster IX
Propionate
Firmicutes
Clostridium cluster IV and XIVa
Butyrate
CH_4
Methanogenic bacteria
(Archaebacteria)

Microbiota-Produced Succinate Improves Glucose Homeostasis via Intestinal Gluconeogenesis



Filipe De Vadder, Petia Kovatcheva-Datchary, Carine Zitoun, Adeline Duchampt, Fredrik Bäckhed, Gilles Mithieux

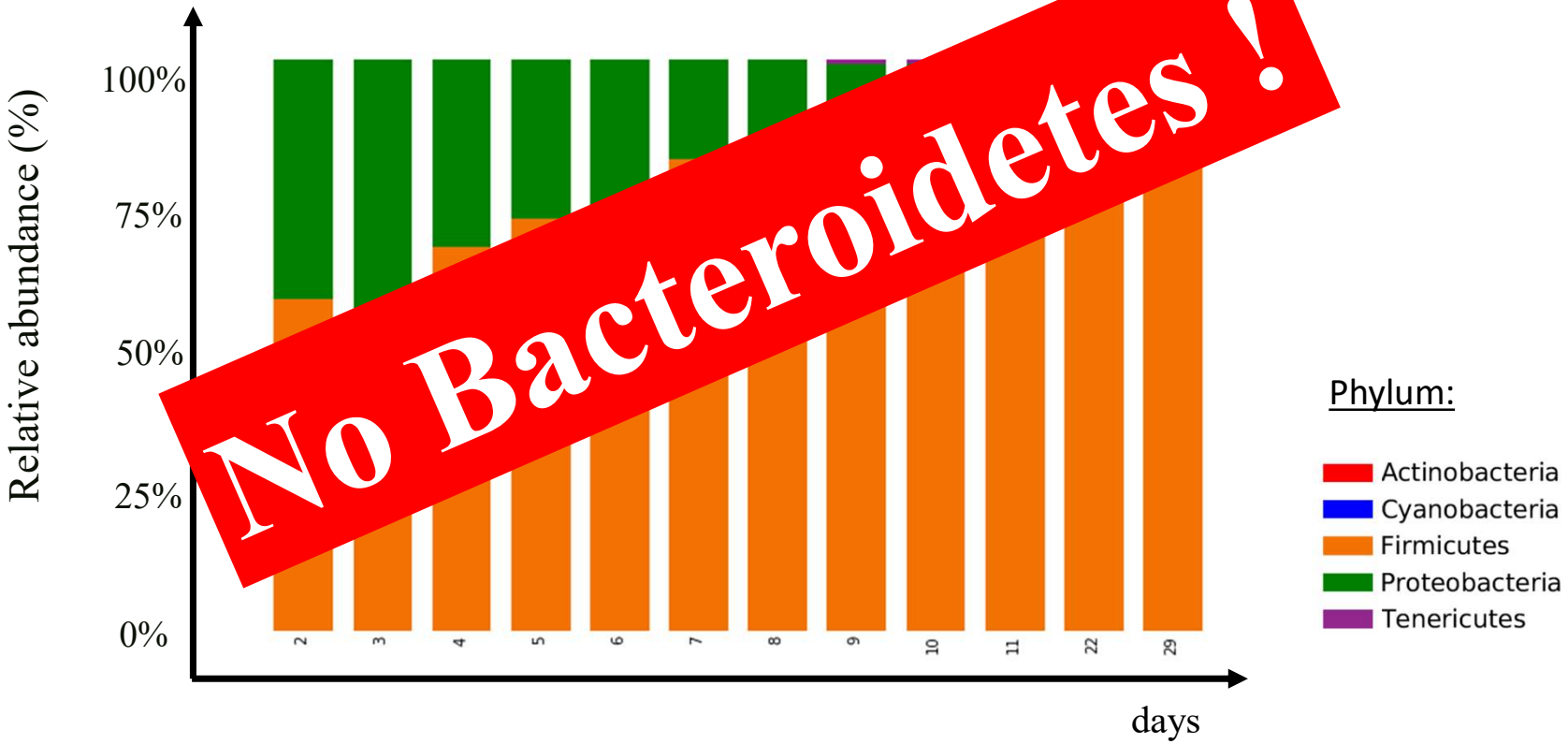
Cell Metabolism, Volume 24, Issue 1, 2016, 151–157

Relative abundance of the families

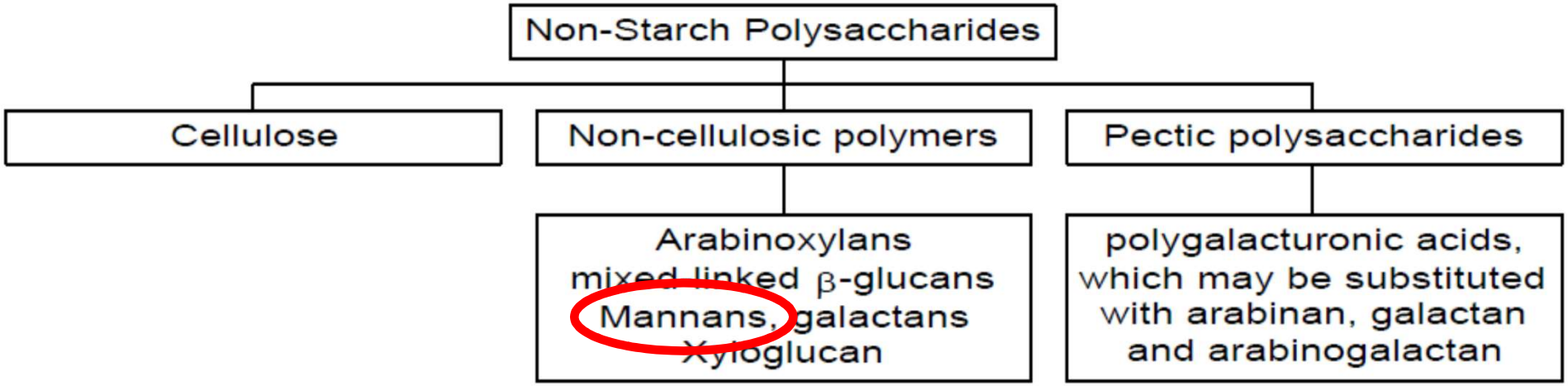
No Rikenellaceae !

D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Corynebacteriales;D_4__Corynebacteriaceae
D_0__Bacteria;D_1__Actinobacteria;D_2__Actinobacteria;D_3__Micrococcales;D_4__Micrococcaceae
D_0__Bacteria;D_1__Actinobacteria;D_2__Coriobacteriia;D_3__Coriobacteriales;D_4__Eggerthellaceae
D_0__Bacteria;D_1__Cyanobacteria;D_2__Oxyphotobacteria;D_3__Chloroplast;D_4__Phaseolus acutifolius (tepary bean)
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Bacillaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Paenibacillaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Bacillales;D_4__Staphylococcaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Enterococcaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Bacilli;D_3__Lactobacillales;D_4__Lactobacillaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Christensenellaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiaceae 1
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Clostridiales vadinBB60 group
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Lachnospiraceae
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Peptostreptococcaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;D_4__Ruminococcaceae
D_0__Bacteria;D_1__Firmicutes;D_2__Clostridia;D_3__Clostridiales;Other
D_0__Bacteria;D_1__Firmicutes;D_2__Erysipelotrichia;D_3__Erysipelotrichales;D_4__Erysipelotrichaceae
D_0__Bacteria;D_1__Proteobacteria;D_2__Alphaproteobacteria;D_3__Rickettsiales;D_4__Mitochondria
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Betaproteobacteriales;D_4__Burkholderiaceae
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Enterobacteriales;D_4__Enterobacteriaceae
D_0__Bacteria;D_1__Proteobacteria;D_2__Gammaproteobacteria;D_3__Pseudomonadales;D_4__Pseudomonadaceae
D_0__Bacteria;D_1__Tenericutes;D_2__Mollicutes;D_3__Mollicutes RF39;D_4__uncultured bacterium

Relative abundance of the phyla



Dietary fiber =



(Choct M., 1997)

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RESEARCH ARTICLE

May/June 2021 Volume 12 Issue 3 e03628-20

Human Gut *Faecalibacterium prausnitzii* Deploys a Highly Efficient Conserved System To Cross-Feed on β-Mannan-Derived Oligosaccharides

Lars J. Lindstad,[a] Galiana Lo,[b] Shaun Leivers,[a] Zijia Lu,[c] Leszek Michalak,[a] Gabriel V. Pereira,[d] Åsmund K. Røhr,[a] Eric C. Martens,[d] Lauren S. McKee,[c] Petra Louis,[b] Sylvia H. Duncan,[b] Bjørge Westereng,[a] Phillip B. Pope,[a,e] Sabina Leanti La Rosa[a,e]

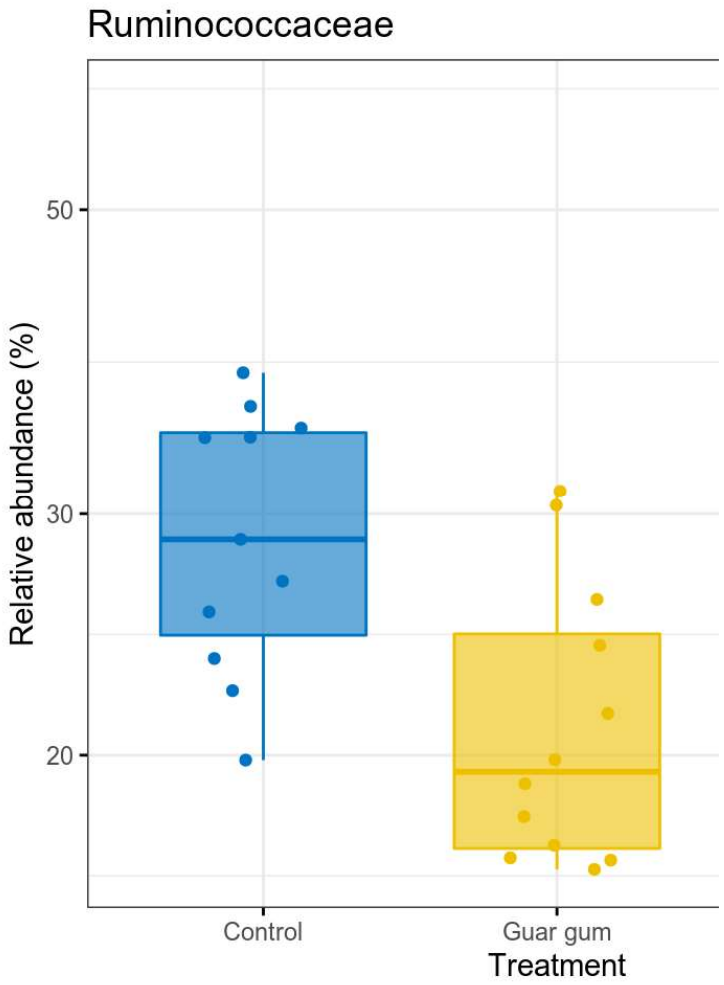
Primary degraders:

Bacteroides ovatus

Roseburia intestinalis

→ Mannan oligosaccharides (MOS)

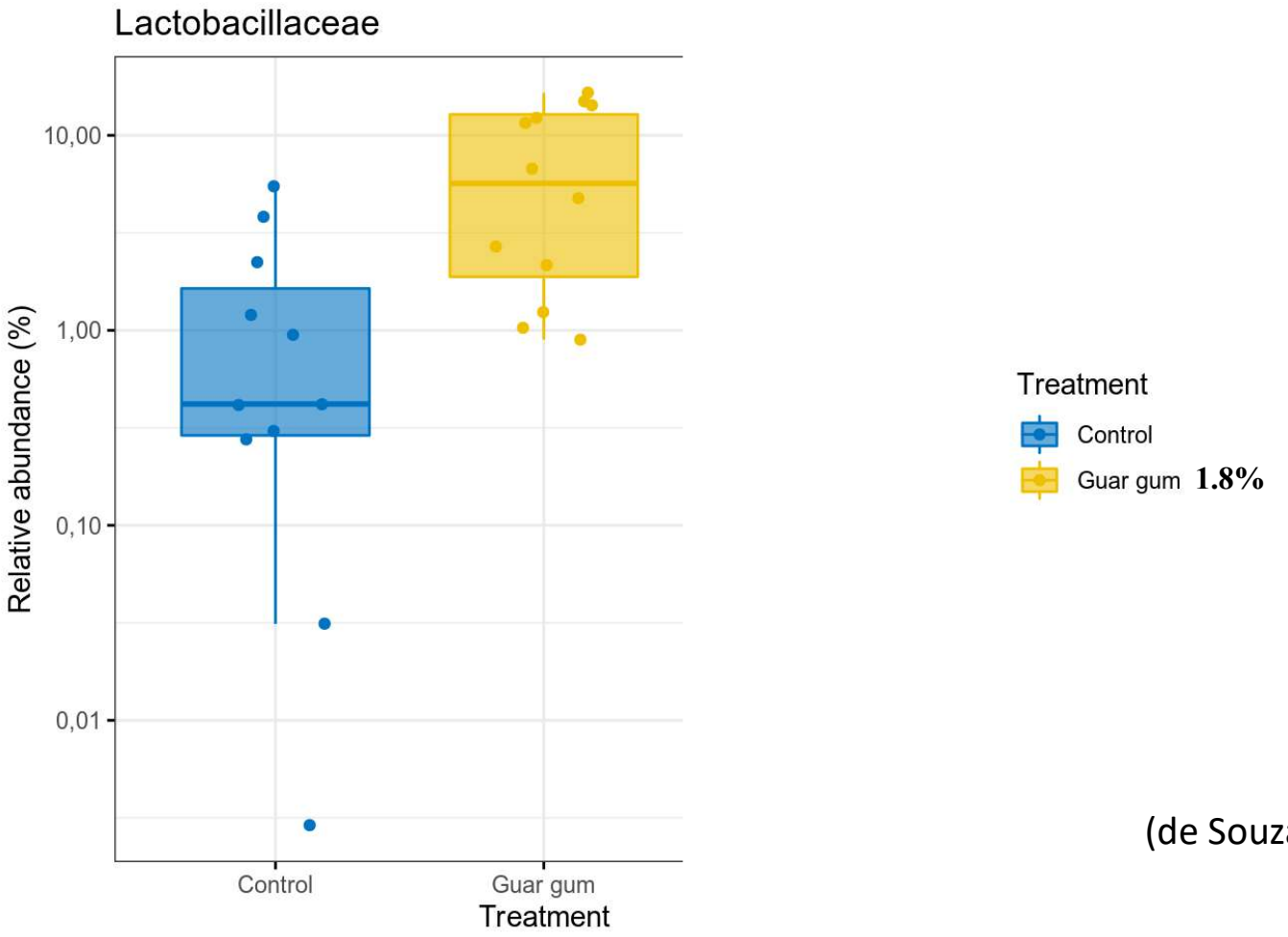
Caecum day 28



Treatment
Control
Guar gum **1.8%**

(de Souza et al., in press)

Caecum day 28



(de Souza et al., in press)

foods

MDPI

Article

Metabolic Conversions by Lactic Acid Bacteria during Plant Protein Fermentations

Wim Engels [1,*], Jamie Siu [1,2], Saskia van Schalkwijk [1], Wilma Wesselink [1], Simon Jacobs [1] and Herwig Bachmann [1,3]

Foods **2022**, *11*, 1005. https://doi.org/10.3390.

GUT MICROBES
2022, VOL. 14, NO. 1, e2046452 (19 pages)
https://doi.org/10.1080/19490976.2022.2046452

Taylor & Francis
Taylor & Francis Group

RESEARCH PAPER

OPEN ACCESS Check for updates

Acids produced by lactobacilli inhibit the growth of commensal *Lachnospiraceae* and S24-7 bacteria

Emma J. E. Brownlie*, Danica Chaharlangi*, Erin Oi-Yan Wong, Deanna Kim, and William Wiley Navarre

Department of Molecular Genetics, University of Toronto, Toronto, ON, Canada

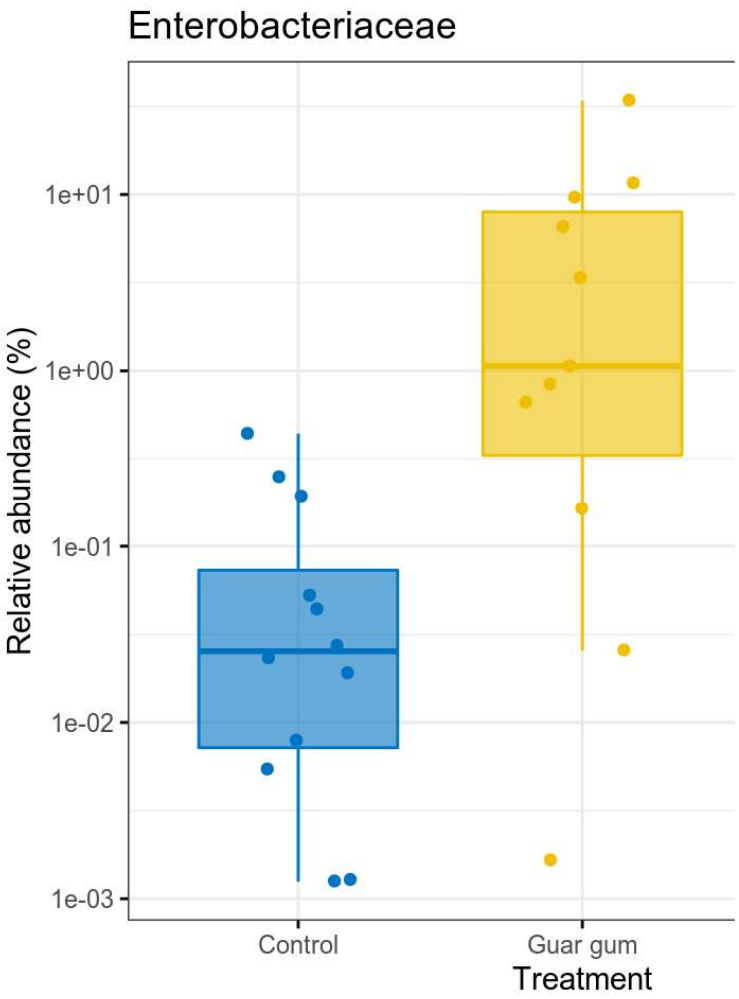
ABSTRACT

The *Lactobacillaceae* are an intensively studied family of bacteria widely used in fermented food and probiotics, and many are native to the gut and vaginal microbiota of humans and other animals. Various studies have shown that specific *Lactobacillaceae* species produce metabolites that can inhibit the colonization of fungal and bacterial pathogens, but less is known about how *Lactobacillaceae* affect individual bacterial species in the endogenous animal microbiota. Here, we show that numerous *Lactobacillaceae* species inhibit the growth of the *Lachnospiraceae* family and the S24-7 group, two dominant clades of bacteria within the gut. We demonstrate that inhibitory activity is a property common to homofermentative *Lactobacillaceae* species, but not to species that use heterofermentative metabolism. We observe that homofermentative *Lactobacillaceae* species robustly acidify their environment, and that acidification alone is sufficient to inhibit growth of *Lachnospiraceae* and S24-7 growth, but not related species from the *Clostridiales* or *Bacteroidales* orders. This study represents one of the first in-depth explorations of the dynamic between *Lactobacillaceae* species and commensal intestinal bacteria, and contributes valuable insight toward deconvoluting their interactions within the gut microbial ecosystem.

ARTICLE HISTORY
Received 28 September 2021
Revised 9 February 2022
Accepted 18 February 2022

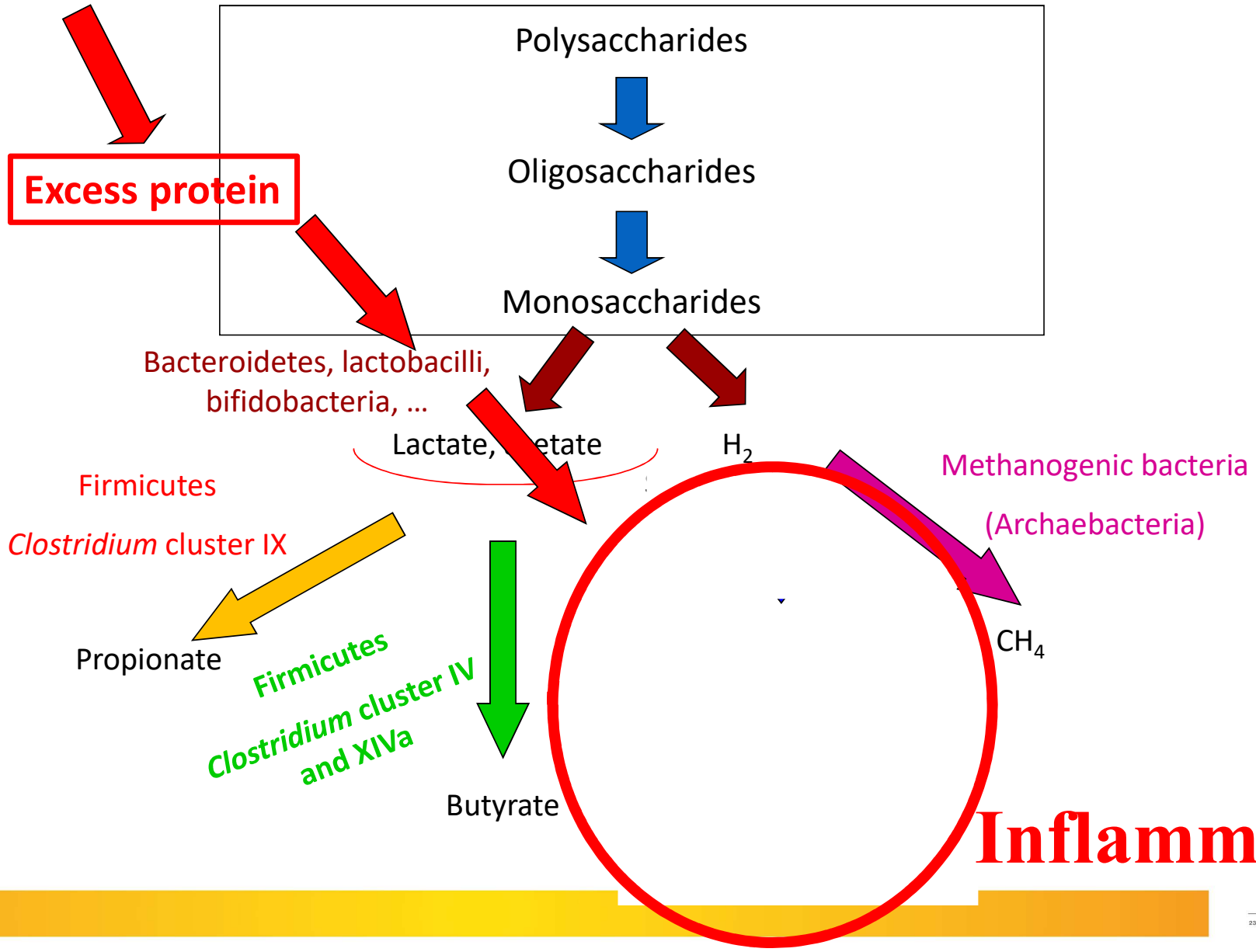
KEYWORDS
Probiotics; lactobacilli; lactic acid bacteria; *Bacteroidales*; *Clostridiales*; microbiota; gut; acid stress; Lachnospiraceae; Muribaculaceae; S24-7

Ileum day 14



Treatment
Control
Guar gum **1.8%**

(de Souza et al., in preparation)


Polysaccharides
Oligosaccharides
Monosaccharides
Excess protein
Bacteroidetes, lactobacilli,
bifidobacteria, …
Lactate,
etate
H_2
Methanogenic bacteria
(Archaebacteria)
Firmicutes
Clostridium cluster IX
Propionate
Firmicutes
Clostridium cluster IV
and XIVa
Butyrate
CH_4
Inflammation !!

Take home messages

* Microbial activity in the caeca determines the efficacy of digestion and absorption in the small intestine

* Most broiler feed formulas lack the necessary NSP to support the caecal microbiota

* Microbiota of young broilers have difficult to degrade the complex network of plant cell wall polysaccharides

* Added pure NSP, prebiotics, enzymes, etc all can support the caecal microbial network

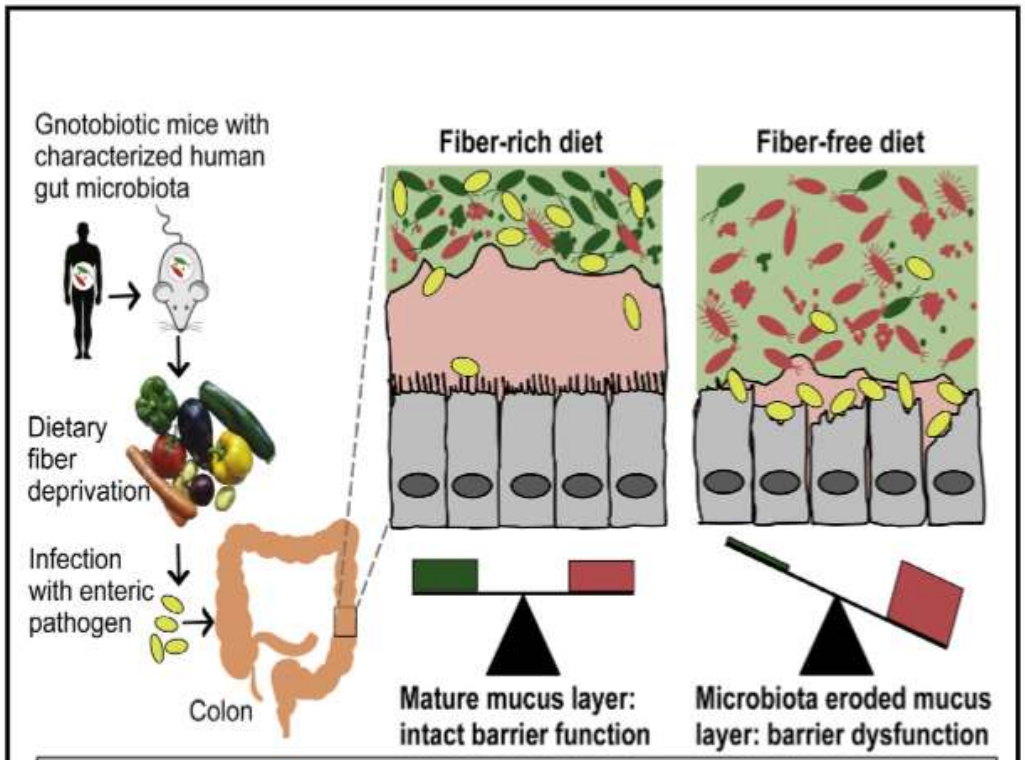
* Proteolytic expansion of Proteobacteria should be avoided

and….

Cell

A Dietary Fiber-Deprived Gut Microbiota Degrades the Colonic Mucus Barrier and Enhances Pathogen Susceptibility

Graphical Abstract



Authors

Mahesh S. Desai, Anna M. Seekatz, Nicole M. Koropatkin, ..., Thaddeus S. Stappenbeck, Gabriel Núñez, Eric C. Martens

Correspondence

mahesh.desai@lih.lu (M.S.D.), emartens@umich.edu (E.C.M.)

In Brief

Regular consumption of dietary fiber helps prevent erosion of the intestinal mucus barrier by the gut microbiome, blunting pathogen infection and reducing the incidence of colitis.

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Thank you for your attention

LIVESTOCK GUT HEALTH TEAM GHENT

richard.ducatelle@ugent.be

LIGHT
Livestock Gut Health Team Ghent

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