Webinar PAIS and butyrate

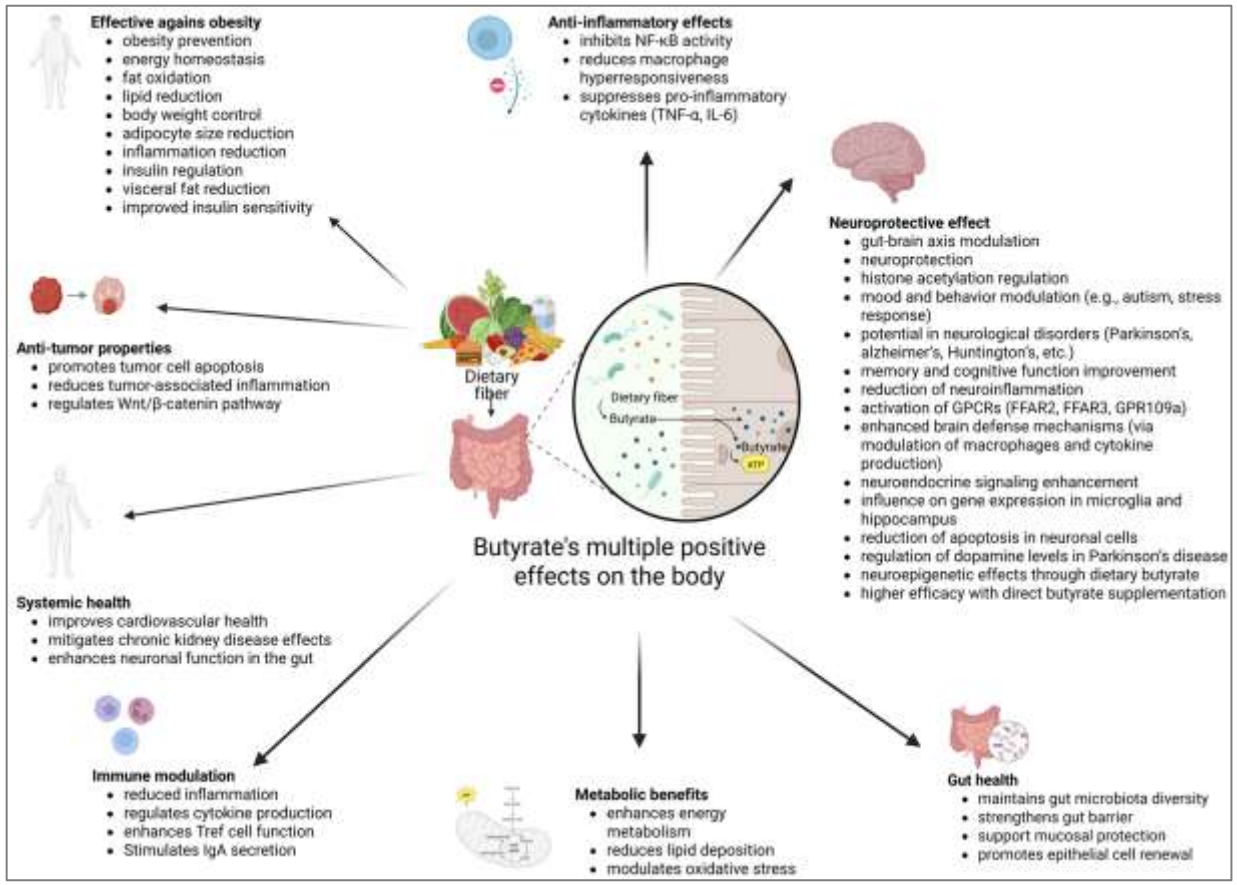
How to treat low butyrate-producing capacity

13-4-2026

Koosje Janssen, Dennis Zeilstra

Conclusions

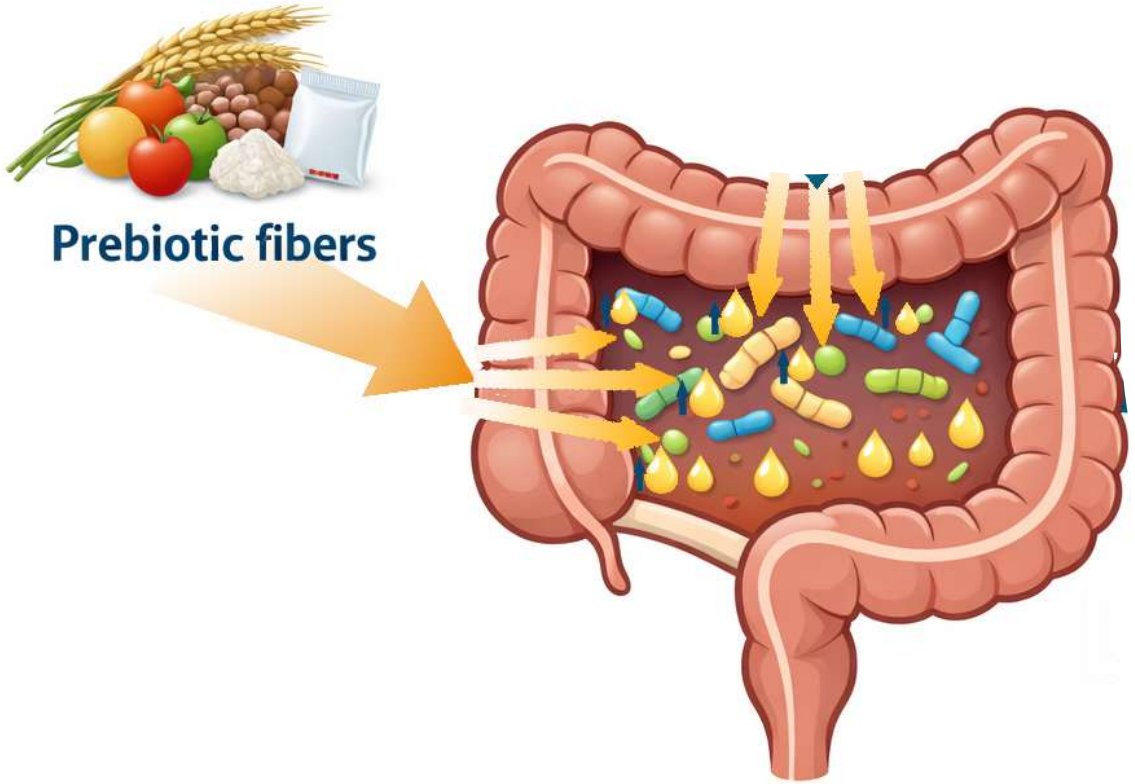
1. **Butyrate is a bacterial metabolite that is key for our health**
2. **It has both local and systemic effects**
3. **Levels are very low in PAIS patients**
4. **Low levels can be treated with several approaches**



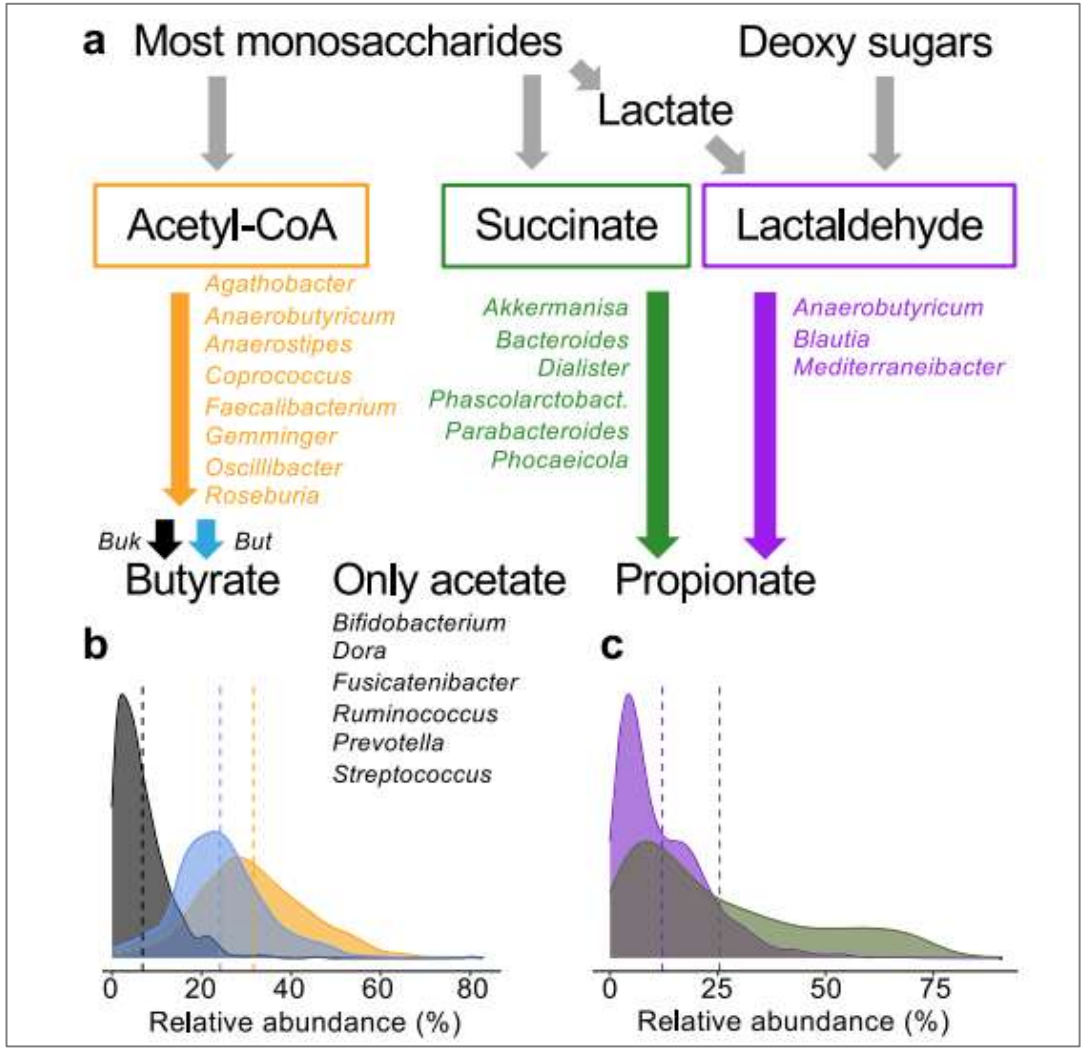
1. Kalkan, A. E. et al.Nutrients.17,.1305.(2025)

Three approaches to treat low butyrate

1



1 Prebiotics: substrate for butyrate production by commensals

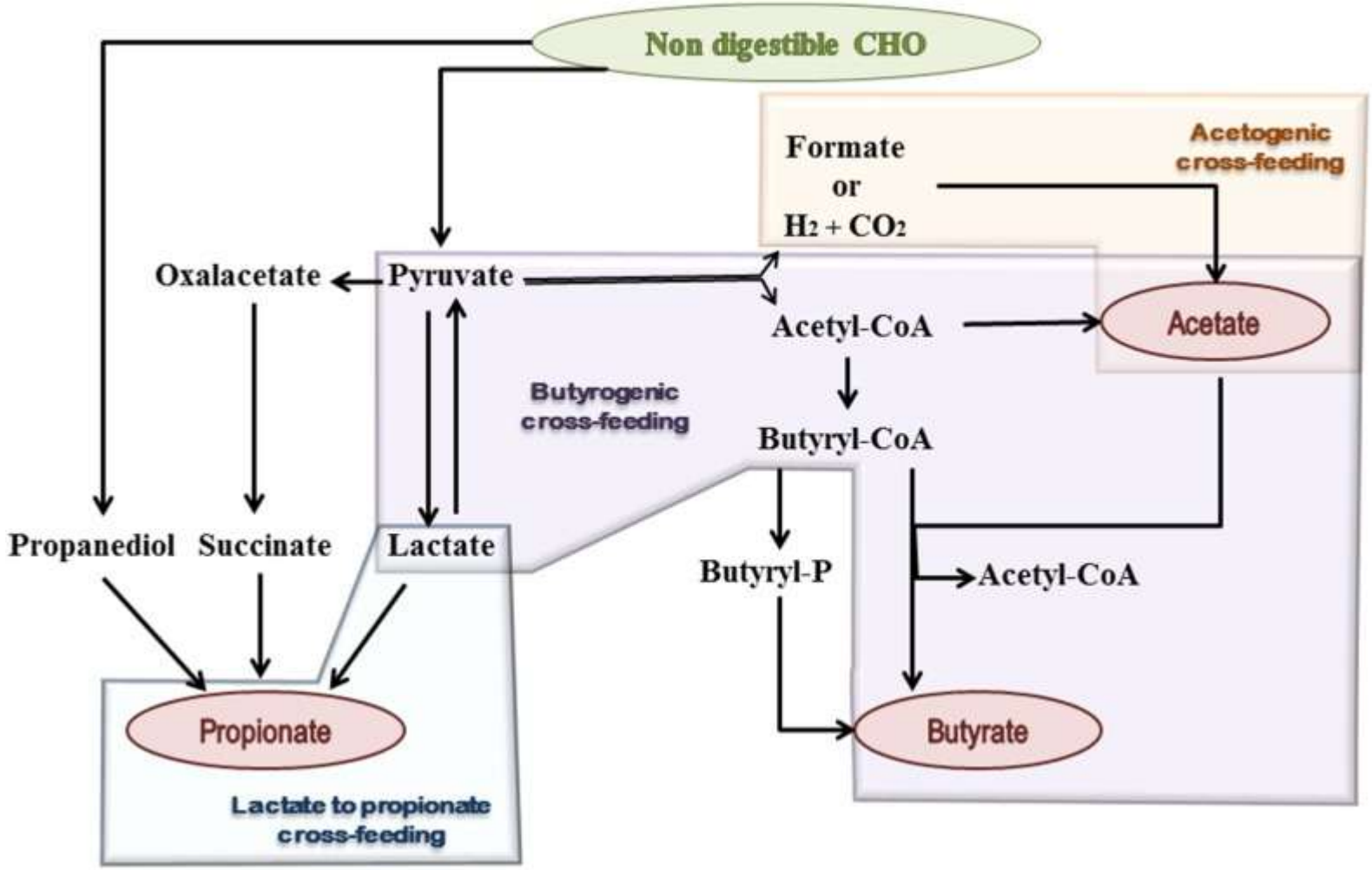


- Short chain fatty acid (SCFA) types[1]:
  - Acetate (most abundant: 60%)
  - Propionate(20%)
  - Butyrate (20%)
- Produced by fermentation of fibers and sugars
- The number of taxa that exhibit the enzymatic capabilities is very different per pathway

1. Parada Venegas, D. et al.Front. Immunol.10,.(2019)
2. Van-Wehle, T. et al.npj Biofilms Microbiomes.10,.63.(2024)

1 Prebiotics: substrate for butyrate production by commensals

- Pathways[1]:
  - Butyrate: 2 main pathways
  - Propionate: 3 pathways, 2 main
  - Acetate: 2 main pathways



1. Ríos-Covián, D. et al.Front Microbiol.7,.185.(2016)

1 Prebiotics: not all fibers are equal (1/2)

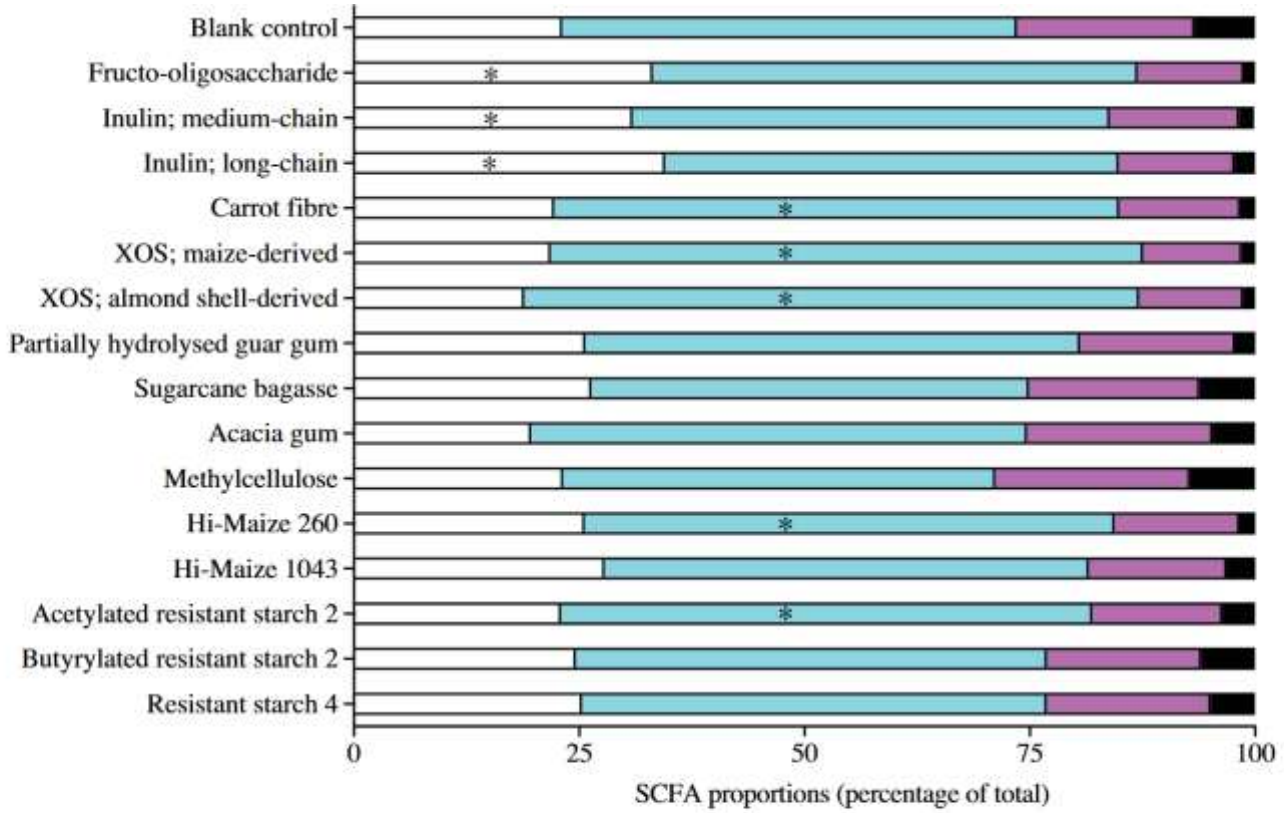
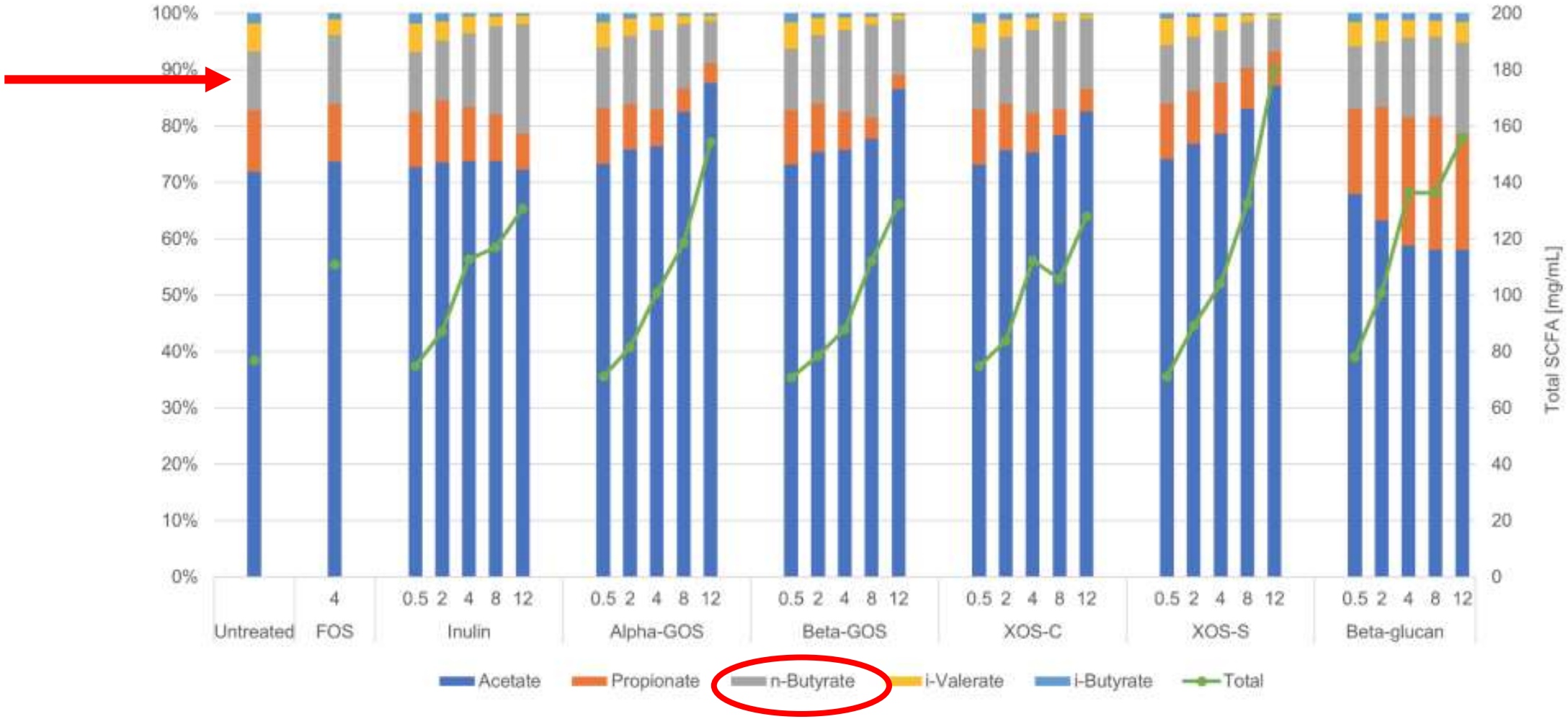


Fig. 2. SCFA proportions for acetate, propionate, butyrate and other (isobutyrate, isovalerate, valerate and caproate), as a proportion of total SCFA concentrations, across fibres investigated following fermentation. Values shown represent the mean SCFA proportions across three replicate experiments conducted using samples provided by three independent participants. Differences between fibres were evaluated using one-way ANOVA. * Significant differences ($P < 0{\cdot}05$; Fisher's least significant difference) between fibres and the blank control for acetate and butyrate proportions. XOS, xylo-oligosaccharide. □, Butyrate; □, acetate; □, propionate; ■, other.

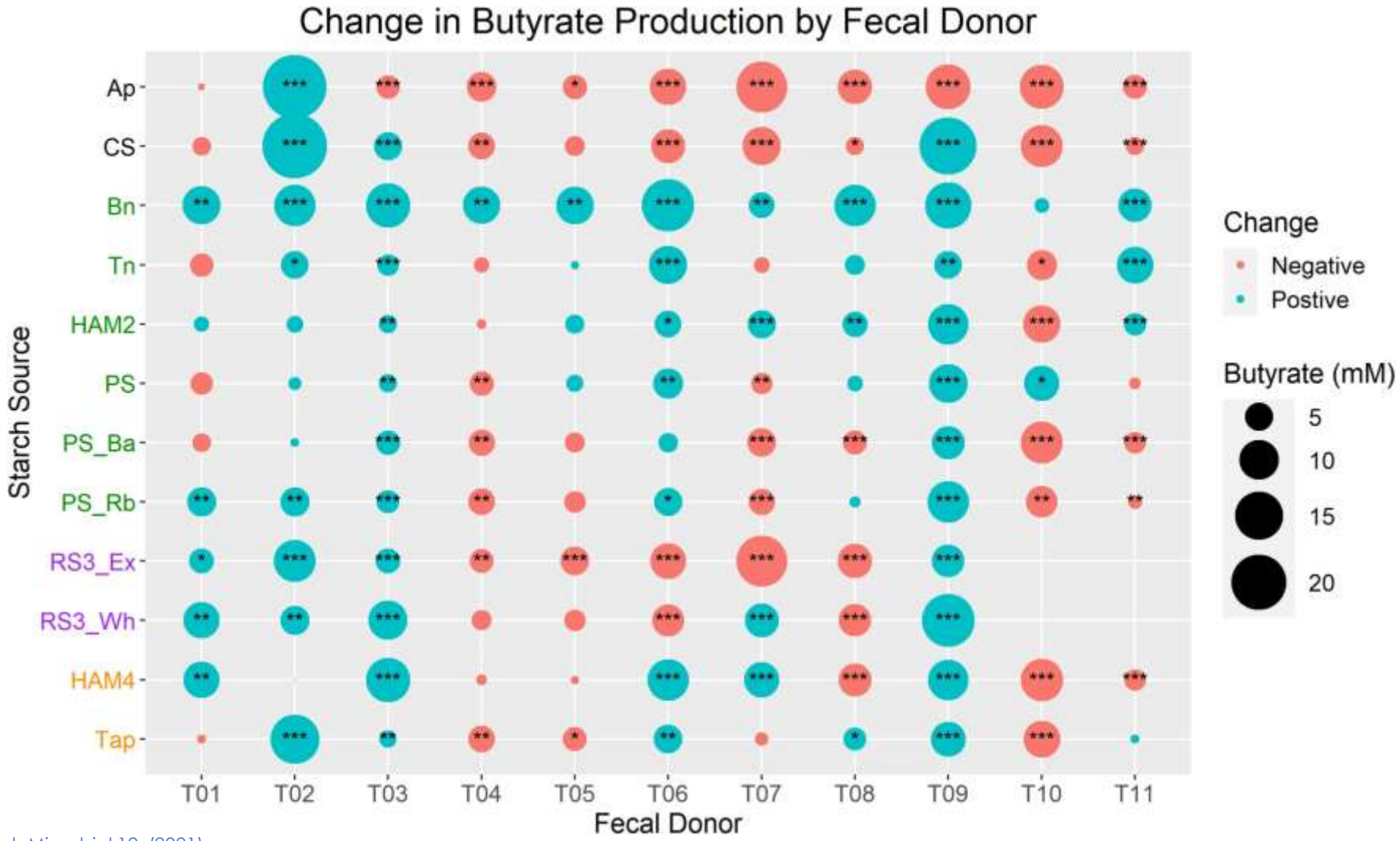
1. So, D. et al.British Journal of Nutrition.126,.208–218.(2021)

1 Prebiotics: not all fibers are equal (2/2)



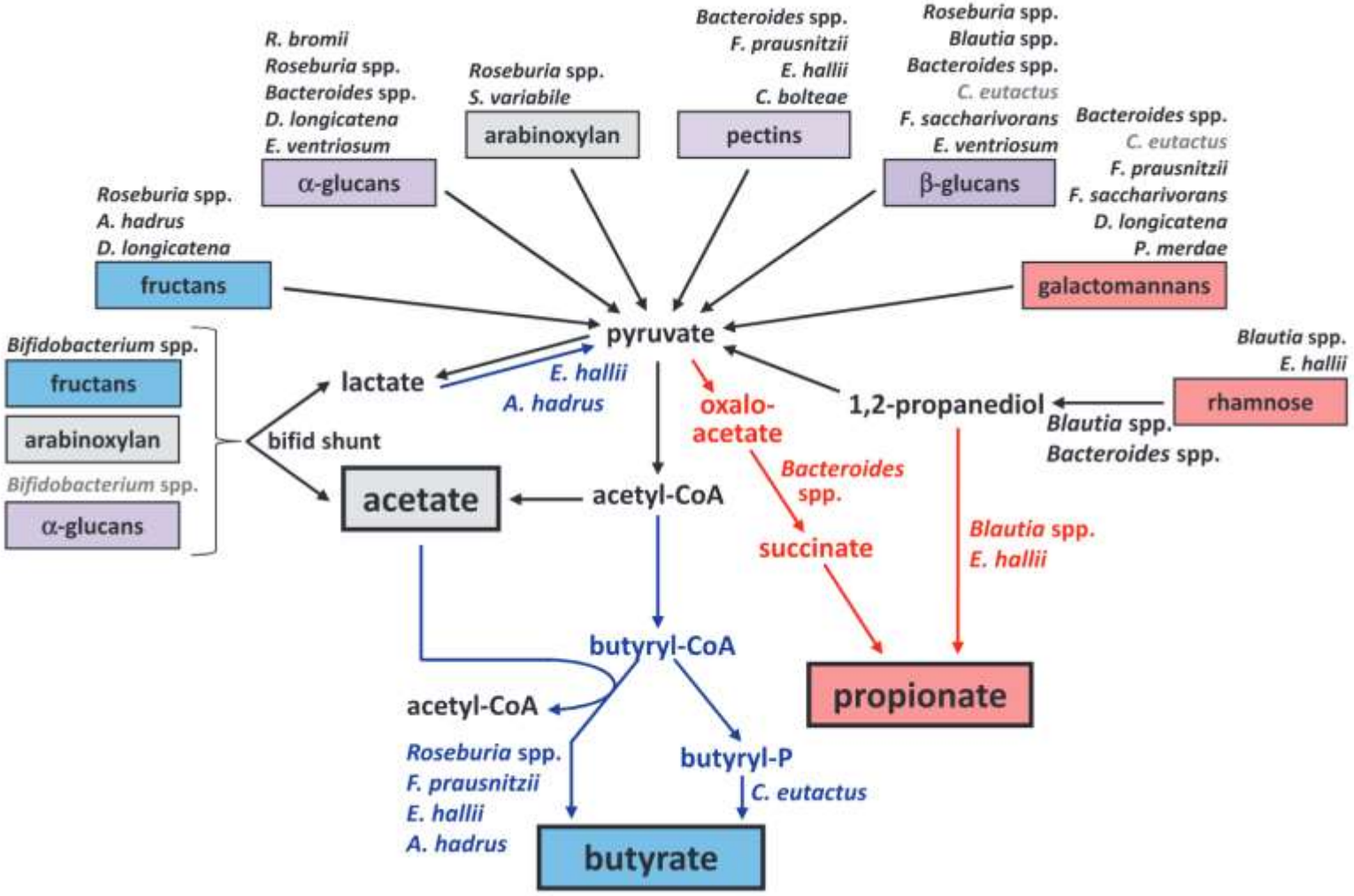
1. Fehlbaum, S. et al.IJMS.19,.3097.(2018)

1 Prebiotics: effects are person-specific[1,2]



1. Teichmann, J. et al.Front. Microbiol.12,.(2021)
2. Simonelli, N. et al.Food Bioscience.62,.105329.(2024)

1 Prebiotics: reasons for differences: composition individual, pathways vary per taxa



1. Reichardt, N. et al.The ISME Journal.(2017)

1 Prebiotics: PHGG is good butyrate stimulator

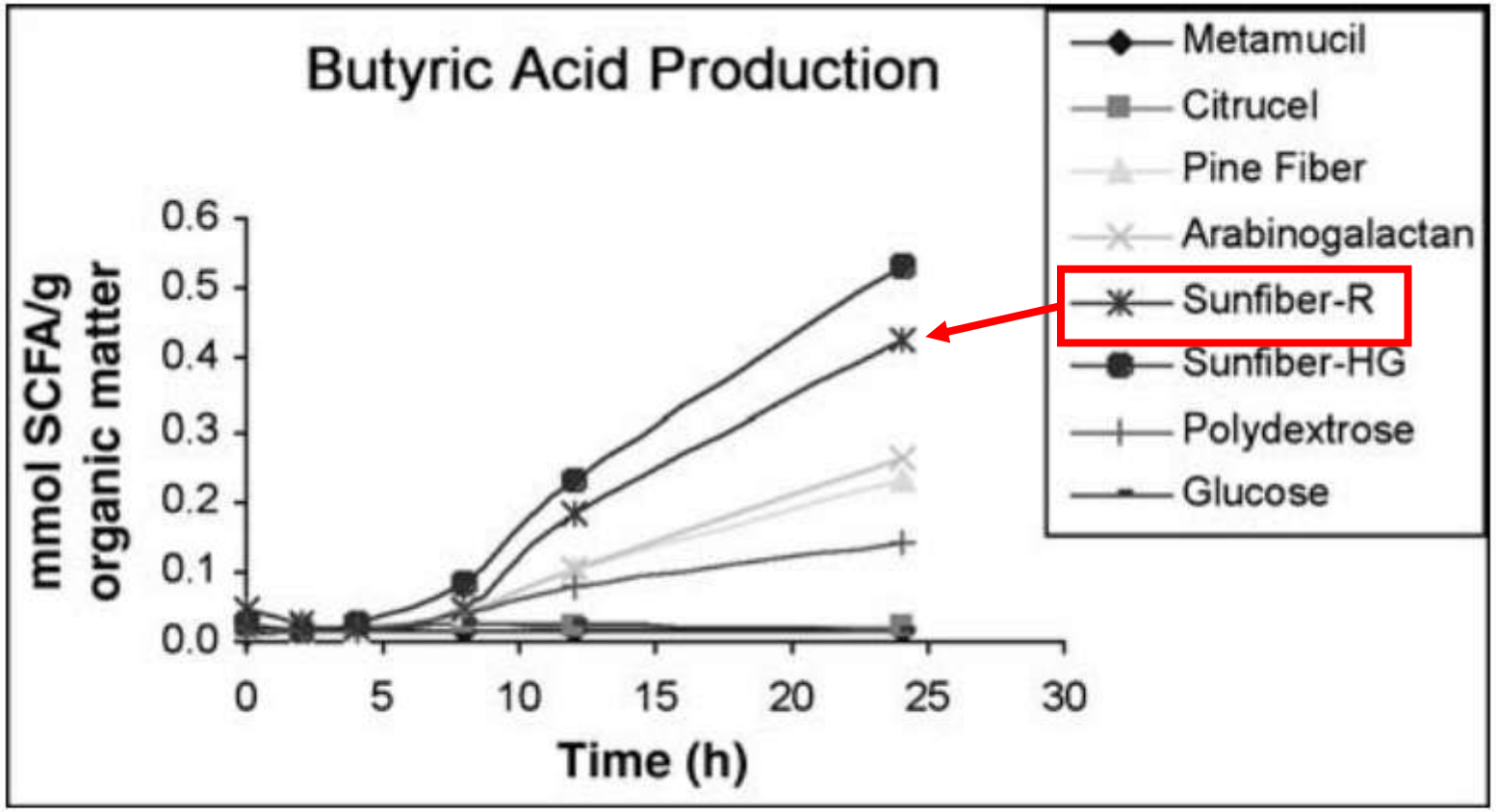


FIG. 4. Butyric acid production from various sources.

1. Pylkas, A. M. et al.Journal of Medicinal Food.(2005)

Example case 1

IBS and low butyrate producers

Case low butyrate formers

Julia, 1978

- Chronic gastrointestinal complaints existing for about 4 years consistent with an irritable bowel with predominantly diarrhea (IBS-D)
- Pronounced fatigue / reduced load capacity
- Lactose intolerance confirmed by lactose breath test
- Strict lactose restriction, but persistent symptoms despite this
- Colonoscopy without abnormalities (exclusion of structural intestinal pathology)

Voorgeschiedenis:

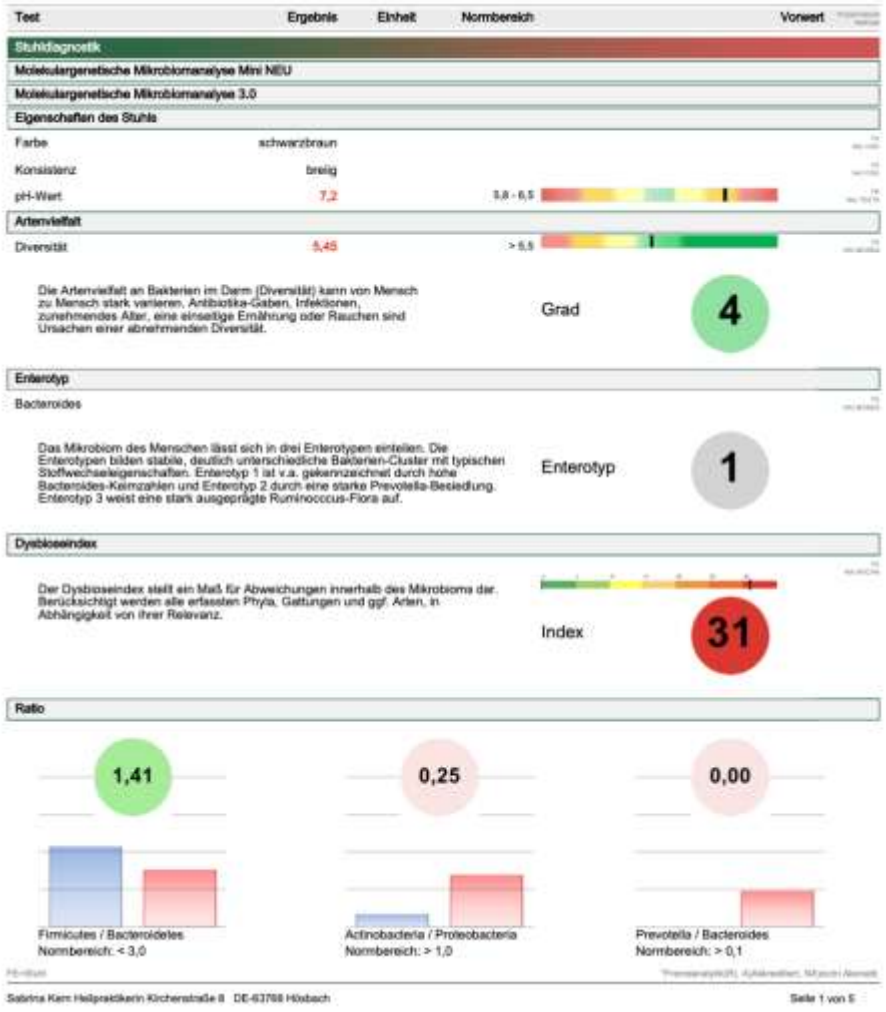
- Emergency section with scarring 2012, appendectomy

Leefstijl / voeding:

- Predominantly whole, vegetable-rich food, little fruit, no soft drinks/alcohol
- Physical activity, endurance athlete

Microbioome analysis july 2024:

Case low butyrate formers



Test	Ergebnis	Einheit	Normbereich	Vorwert
Stuhldiagnostik				
Molekulargenetische Mikrobiomanalyse Mini NEU				
Molekulargenetische Mikrobiomanalyse 3.0				
Eigenschaften des Stuhls				
Farbe	schwarzbraun			
Konsistenz	breiig			
pH-Wert	7,2		5,8 - 6,5	
Artenvielfalt				
Diversität	5,45		> 6,5	

Die Artenvielfalt an Bakterien im Darm (Diversität) kann von Mensch zu Mensch stark variieren. Antibiotika-Gaben, Infektionen, zunehmendes Alter, eine einseitige Ernährung oder Rauchen sind Ursachen einer abnehmenden Diversität.

Grad **4**

Enterotyp

Bacteroides

Das Mikrobiom des Menschen lässt sich in drei Enterotypen einteilen. Die Enterotypen bilden stabile, deutlich unterschiedliche Bakterien-Cluster mit typischen Stoffwechseleigenschaften. Enterotyp 1 ist v.a. gekennzeichnet durch hohe Bacteroides-Keimzahlen und Enterotyp 2 durch eine starke Prevotella-Besiedlung. Enterotyp 3 weist eine stark ausgeprägte Ruminococcus-Flora auf.

Enterotyp **1**

Dysbioseindex

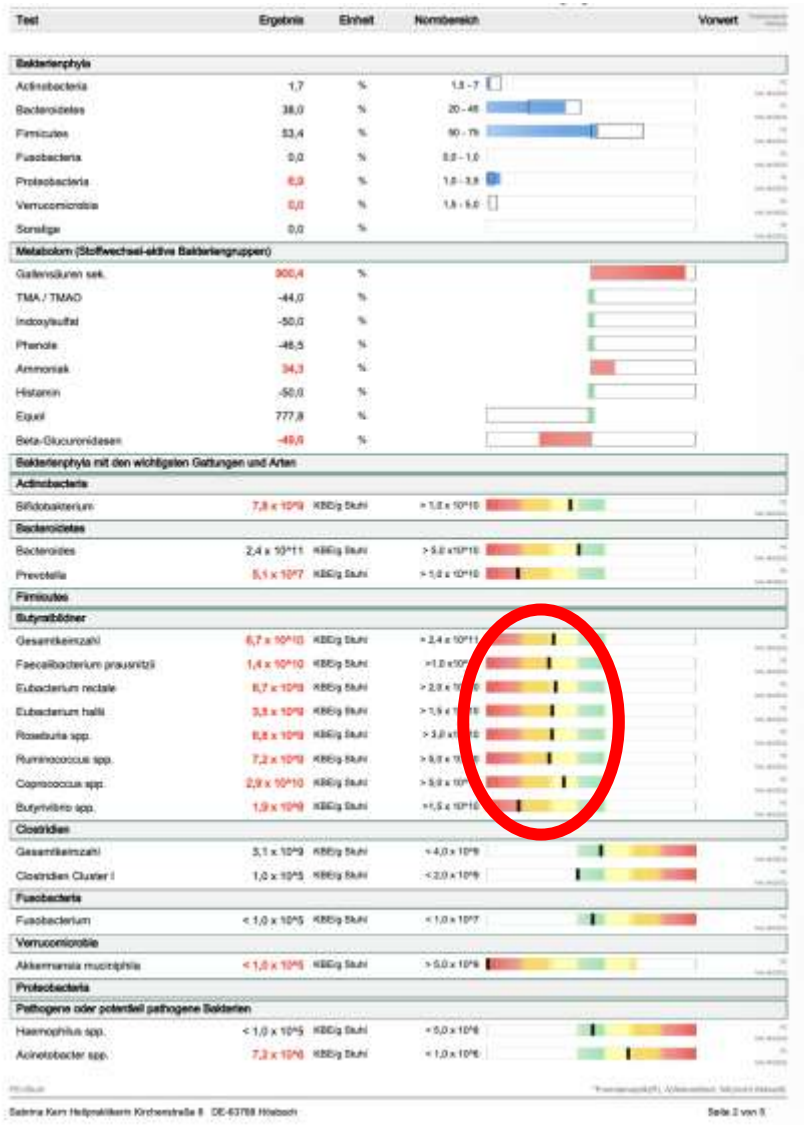
Der Dysbioseindex stellt ein Maß für Abweichungen innerhalb des Mikrobioms dar. Berücksichtigt werden alle erfassten Phyla, Gattungen und ggf. Arten, in Abhängigkeit von ihrer Relevanz.

Index **31**

Ratio

1,41	0,25	0,00
Firmicutes / Bacteroidetes	Actinobacteria / Proteobacteria	Prevotella / Bacteroides
Normbereich: < 3,0	Normbereich: > 1,0	Normbereich: > 0,1

Sabrina Kern Heilpraktikerin Kirchenstraße 8 DE-63768 Hösbach Seite 1 von 5



Test	Ergebnis	Einheit	Normbereich	Vorwert
Bakterienphyla				
Actinobacteria	1,7	%	1,8 - 7	
Bacteroidetes	38,0	%	20 - 48	
Firmicutes	53,4	%	50 - 76	
Fusobacteria	0,0	%	0,0 - 1,0	
Proteobacteria	6,9	%	1,0 - 3,8	
Verrucomicrobia	0,0	%	1,8 - 5,0	
Sonstige	0,0	%		
Metabolom (Stoffwechsel-aktive Bakteriengruppen)				
Gallensäuren sek.	900,4	%		
TMA / TMAO	-44,0	%		
Indoxylsulfat	-50,0	%		
Phenole	-46,5	%		
Ammoniak	34,3	%		
Histamin	-50,0	%		
Equol	777,8	%		
Beta-Glucuronidasen	-49,0	%		
Bakterienphyla mit den wichtigsten Gattungen und Arten				
Actinobacteria				
Bifidobakterium	7,8 x 10^9	KBE/g Stuhl	> 1,0 x 10^10	
Bacteroidetes				
Bacteroides	2,4 x 10^11	KBE/g Stuhl	> 5,0 x 10^10	
Prevotella	5,1 x 10^7	KBE/g Stuhl	> 1,0 x 10^10	
Firmicutes				
Butyratbildner				
Gesamtkeimzahl	6,7 x 10^10	KBE/g Stuhl	> 2,4 x 10^11	
Faecalibacterium prausnitzii	1,4 x 10^10	KBE/g Stuhl	> 1,0 x 10^	
Eubacterium rectale	8,7 x 10^9	KBE/g Stuhl	> 2,0 x 10^	
Eubacterium hallii	3,8 x 10^9	KBE/g Stuhl	> 1,9 x 10^	
Roseburia spp.	8,8 x 10^9	KBE/g Stuhl	> 3,0 x 10^	
Ruminococcus spp.	7,2 x 10^9	KBE/g Stuhl	> 9,0 x 10^	
Coprococcus spp.	2,9 x 10^10	KBE/g Stuhl	> 5,0 x 10^	
Butyrivibrio spp.	1,9 x 10^9	KBE/g Stuhl	> 1,5 x 10^10	
Clostridien				
Gesamtkeimzahl	5,1 x 10^9	KBE/g Stuhl	< 4,0 x 10^9	
Clostridien Cluster I	1,0 x 10^5	KBE/g Stuhl	< 2,0 x 10^9	
Fusobacteria				
Fusobacterium	< 1,0 x 10^5	KBE/g Stuhl	< 1,0 x 10^7	
Verrucomicrobia				
Akkermansia muciniphila	< 1,0 x 10^5	KBE/g Stuhl	> 5,0 x 10^9	
Proteobacteria				
Pathogene oder potentiell pathogene Bakterien				
Haemophilus spp.	< 1,0 x 10^5	KBE/g Stuhl	< 5,0 x 10^8	
Acinetobacter spp.	7,2 x 10^6	KBE/g Stuhl	< 1,0 x 10^8	

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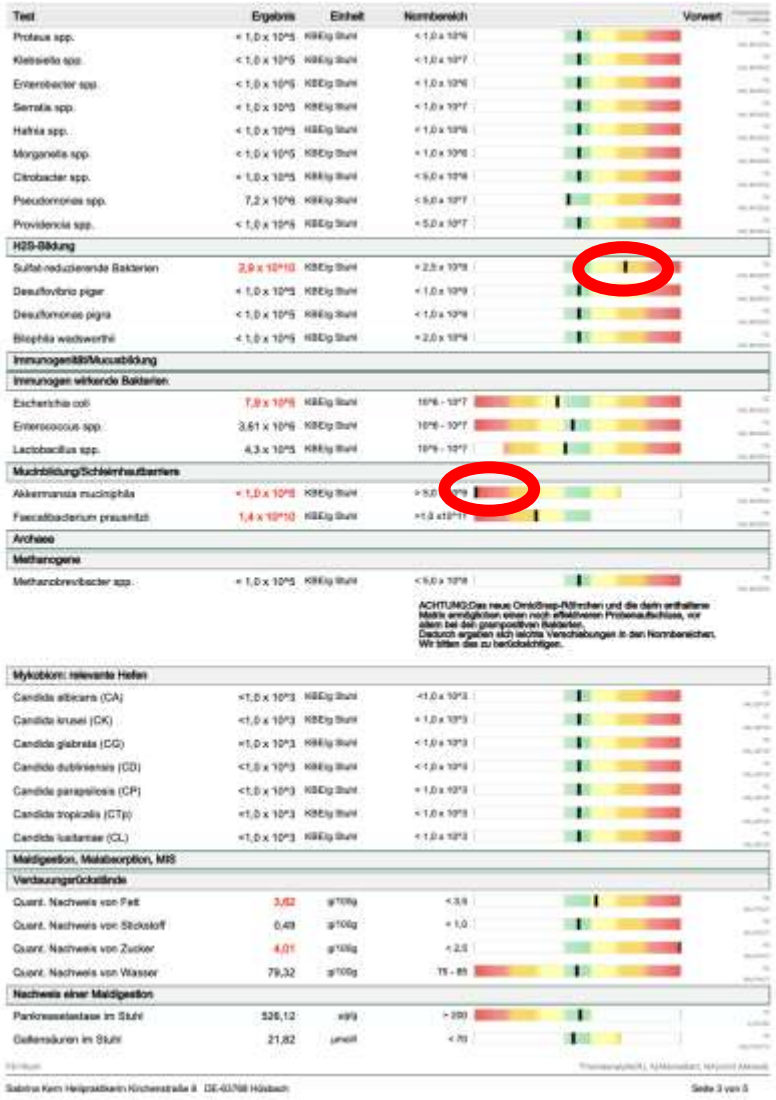
Case low butyrate formers



Test	Ergebnis	Einheit	Normbereich	Vorwert
Nachweis einer Malabsorption				
Calprotectin	31,00	mg/l	< 50	
Alpha 1-Antitrypsin	8,8	mg/dl	< 27,5	
Einzelparameter				
Sekretorisches Immunglobulin A (sIgA)	195,0	µg/ml	510 - 2040	

Case low butyrate formers

Therapy:

- Based on microbiological stool analysis started with an individual therapy with MyOwnBlend for 8 weeks
- In addition, manual treatment of the cesarean scar, control and replenishment of micronutrients

Course:

- After about 6 weeks a severe flu-like infection, according to patient more serious than before
  At that time increased psychological strain, but already physical stabilization of the intestinal complaints
- Another 8 weeks of MyOwnBlend for further stabilization

Rezept **Datum:** 05-10-2024

MyOwnBlend, Magistral-Preparat 2 Monaten (oral)	**Pro Tag (gramm)**	**Gesamt (gramm)**
PHGG	6	360
L. plantarum P-8	2	120
Bifidobacterium lactis HN019	3	180
Lactiplantibacillus plantarum DR7	2	120
Bacillus coagulans Unique IS-2	1	60
Akkermansia muciniphila, pasteurisiertes	1	60
Gesamt	**15**	**900**

Case low butyrate formers

Results:

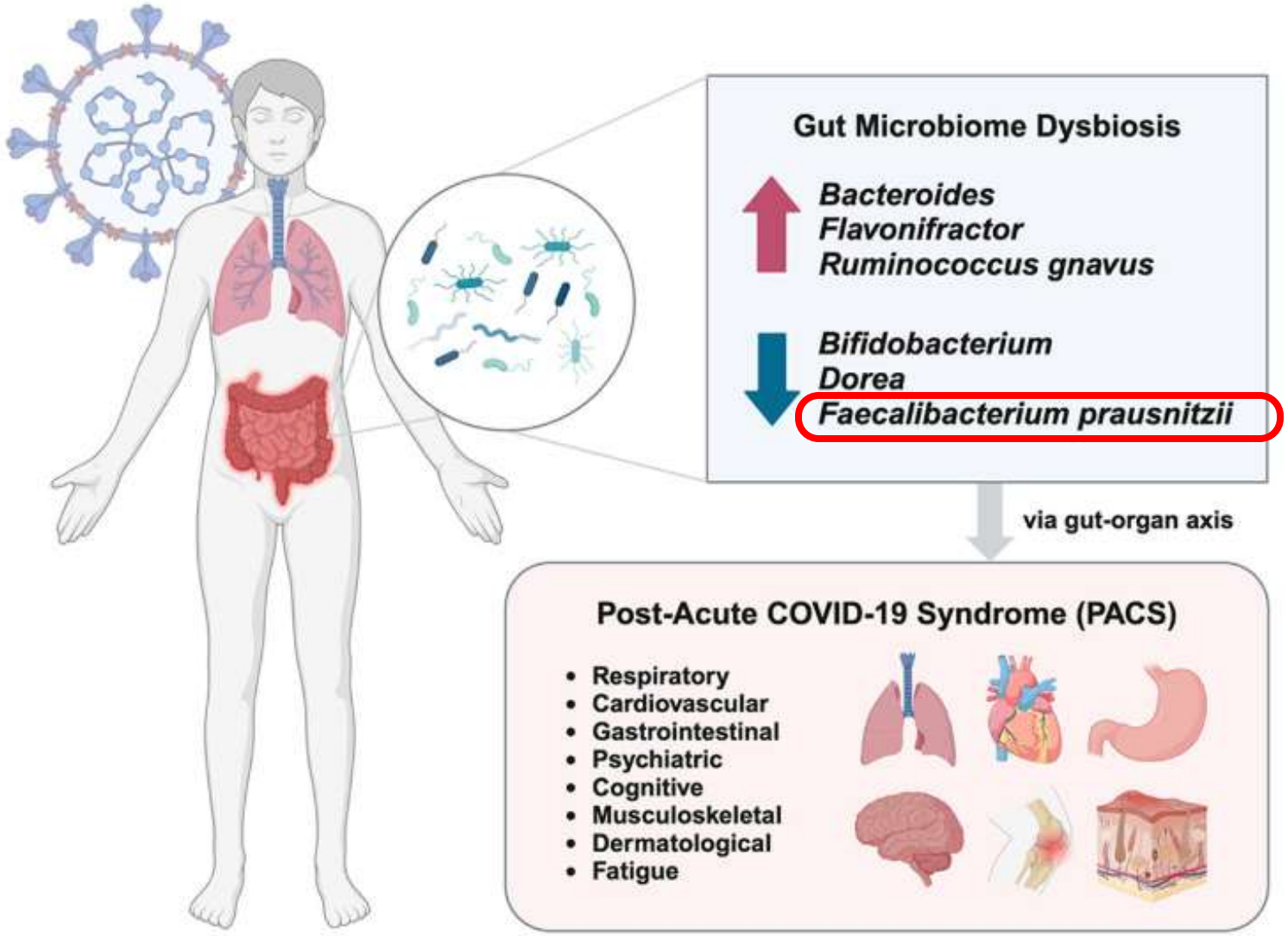
- November 2024 no more diarrhoea complaints
- Increase in energy and load capacity (marathon in 2025)

Current status:

- Significantly improved overall condition
- Good gastrointestinal stability
- In view of the enormous progress, patient and practitioner have chosen not to do a retest

Butyrate in PAIS

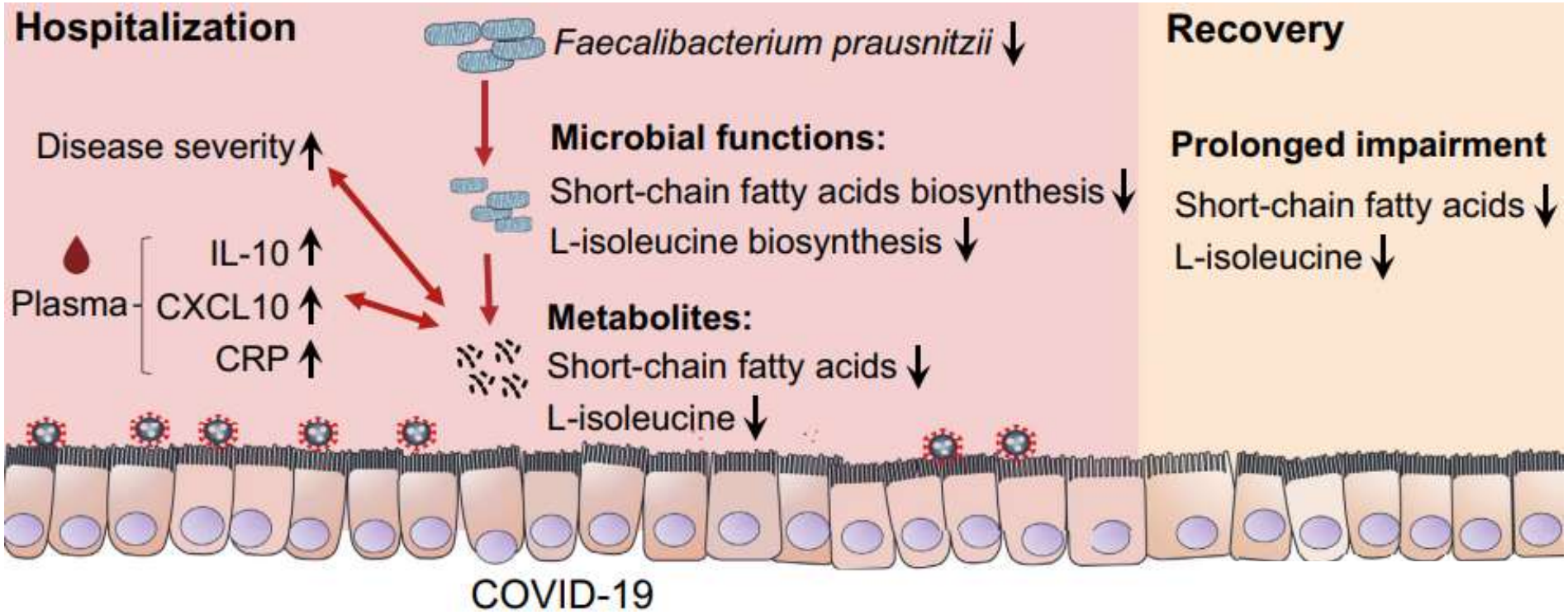
Long COVID and Dysbiosis: reduced butyrate producers



Lau RI, Su Q, Ng SC. Long COVID and gut microbiome: insights into pathogenesis and therapeutics. Gut Microbes. 2025

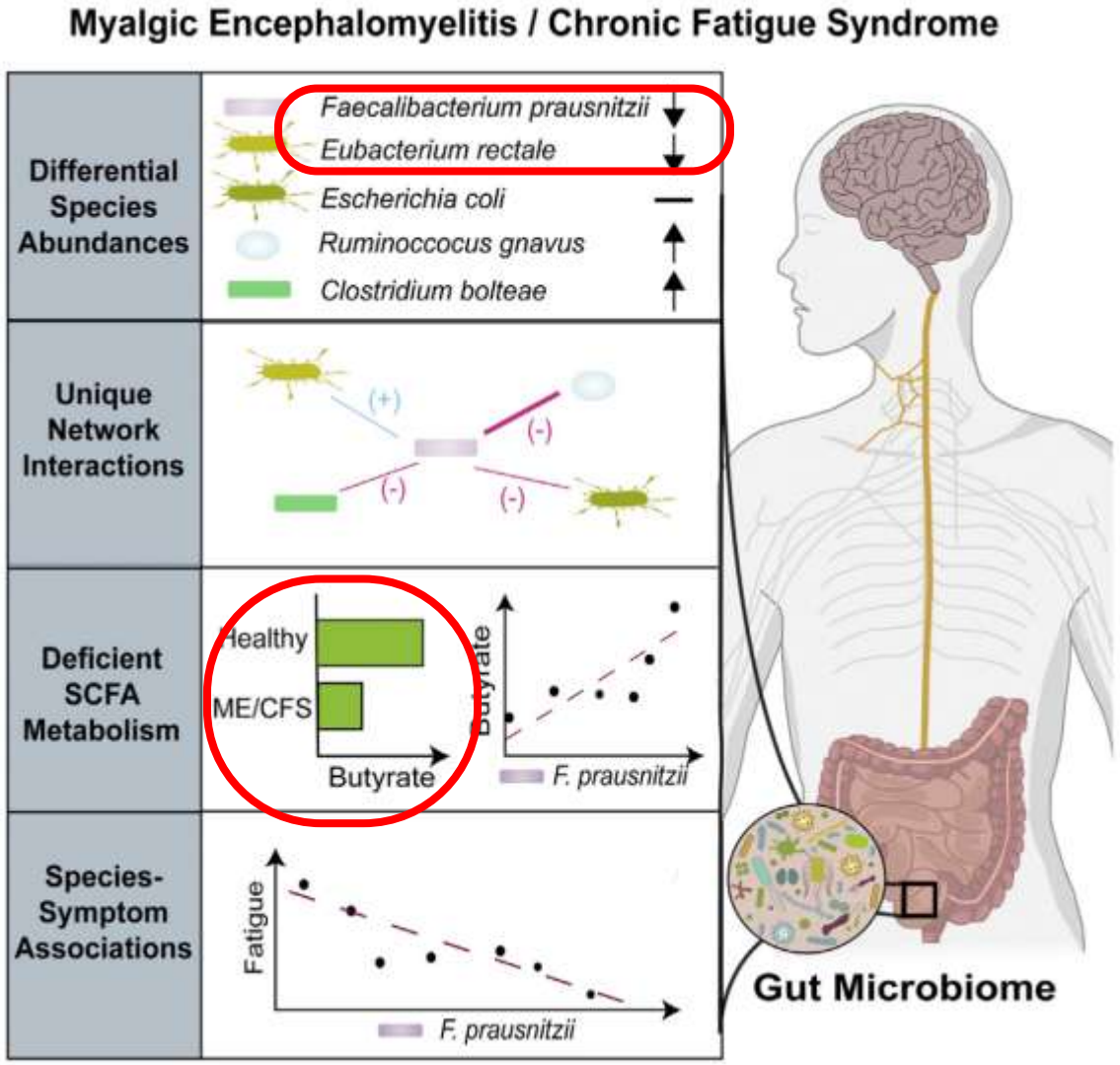
Long COVID: low SCFAs

Production of SCFA is low in Long-Covid



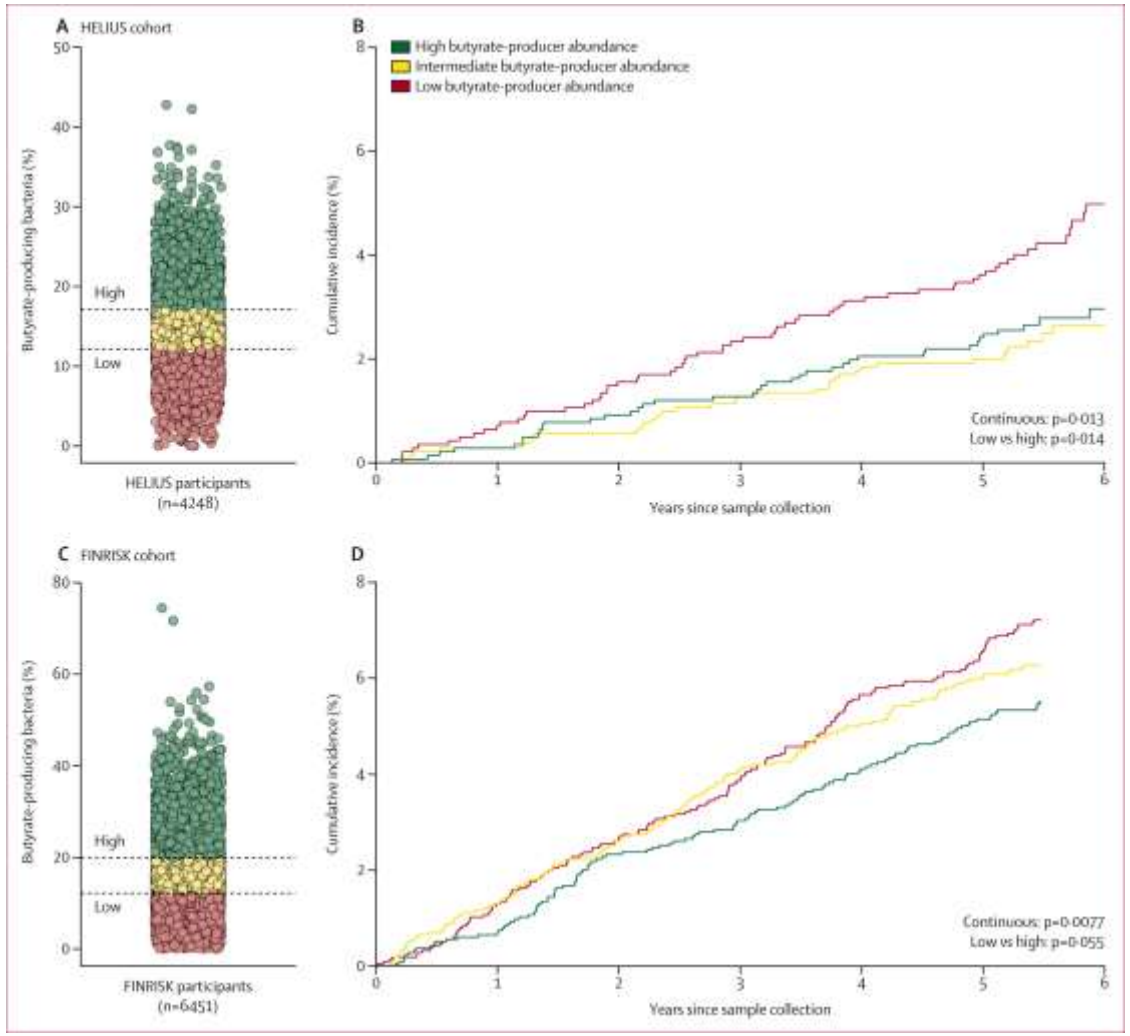
Fen Zhang et al., Prolonged Impairment of Short-Chain Fatty Acid and L-Isoleucine Biosynthesis in Gut Microbiome in Patients With COVID-19. Gastroenterology

ME/CFS: low SCFAs[1]

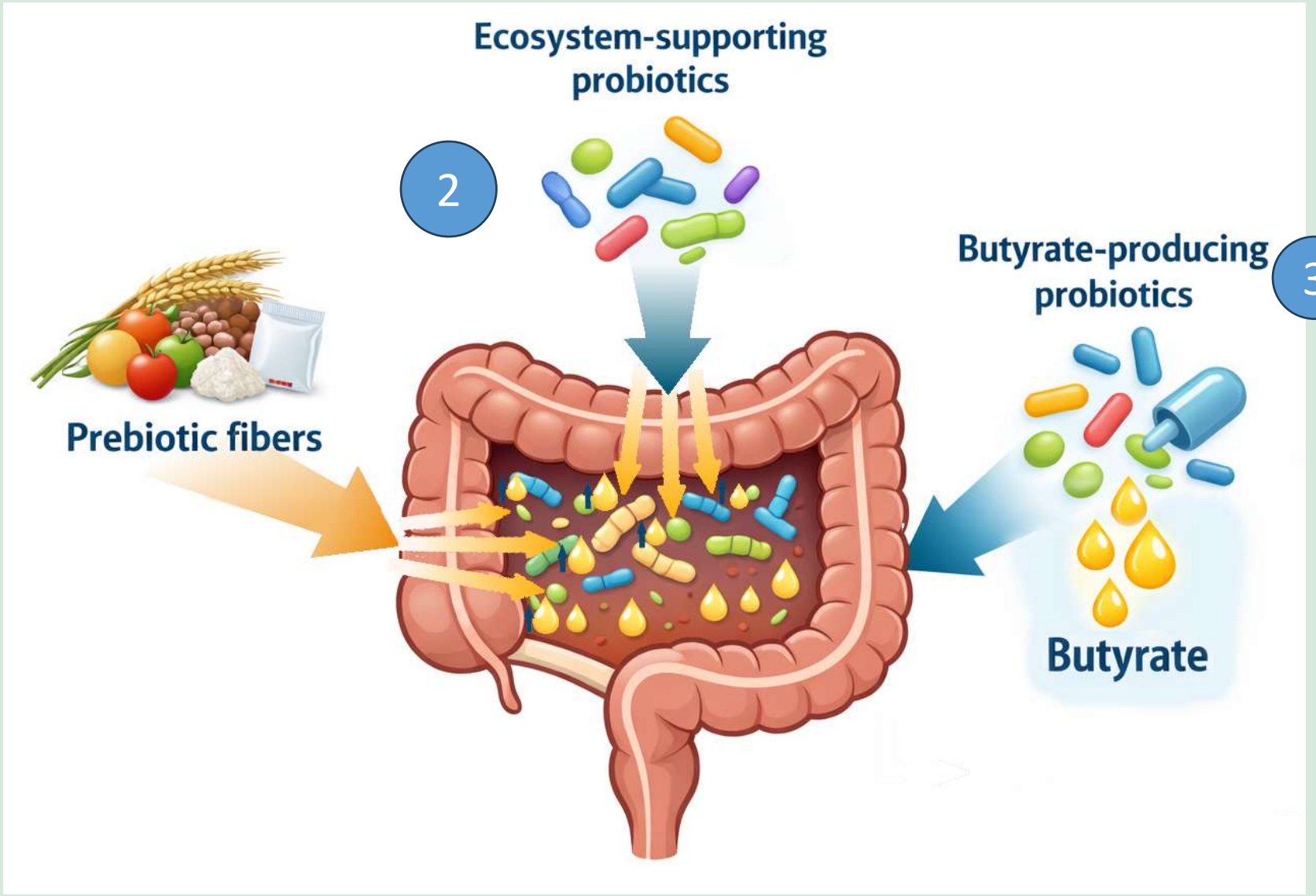


1. Guo, C. et al.Cell Host & Microbe.31,.288-304.e8.(2023)

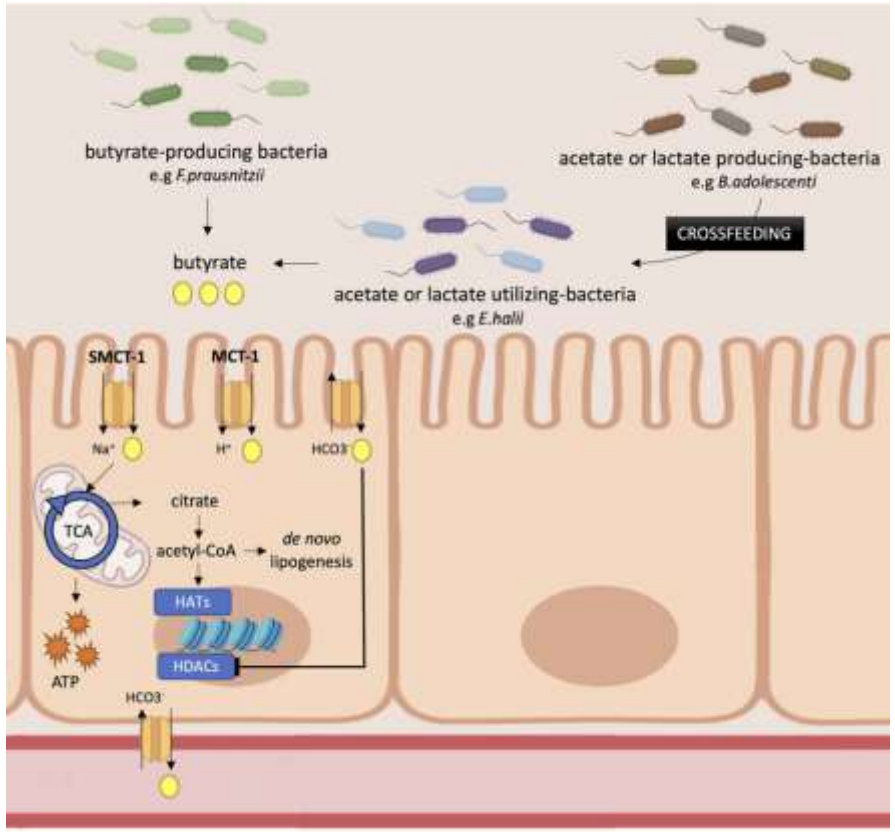
NB: butyrate protects against severe infectious disease[1]



1. Kullberg, R. F. J. et al.The Lancet Microbe.5,.(2024)

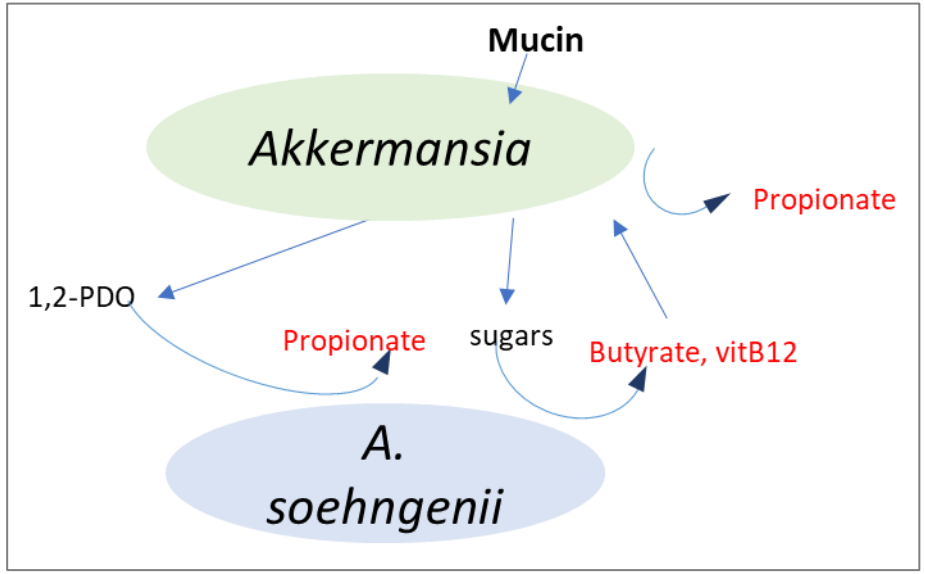


2 Influence the microbiome ecosystem to boost butyrate production



Various mechanisms indirectly influence butyrate production, including via[1]:

- Cross-feeding
- Production and excretion of vitamins and other nutrients
- Changing composition of microbiome via competition, bacteriocins, network effects, etc.

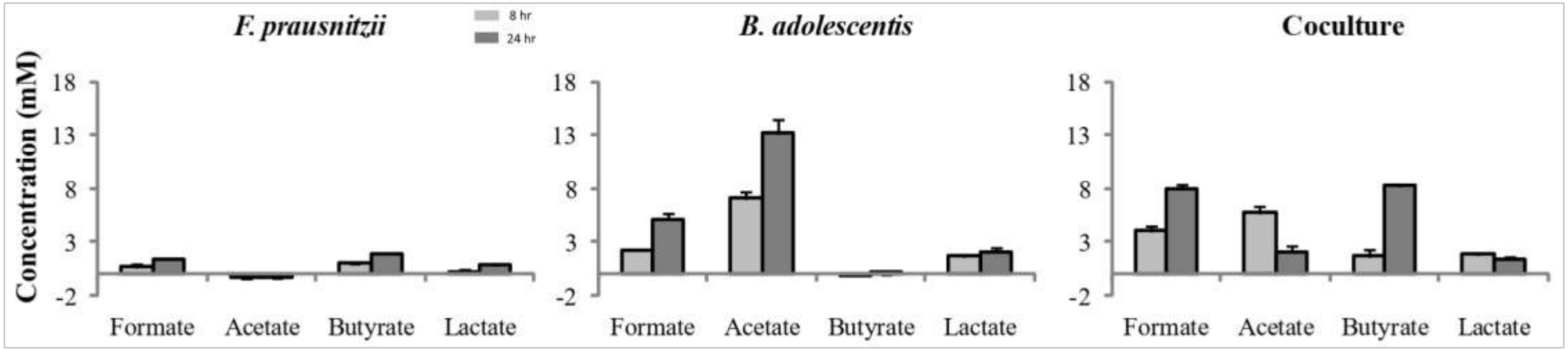


1,2-PDO: 1,2-Propanediol

1. van Deuren, T. et al.Obesity Reviews.n/a,.e13498.(2022)
2. Belzer, C. et al. mBio 8, e00770-17 (2017)

2 Influence the microbiome ecosystem *Bifidobacterium adolescentis* SH001

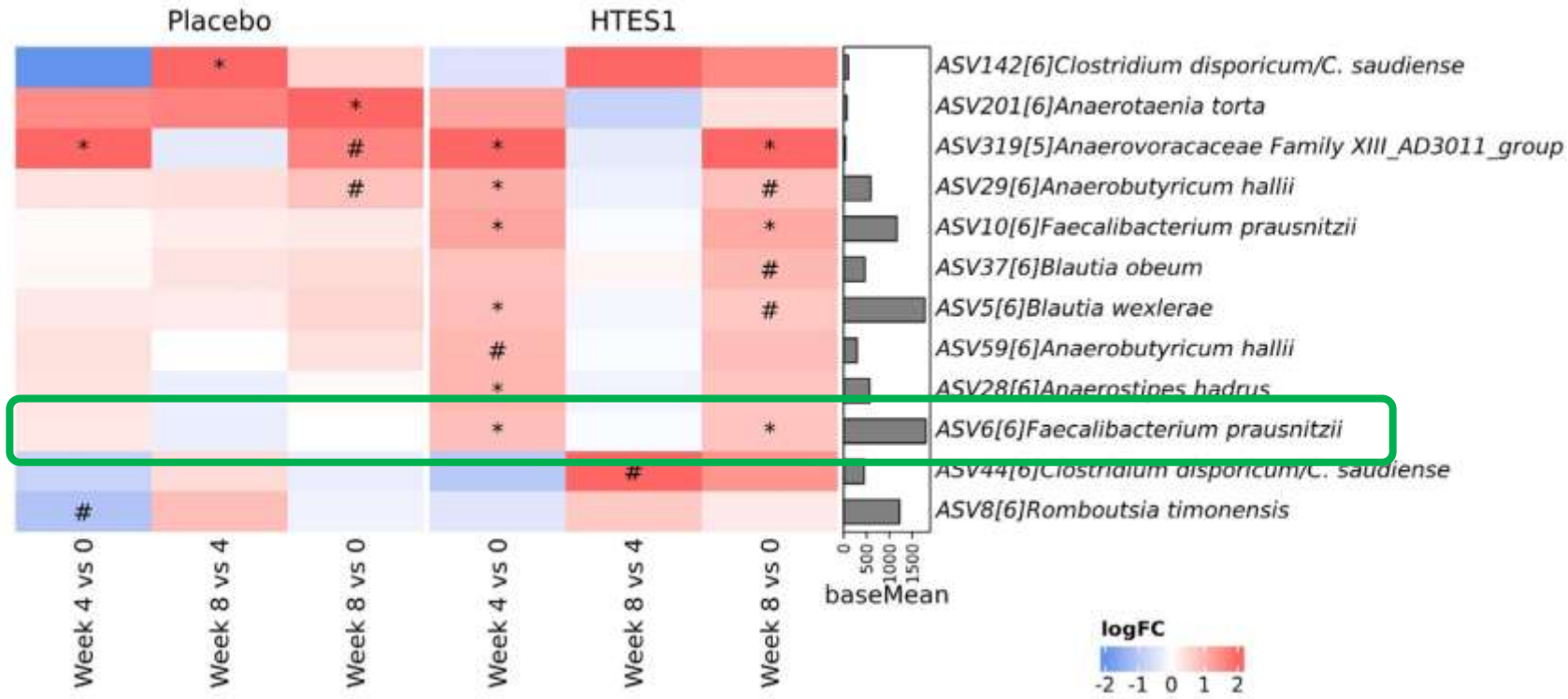
B. adolescentis is known cross-feeder for _F. prausnitzii_ (most abundant butyrate producer in our gut)[1]



1. Rios-Covian, D. et al.FEMS Microbiology Letters.362,.fnv176.(2015)

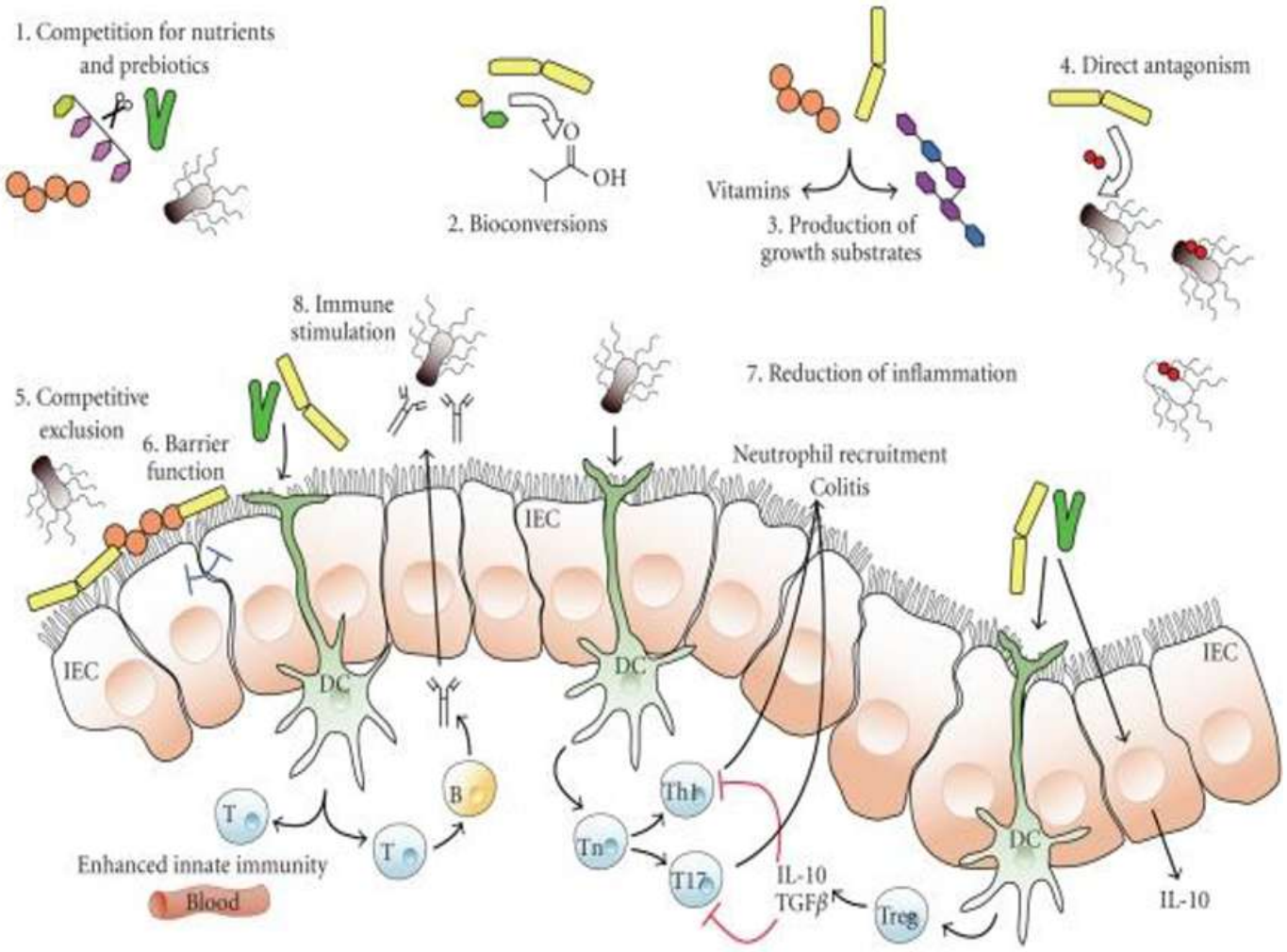
2 Influence the microbiome ecosystem *Bifidobacterium longum* ES1

***B. Longum* ES1** also increases *F. prausnitzii*, but not (only) as cross-feeder, since it was heat-killed (i.e. postbiotic) in this study[1]. This shows how **modulation of the ecosystem** can boost butyrate-production



1. Naghibi, M. et al.Nutrients.16,.3952.(2024)

2 Influence the microbiome ecosystem the many actions of probiotics



1. Khalighi, A. et al.in.Probiotics and Prebiotics in Human Nutrition and Health.(IntechOpen, 2016)

2 Influence the microbiome ecosystem *Saccharomyces boulardii* CNCM-I-1079

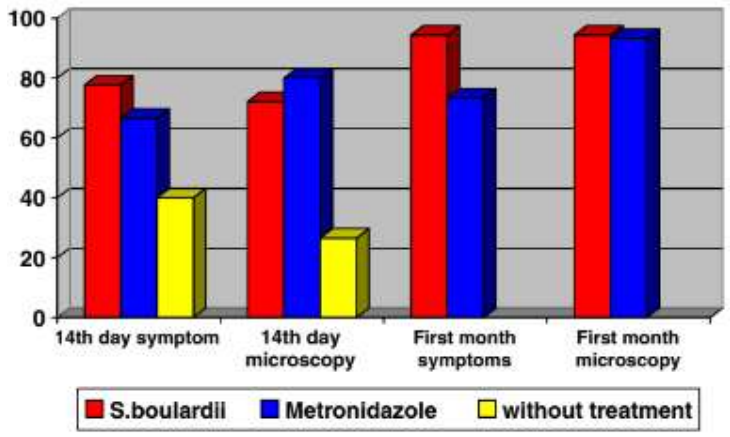


Fig. 1 Cure rate for clinical findings and parasitological examinations between study groups on the 14th day and first month

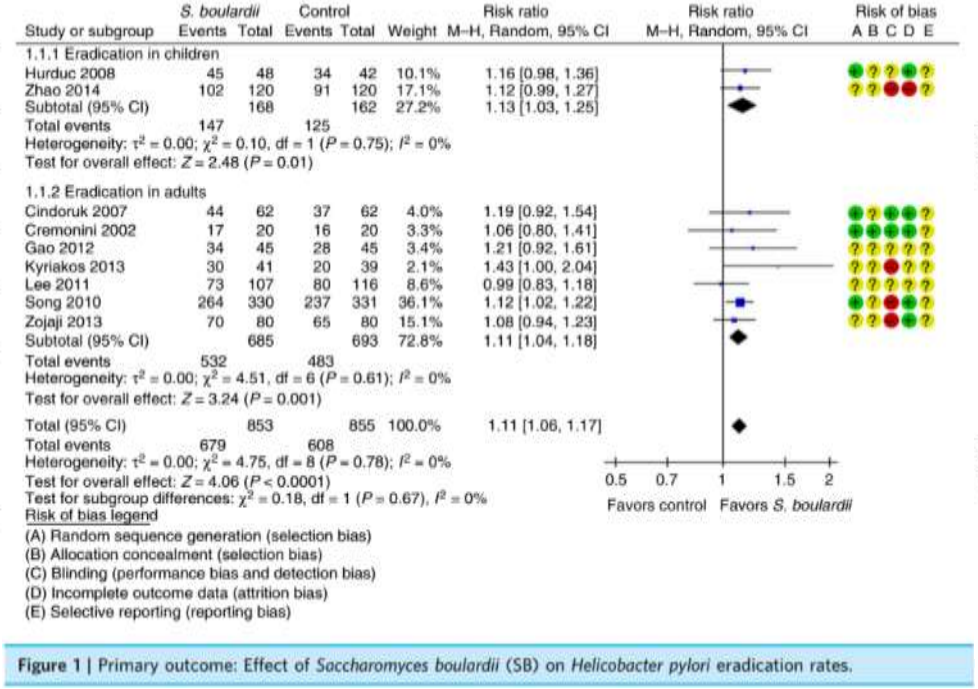
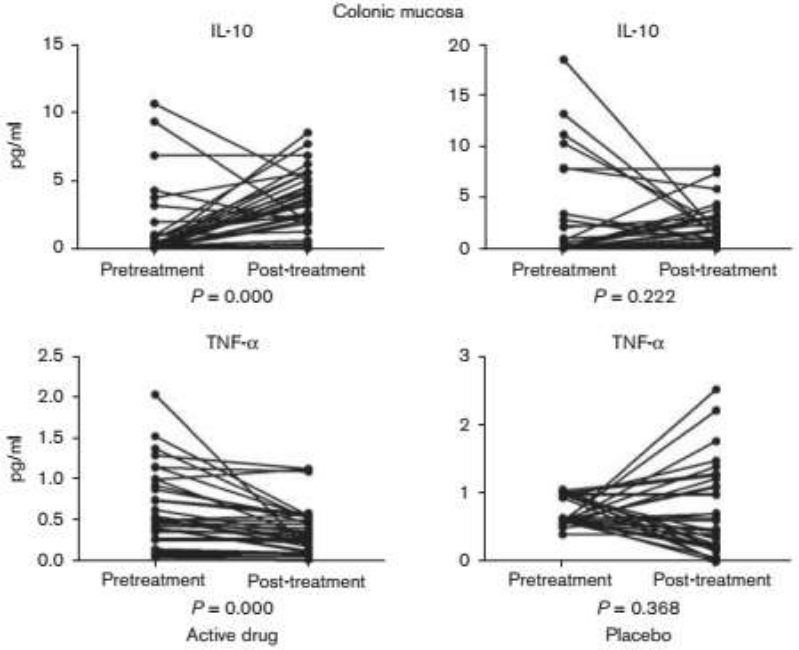


Figure 1 | Primary outcome: Effect of *Saccharomyces boulardii* (SB) on *Helicobacter pylori* eradication rates.



Inhibits parasites(*Entameba histolytica, Blastocystis hominis, Giardia lamblia*)[1-3]

Inhibits *Helicobacter pylori*[4]

Anti-inflammatory and intestinal barrier function-enhancing effects[5,6]

1. Dinleyici, E. C. et al. Am. J. Trop. Med. Hyg. 80, 953–955 (2009)
2. Dinleyici, E. C. et al. Parasitol. Res. 108, 541–545 (2011)
3. Besirbellioglu, B. A. et al. Scandinavian Journal of Infectious Diseases 38, 479–481 (2006)
4. Szajewska, H. et al. Alimentary Pharmacology & Therapeutics 41, 1237–1245 (2015)
5. Abbas, Z. et al. European Journal of Gastroenterology & Hepatology 1 (2014)
6. Garcia Vilela, E. et al.Scandinavian Journal of Gastroenterology.43,.842–848.(2008)

Example case 2

Crohn’s disease and low butyrate producers

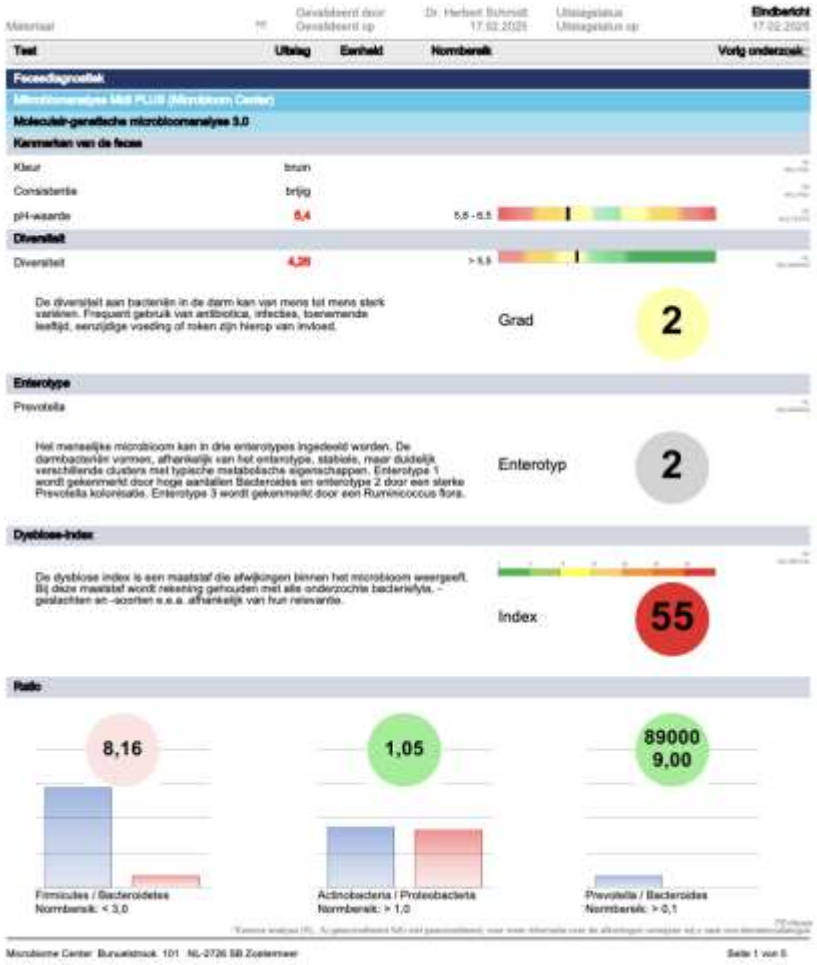
Case Crohn’s disease and low butyrate formers

Guido, 2011

- Crohn's with very high calprotectin, many complaints
- Since 3 years of joint inflammation, CRP increased, juvenile rheumatism was first thought.
- Nauseous, no appetite, lost 10 kilos in the past 3 months
- Def: diarrhea, lots of undigested remains
- Low energy, no focus, can't exercise
- Biologicals started but insufficient effect

- Microbiome analysis February2025

Case Crohn's disease a



Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Feces diagnostiek				
Microbiomeanalyse Mdl PLUS (Microbiom Center)				
Moleculair-genetische microbioomanalyse 3.0				
Kenmerken van de feces				
Kleur	bruin			
Consistentie	brijig			
pH-waarde	6,4		5,6 - 6,5	
Diversiteit				
Diversiteit	4,28		> 5,5	

De diversiteit aan bacteriën in de darm kan van mens tot mens sterk variëren. Frequent gebruik van antibiotica, infecties, toenemende leeftijd, eenzijdige voeding of roken zijn hiervan van invloed.

Grad 2

Enterotype

Prevotella

Het menselijke microbioom kan in drie enterotypes ingedeeld worden. De darmbacteriën vormen, afhankelijk van het enterotype, stabiele, maar duidelijk verschillende clusters met typische metabolische eigenschappen. Enterotype 1 wordt gekenmerkt door hoge aantallen Bacteroides en enterotype 2 door een sterke Prevotella kolonisatie. Enterotype 3 wordt gekenmerkt door een Ruminococcus flora.

Enterotyp 2

Dysbiose-Index

De dysbiose index is een maatstaf die afwijkingen binnen het microbioom weergeeft. Bij deze maatstaf wordt rekening gehouden met alle onderzochte bacterieflyta, -geslachten en -soorten e.e.a. afhankelijk van hun relevantie.

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Ratio

8,16	1,05	89000 9,00
Firmicutes / Bacteroidetes	Actinobacteria / Proteobacteria	Prevotella / Bacteroides
Normbereik: < 3,0	Normbereik: > 1,0	Normbereik: > 0,1

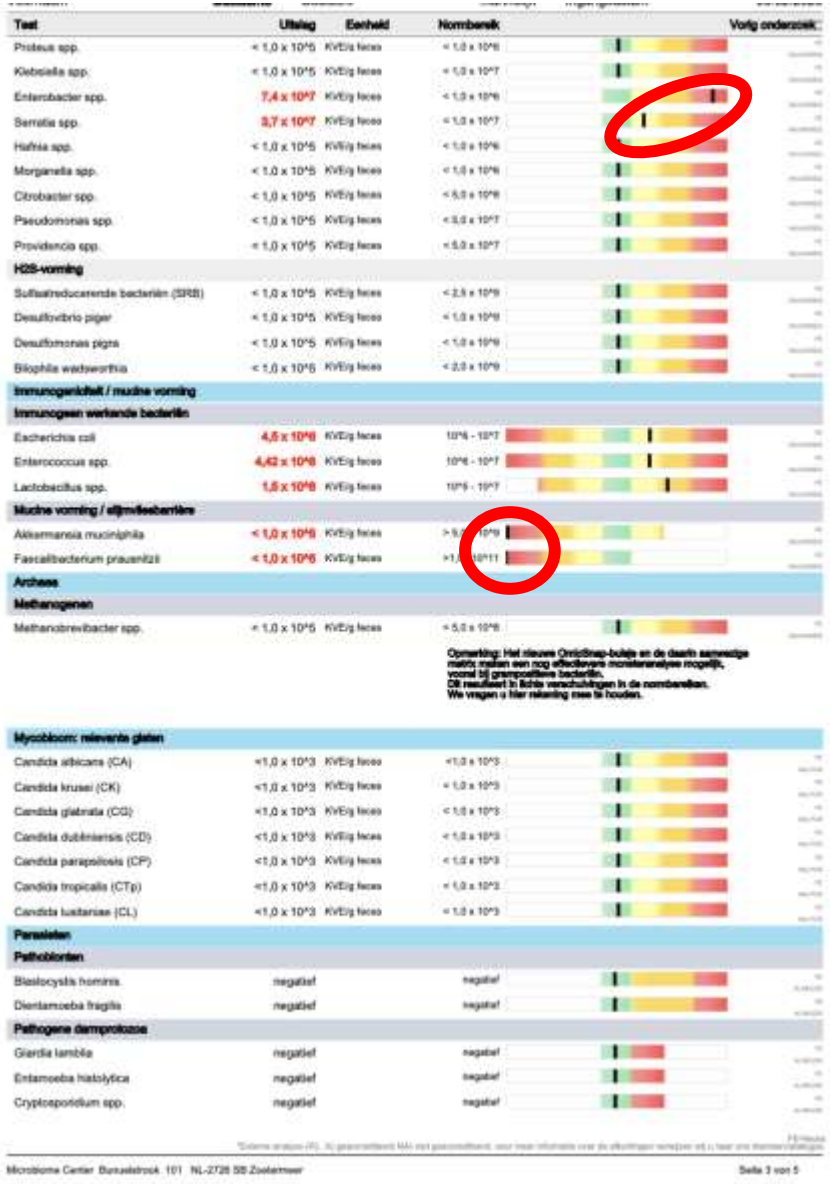
Microbiome Center Bunuelstrook 101 NL-2726 SB Zoetermeer Seite 1 von 5

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Indeling van bacteriën naar fylum				
Actinobacteria	8,8	%	1,5 - 7	
Bacteroidetes	8,9	%	20 - 45	
Firmicutes	72,6	%	50 - 75	
Fusobacteria	1,3	%	0,0 - 1,0	
Proteobacteria	8,4	%	1,0 - 3,5	
Verrucomicrobia	0,0	%	1,5 - 5,0	
Overige	0,0	%		
Metaboloom (stofwisselingsactieve bacteriegroepen)				
Secundaire galzuren	-49,8	%		
TMA / TMAO	4971,5	%		
Indoxylsulfaat	-50,0	%		
Fenolen	1242,8	%		
Ammoniak	178,2	%		
Histamine	-50,0	%		
Equol	-50,0	%		
Beta-glucuronidasen	516,2	%		
Indeling van bacteriën naar fylum met de belangrijkste bacteriegeslachten en -soorten				
Actinobacteria				
Bifidobacterium	8,5 x 10^10	KVE/g feces	> 1,0 x 10^10	
Bacteroidetes				
Bacteroides	< 1,0 x 10^5	KVE/g feces	> 5,0 x10^10	
Prevotella	8,9 x 10^10	KVE/g feces	> 1,0 x 10^10	
Firmicutes				
Butyraatproducerende bacteriën				
Totaal kiemgetal	2,6 x 10^9	KVE/g feces	> 2,4 x 10^1	
Faecalibacterium prausnitzii	< 1,0 x 10^5	KVE/g feces	>1,0 x10 1	
Eubacterium rectale	1,8 x 10^7	KVE/g feces	> 2,0 x 10	
Eubacterium hallii	2,4 x 10^8	KVE/g feces	> 1,5 x 10	
Roseburia spp.	1,8 x 10^7	KVE/g feces	> 3,0 x 10	
Ruminococcus spp.	2,4 x 10^8	KVE/g feces	> 5,0 x 10	
Coprococcus spp.	2,8 x 10^8	KVE/g feces	> 5,0 x 10	
Butyrivibrio spp.	< 1,0 x 10^5	KVE/g feces	>1,5 x 10^	
Clostridia				
Totaal kiemgetal	2,7 x 10^11	KVE/g feces	< 4,0 x 10^9	
Clostridia Cluster I	6,8 x 10^10	KVE/g feces	< 2,0 x 10^9	
Fusobacteria				
Fusobacterium	1,3 x 10^10	KVE/g feces	< 1,0 x 10^7	
Verrucomicrobia				
Akkermansia muciniphila	< 1,0 x 10^5	KVE/g feces	> 5,0 x 10^9	
Proteobacteria				
Pathogene of potentieel pathogene bacteriën				
Haemophilus spp.	3,9 x 10^10	KVE/g feces	< 5,0 x 10^8	
Acinetobacter spp.	9,2 x 10^6	KVE/g feces	< 1,0 x 10^6	

*Externe analyse (R), A) geaccrediteerd NA) niet geaccrediteerd, voor meer informatie over de afkortingen verwijzen wij u naar ons dienstencatalogus. FE=feces

Microbiome Center Bunuelstrook 101 NL-2726 SB Zoetermeer Seite 2 von 5

Case Crohn's disease and low butyrate formers



Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Proteus spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Klebsiella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7	
Enterobacter spp.	7,4 x 10^7	KVE/g feces	< 1,0 x 10^6	
Serratia spp.	3,7 x 10^7	KVE/g feces	< 1,0 x 10^7	
Hafnia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Morganella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Citrobacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^6	
Pseudomonas spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7	
Providencia spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7	
H2S-vorming				
Sulfaatreducerende bacteriën (SRB)	< 1,0 x 10^5	KVE/g feces	< 2,5 x 10^6	
Desulfovibrio piger	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Desulfomonas pigra	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Bilophila wadsworthia	< 1,0 x 10^5	KVE/g feces	< 2,0 x 10^6	
Immunogeniciteit / mucine vorming				
Immunogeen werkende bacteriën				
Escherichia coli	4,5 x 10^6	KVE/g feces	10^6 - 10^7	
Enterococcus spp.	4,42 x 10^6	KVE/g feces	10^6 - 10^7	
Lactobacillus spp.	1,5 x 10^6	KVE/g feces	10^5 - 10^7	
Mucine vorming / slijmviseberiere				
Akkermansia muciniphila	< 1,0 x 10^5	KVE/g feces	> 5,0 x 10^9	
Faecalibacterium prausnitzii	< 1,0 x 10^6	KVE/g feces	>1,0 x 10^11	
Archaea				
Methanogenen				
Methanobrevibacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^6	

Opmerking: Het nieuwe OmicSnap-buisje en de daarin aanwezige matrix maken een nog effectievere moleculeanalyse mogelijk, vooral bij grampositieve bacteriën.
Dit resulteert in licht verschuivingen in de normbereiken.
We vragen u hier rekening mee te houden.

Mycobloom: relevante gisten				
Candida albicans (CA)	<1,0 x 10^3	KVE/g feces	<1,0 x 10^3	
Candida krusei (CK)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida glabrata (CG)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida dubliniensis (CD)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida parapsilosis (CP)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida tropicalis (CTp)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida lusitaniae (CL)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Parasieten				
Pathobionten				
Blastocystis hominis	negatief		negatief	
Dientamoeba fragilis	negatief		negatief	
Pathogene dampprotozoa				
Giardia lamblia	negatief		negatief	
Entamoeba histolytica	negatief		negatief	
Cryptosporidium spp.	negatief		negatief	

Microbiome Center Burgerstraat 101 NL-2726 SB Zoetermeer Seite 3 van 5

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Cyclospora cayetanensis	negatief		negatief	
Vertering				
Vetgehalte	7,20	g/100g	< 3,5	
Stikstofgehalte	0,40	g/100g	< 1,0	
Suikergehalte	5,60	g/100g	< 2,5	
Watergehalte	78,80	g/100g	75 - 85	
Extra parameter(s)				
Calprotectine	>800,00	mg/l	< 50	
Alfa-1-antitripsine	44,9	mg/dl	< 27,5	
Secretoir Immunoglobuline A	4562,3	µg/ml	510 - 2040	
Zonuline	91,25	ng/ml	< 55	

Case Crohn’s disease and low butyrate formers

MyOwnBlend

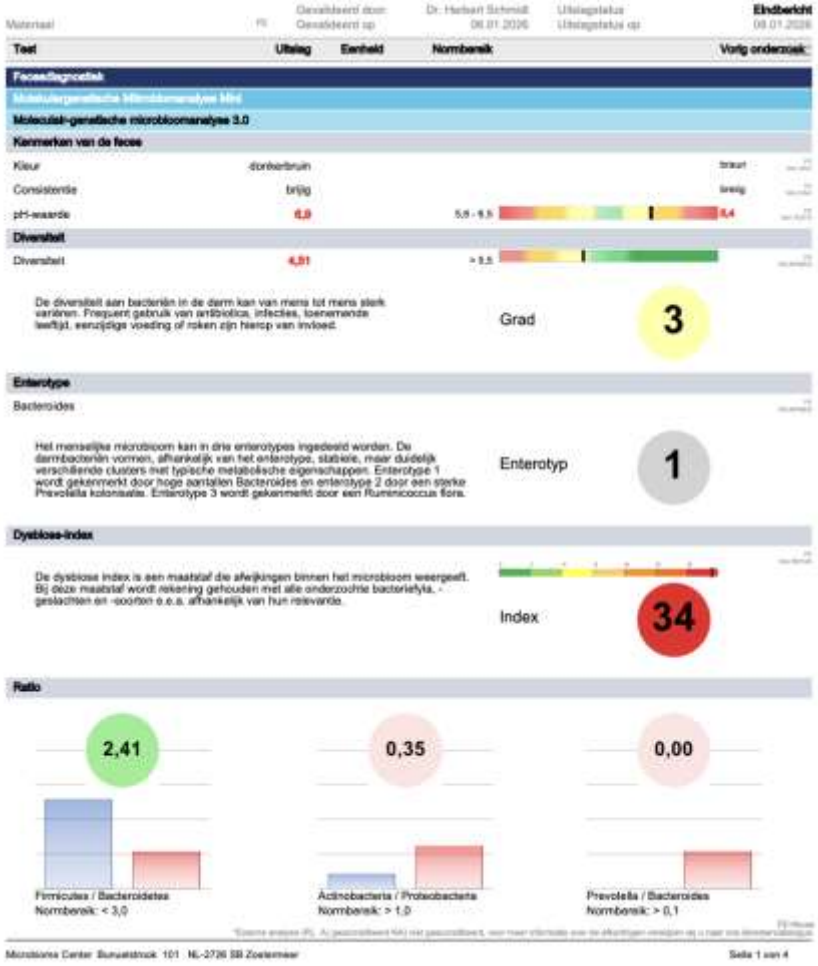
Code	Element	Dagdosering
M002	MyOwnBlend, magistrale bereiding 2 maanden (oraal)	
BB021	Bacillus coagulans Unique IS-2	2
BB061	Bifidobacterium lactis HN019	2
BB022	Enterococcus faecium + Bacillus subtilis	1
BB028	L. plantarum P-8	1
BB027	L. rhamnosus SP1	1
BB075	Lacticaseibacillus paracasei Lpc-37	1
BB029	PHGG	5
BB058	S. Boulardii CNCM-I-1079	2

Case Crohn’s disease and low butyrate formers

- **Result**
  - Feb-July: have not been sick anymore, stools more stable and more energy, gained weight
  - July epididymitis requiring antibiotics, after which again dysregulation
  - Started school in Sept, went well, started phasing out biologicals on my own initiative and MOB was finished

- **Follow-up:**
  - Nov stool restless again, energy still good
  - Restart biologicals and MOB after which improvement again
  - Retest January 2026

Case Crohn's disease



Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Feces/fagocytisk				
Molecular-genetische microbioomanalyse 3.0				
Kenmerken van de feces				
Kleur	donkerbruin			bruin
Consistentie	brijig			brijig
pH-waarde	6,9		5,5 - 6,5	6,4
Diversiteit				
Diversiteit	4,01		> 3,5	

De diversiteit aan bacteriën in de darm kan van mens tot mens sterk variëren. Frequent gebruik van antibiotica, infecties, loenemende leeftijd, eenzijdige voeding of roken zijn hiervp van invloed.

Grad **3**

Enterotype

Bacteroides

Het menselijke microbioom kan in drie enterotypes ingedeeld worden. De darmbacteriën vormen, afhankelijk van het enterotype, stabiele, maar duidelijk verschillende clusters met typische metabolische eigenschappen. Enterotype 1 wordt gekenmerkt door hoge aantallen Bacteroides en enterotype 2 door een sterke Prevotella kolonisatie. Enterotype 3 wordt gekenmerkt door een Ruminococcus flora.

Enterotyp **1**

Dysbiose-index

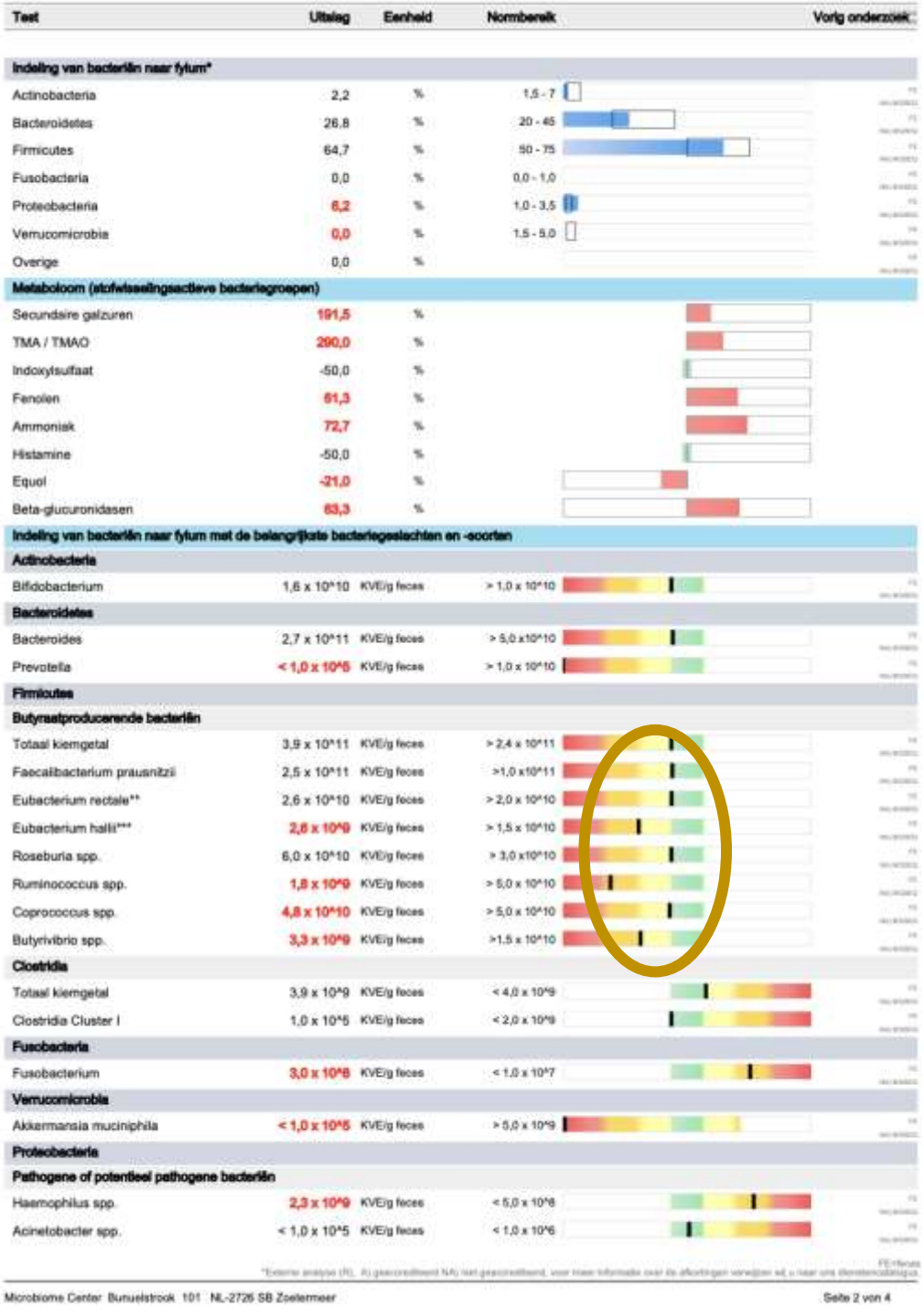
De dysbiose index is een maatstaf die afwijkingen binnen het microbioom weergeeft. Bij deze maatstaf wordt rekening gehouden met alle onderzochte bacterievlya, -geslachten en -soorten o.e.a. afhankelijk van hun relevantie.

Index **34**

Ratio

2,41	0,35	0,00
Firmicutes / Bacteroidetes	Actinobacteria / Proteobacteria	Prevotella / Bacteroides
Normbereik: < 3,0	Normbereik: > 1,0	Normbereik: > 0,1

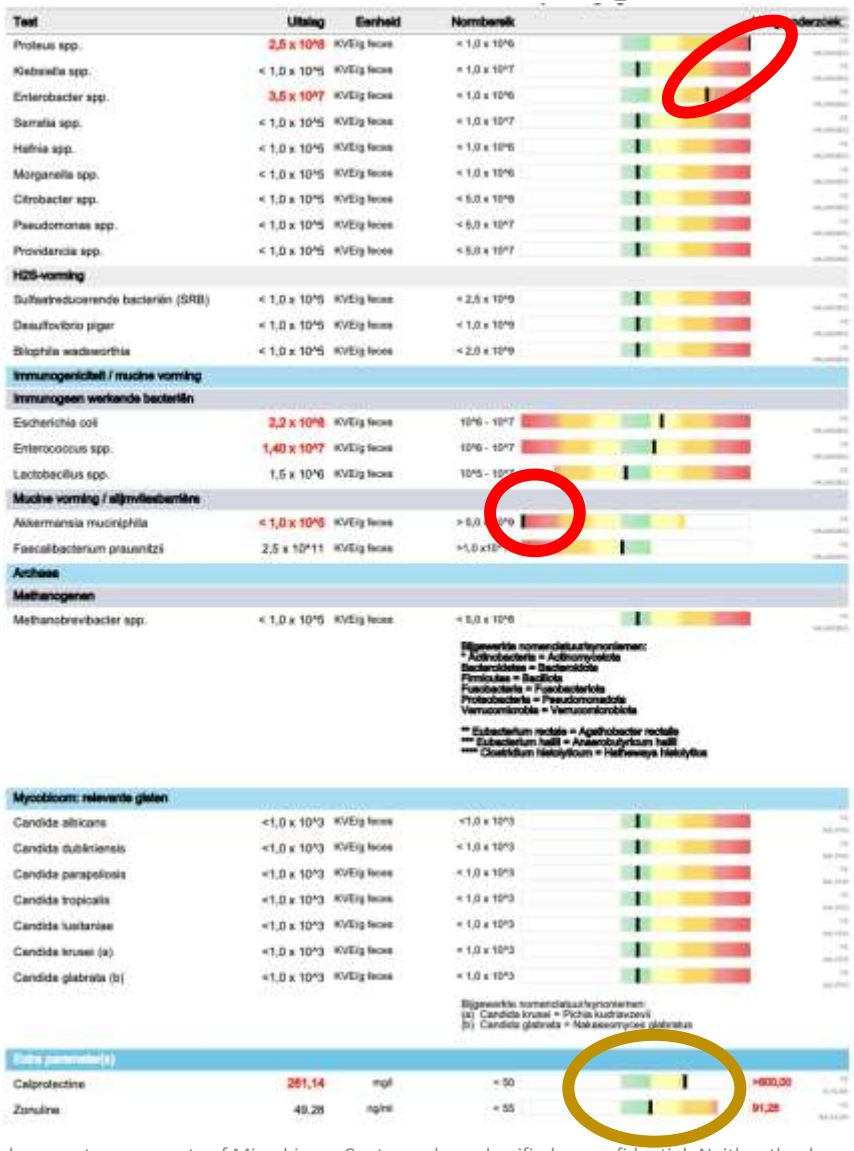
Microbiome Center Bunuelstrook 101 NL-2726 SB Zoetermeer Seite 1 van 4



Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Indeling van bacteriën naar fylum*				
Actinobacteria	2,2	%	1,5 - 7	
Bacteroidetes	26,8	%	20 - 45	
Firmicutes	64,7	%	50 - 75	
Fusobacteria	0,0	%	0,0 - 1,0	
Proteobacteria	6,2	%	1,0 - 3,5	
Verrucomicrobia	0,0	%	1,5 - 5,0	
Overige	0,0	%		
Metaboloom (stofwisselingsactieve bacteriegroepen)				
Secundaire galzuren	191,5	%		
TMA / TMAO	290,0	%		
Indoxylsulfaat	-50,0	%		
Fenolen	61,3	%		
Ammoniak	72,7	%		
Histamine	-50,0	%		
Equol	-21,0	%		
Beta-glucuronidasen	63,3	%		
Indeling van bacteriën naar fylum met de belangrijkste bacteriegeslachten en -soorten				
Actinobacteria				
Bifidobacterium	1,6 x 10^10	KVE/g feces	> 1,0 x 10^10	
Bacteroidetes				
Bacteroides	2,7 x 10^11	KVE/g feces	> 5,0 x10^10	
Prevotella	< 1,0 x 10^5	KVE/g feces	> 1,0 x 10^10	
Firmicutes				
Butyraatproducerende bacteriën				
Totaal kiemgetal	3,9 x 10^11	KVE/g feces	> 2,4 x 10^11	
Faecalibacterium prausnitzii	2,5 x 10^11	KVE/g feces	>1,0 x10^11	
Eubacterium rectale**	2,6 x 10^10	KVE/g feces	> 2,0 x 10^10	
Eubacterium hallii***	2,6 x 10^9	KVE/g feces	> 1,5 x 10^10	
Roseburia spp.	6,0 x 10^10	KVE/g feces	> 3,0 x10^10	
Ruminococcus spp.	1,8 x 10^9	KVE/g feces	> 5,0 x 10^10	
Coprococcus spp.	4,8 x 10^10	KVE/g feces	> 5,0 x 10^10	
Butyrivibrio spp.	3,3 x 10^9	KVE/g feces	>1,5 x 10^10	
Clostridia				
Totaal kiemgetal	3,9 x 10^9	KVE/g feces	< 4,0 x 10^9	
Clostridia Cluster I	1,0 x 10^5	KVE/g feces	< 2,0 x 10^9	
Fusobacteria				
Fusobacterium	3,0 x 10^8	KVE/g feces	< 1,0 x 10^7	
Verrucomicrobia				
Akkermansia muciniphila	< 1,0 x 10^5	KVE/g feces	> 5,0 x 10^9	
Proteobacteria				
Pathogene of potentieel pathogene bacteriën				
Haemophilus spp.	2,3 x 10^9	KVE/g feces	< 5,0 x 10^8	
Acinetobacter spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	

Microbiome Center Bunuelstrook 101 NL-2726 SB Zoetermeer Seite 2 van 4

Case Crohn’s disease and low butyrate formers



Test	Uitslag	Eenheid	Normbereik
Proteus spp.	2,5 x 10^8	KVE/g feces	< 1,0 x 10^6
Klebsiella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7
Enterobacter spp.	3,5 x 10^7	KVE/g feces	< 1,0 x 10^6
Serratia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7
Hafnia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6
Morganella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6
Citrobacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^6
Pseudomonas spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7
Providencia spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7
H2S-vorming			
Sulfaatreducerende bacteriën (SRB)	< 1,0 x 10^5	KVE/g feces	< 2,5 x 10^9
Desulfovibrio piger	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^9
Bilophila wadsworthia	< 1,0 x 10^5	KVE/g feces	< 2,0 x 10^9
Immunogeniciteit / mucine vorming			
Immunogeen werkende bacteriën			
Escherichia coli	2,2 x 10^8	KVE/g feces	10^6 - 10^7
Enterococcus spp.	1,40 x 10^7	KVE/g feces	10^6 - 10^7
Lactobacillus spp.	1,5 x 10^6	KVE/g feces	10^5 - 10^7
Mucine vorming / slijmvliesbarrière			
Akkermansia muciniphila	< 1,0 x 10^5	KVE/g feces	> 5,0 x 10^9
Faecalibacterium prausnitzii	2,5 x 10^11	KVE/g feces	>1,0 x10^9
Archaea			
Methanogenen			
Methanobrevibacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^6

Bijgewerkte nomenclatuur/synoniemen:
* Actinobacteria = Actinomycetota
Bacteroidetes = Bacteroidota
Firmicutes = Bacillota
Fusobacteria = Fusobacteriota
Proteobacteria = Pseudomonadota
Verrucomicrobia = Verrucomicrobiota

** Eubacterium rectale = Agathobacter rectalis
*** Eubacterium hallii = Anaerobutyricum hallii
**** Clostridium hiolytlcum = Hathewaya histolytica

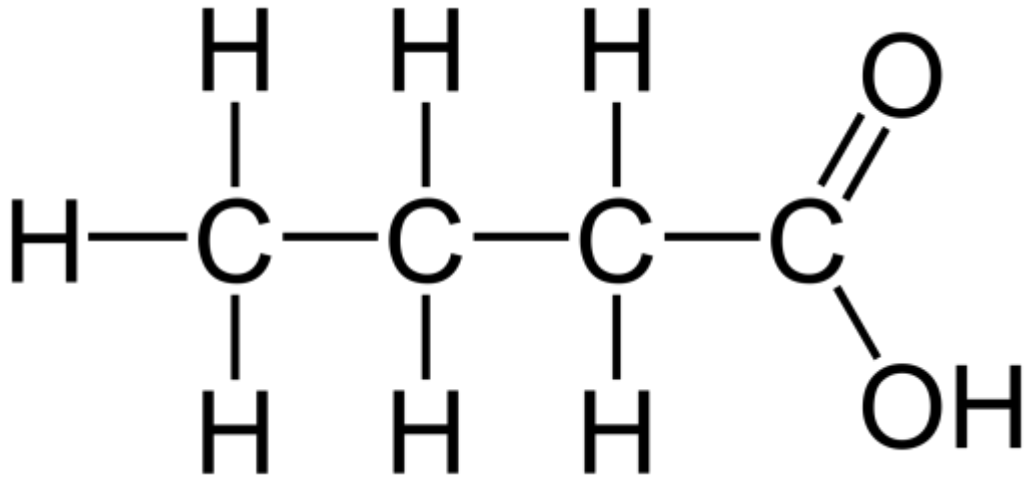
Mycobiom: relevante gisten			
Candida albicans	<1,0 x 10^3	KVE/g feces	<1,0 x 10^3
Candida dubliniensis	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3
Candida parapsilosis	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3
Candida tropicalis	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3
Candida lusitaniae	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3
Candida krusei (a)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3
Candida glabrata (b)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3

Bijgewerkte nomenclatuur/synoniemen:
(a) Candida krusei = Pichia kudriavzevii
(b) Candida glabrata = Nakaseomyces glabratus

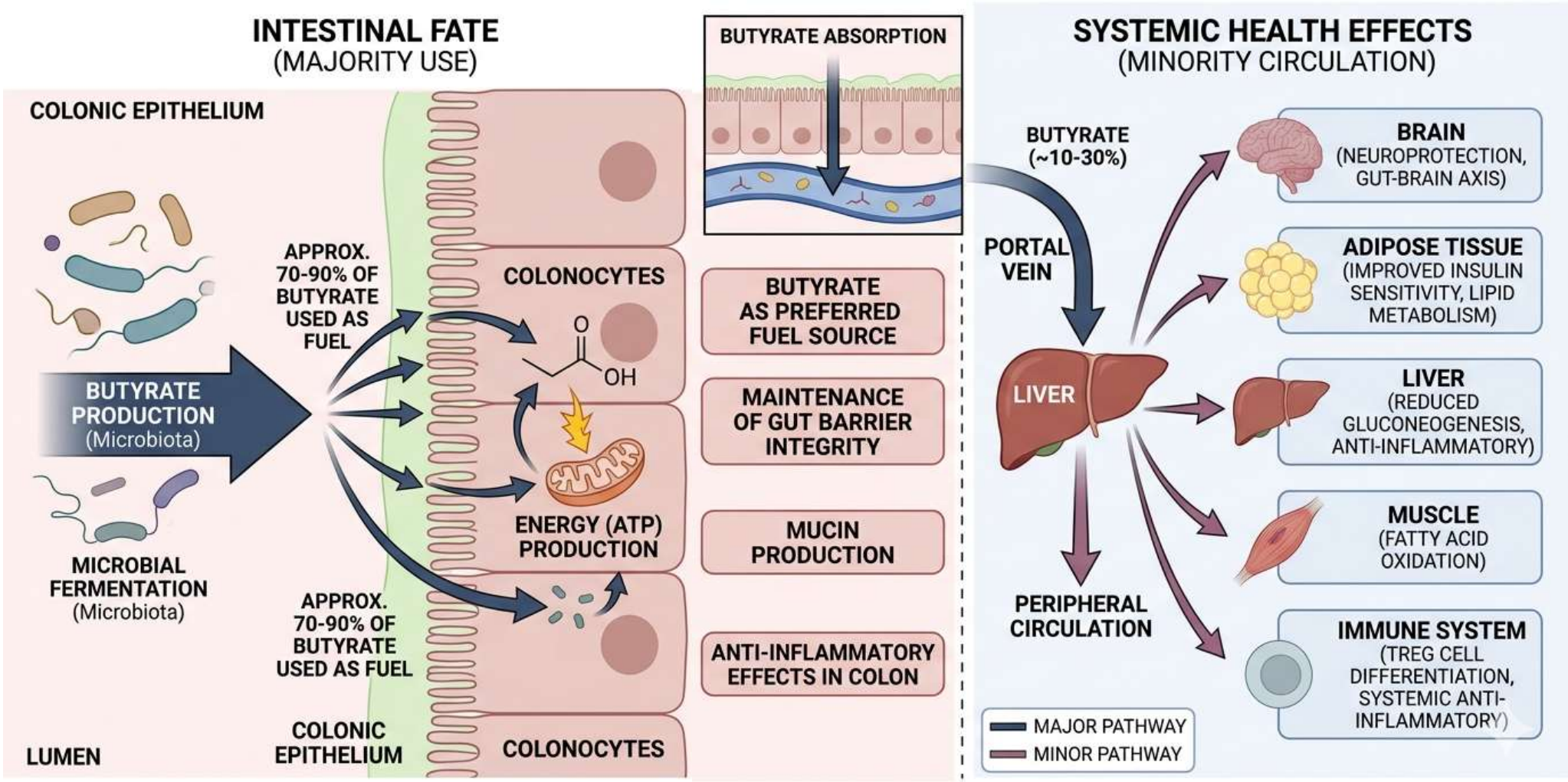
Extra parameter(s)				
Calprotectine	261,14	mg/l	< 50	>600,00
Zonuline	49,28	ng/ml	< 55	91,28

Butyrate

Health effects

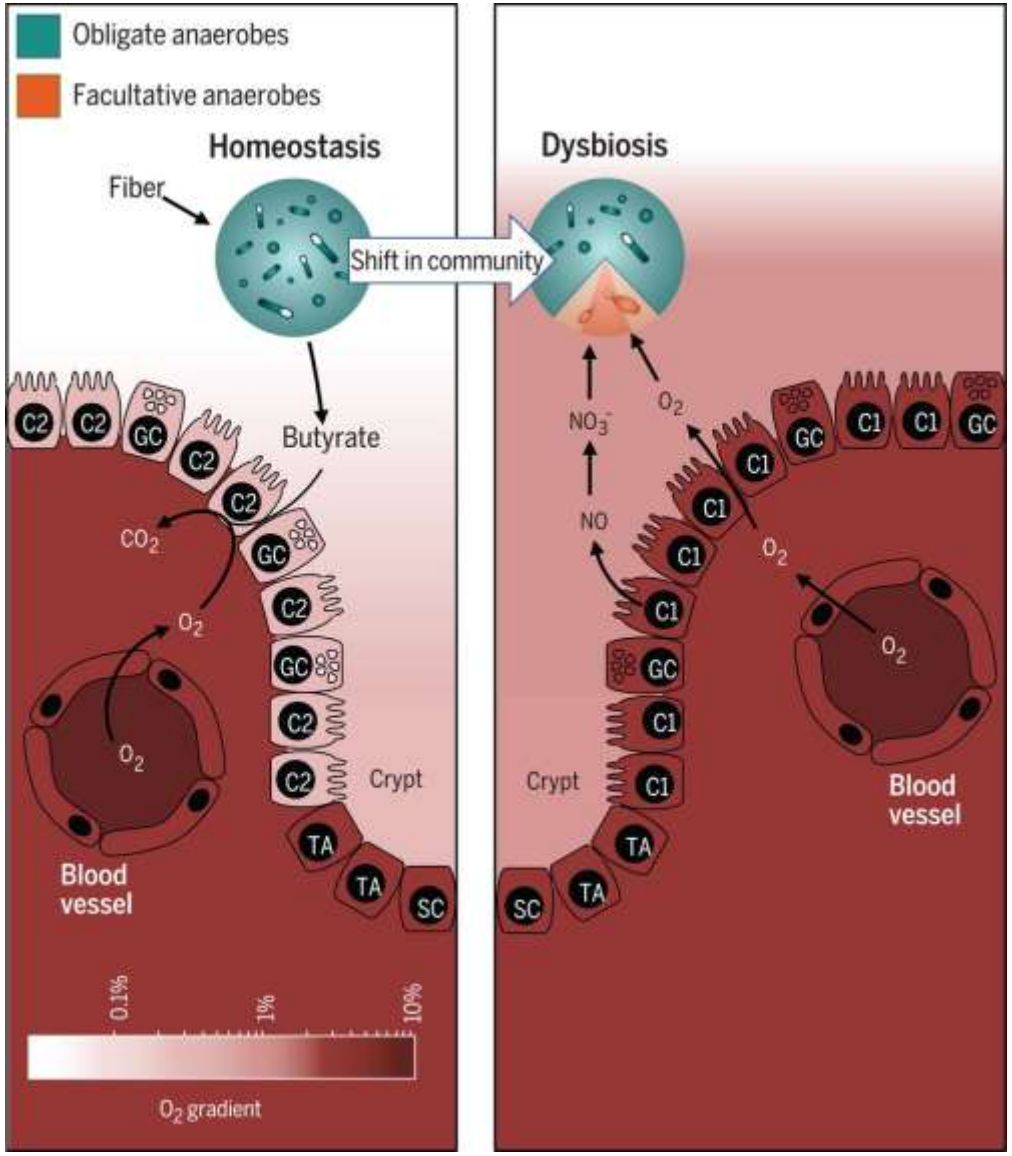


Butyrate metabolism and systemic health effects



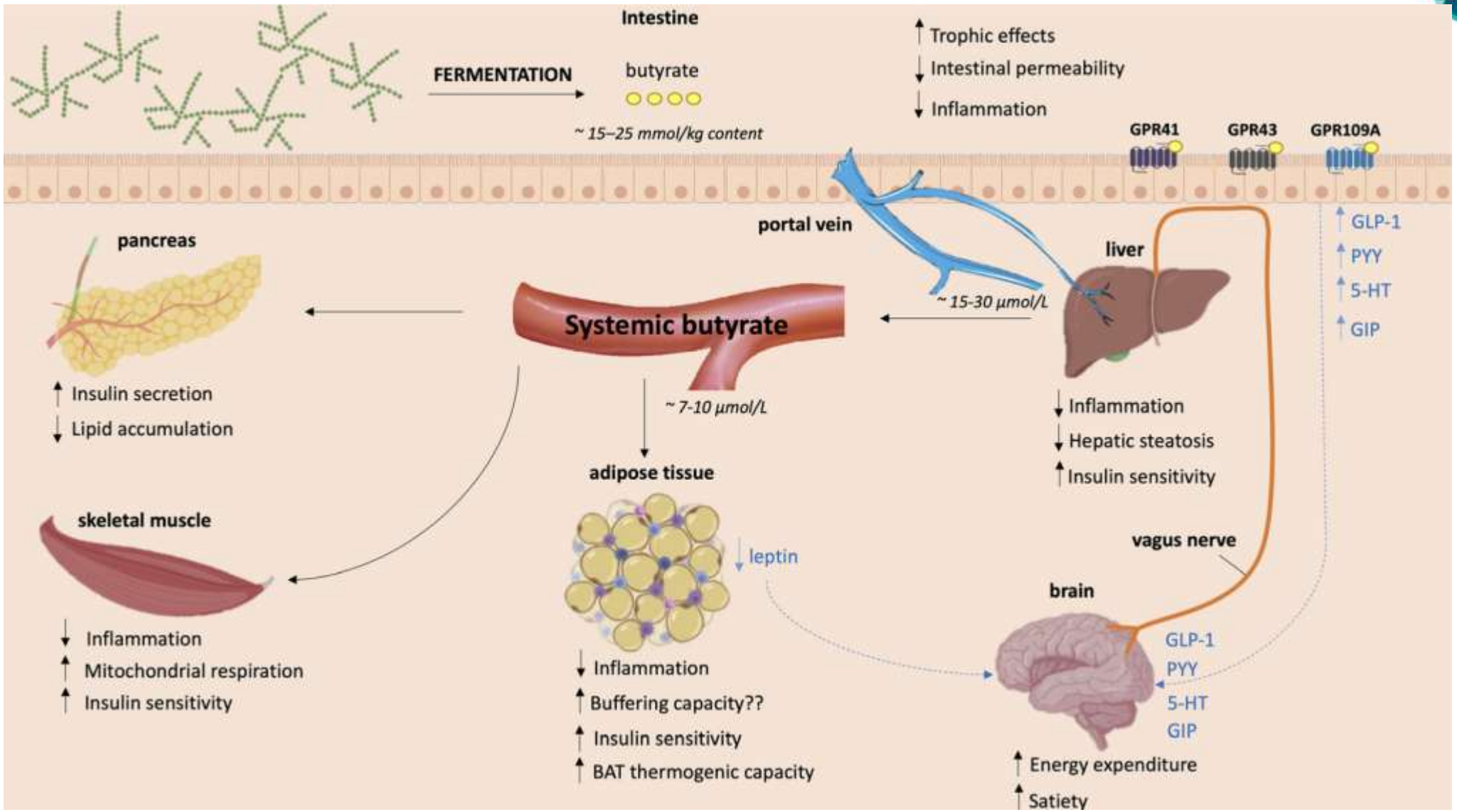
1. McNabney, S. M. et al.Nutrients.9,.1348.(2017)
2. Singh, V. et al.Front. Microbiol.13,.1103836.(2023)
3. Hays, K. E. et al.Gut Microbes.16,.2393270.(2024)

Butyrate local health effects

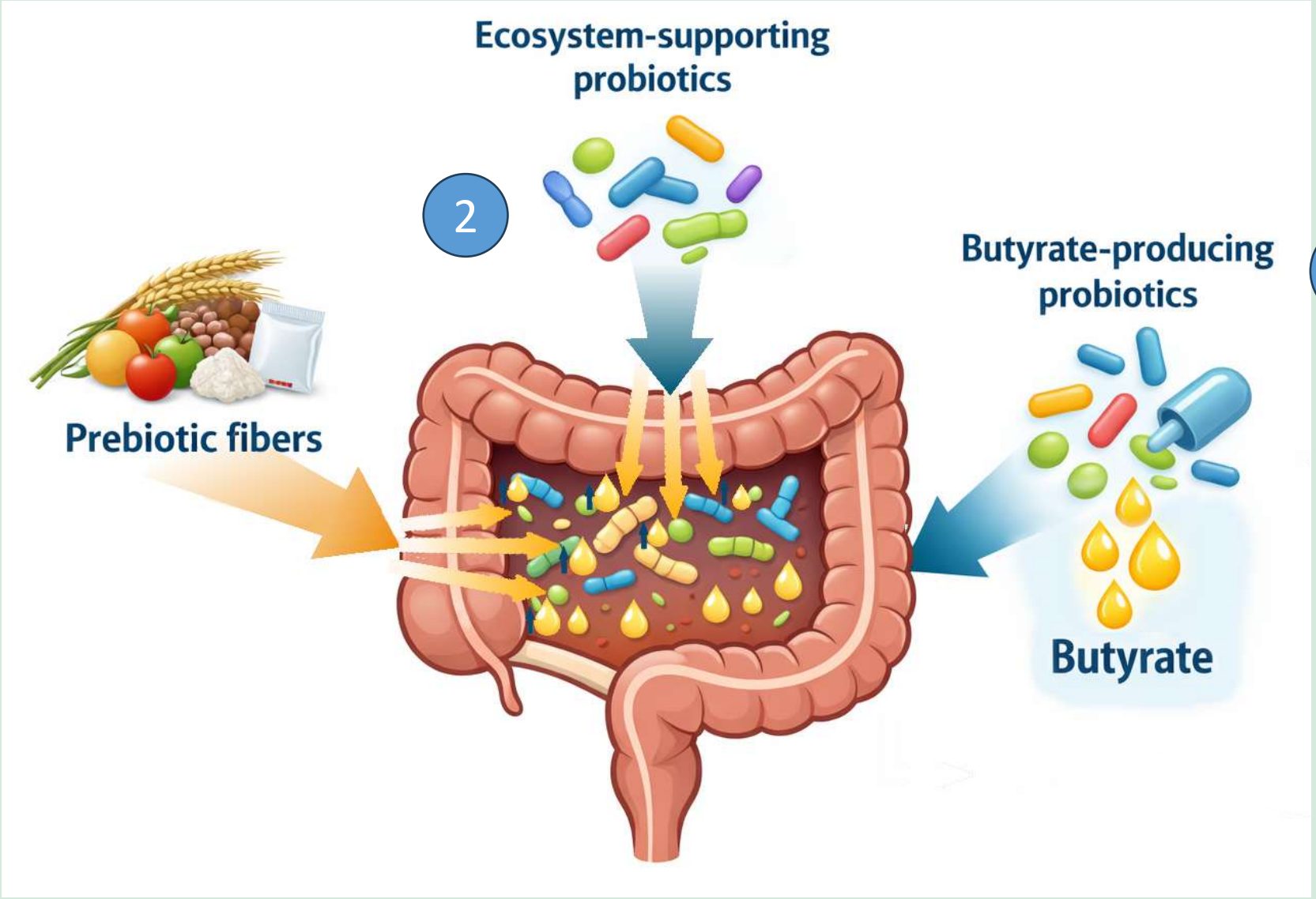


Litvak, Y. et al.Science.362,.eaat9076.(2018)

Butyrate systemic health effects

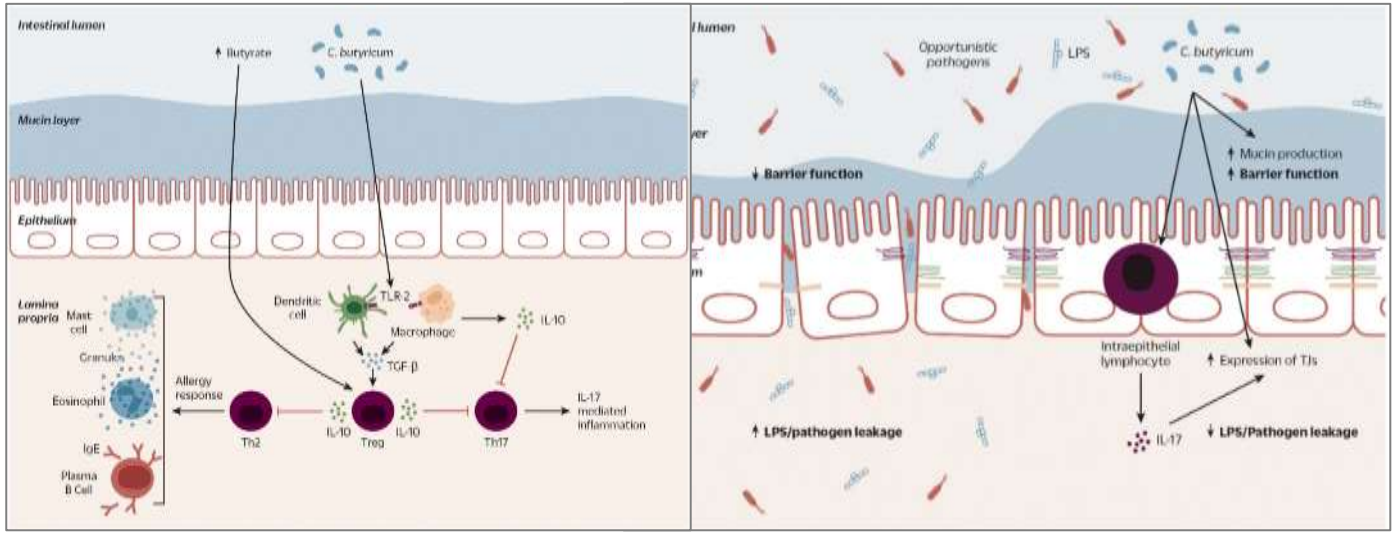


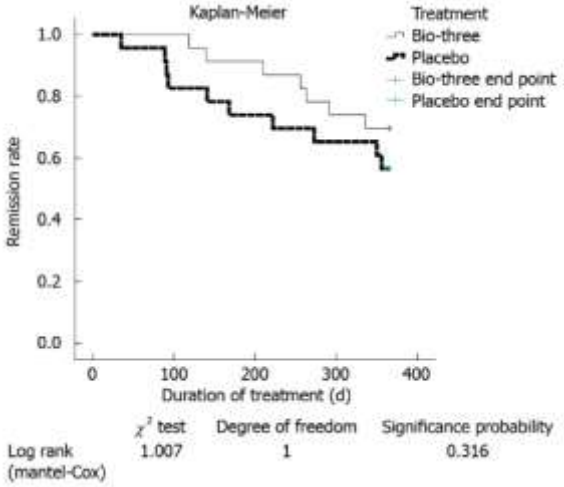
van Deuren, T. et al.Obesity Reviews.n/a,.e13498.(2022)



3 Butyrate-producing probiotics: "Butyrate generator"

- This building block contains three strains:
  - *Enterococcus faecium* T-110
  - *Clostridium butyricum* TO-A
  - *Bacillus subtilis* TO-A
- On the Japanese market as medicine since 1963
- Strains act symbiotically, yielding *in situ* butyrate production of *C. butyricum*
- **Butyrate** has strong anti-inflammatory properties[1-3]
  - Exemplified by effect of this building block on ulcerative colitis[4-6]
- For this building block there is also evidence for:
  - Anti-inflammatory effects[4,7,8]
  - Infectious diarrhea[7,8]
- Data analysis: favorable effect in patients with allergy.
- Typical use: inflammation with low butyrate-producing capacity.





1. Brahe, L. K. et al. Obesity Reviews 14, 950–959 (2013)
2. Chang, P. V. et al. PNAS 111, 2247–2252 (2014)
3. Stoeva, M. K. et al. Gut Microbes 13, 1907272 (2021)
4. Yoshimatsu, Y. et al. World J Gastroenterol 21, 5985–5994 (2015)
5. Tsuda, Y. et al. Scand. J. Gastroenterol. 42, 1306–1311 (2007)
6. Lee, J. et al. Gastroenterology Research and Practice 2022, 1–5 (2022)
7. Chen, C.-C. et al. Pediatr. Infect. Dis. J. 29, 135–138 (2010)
8. Huang, Y.-F. et al. J. Clin. Gastroenterol. 48, 37–42 (2014)
9. Aisu, N. et al. Experimental and Therapeutic Medicine 10, 966–972 (2015)

3 Butyrate-producing probiotics: “Butyrate generator” (Bio-three)

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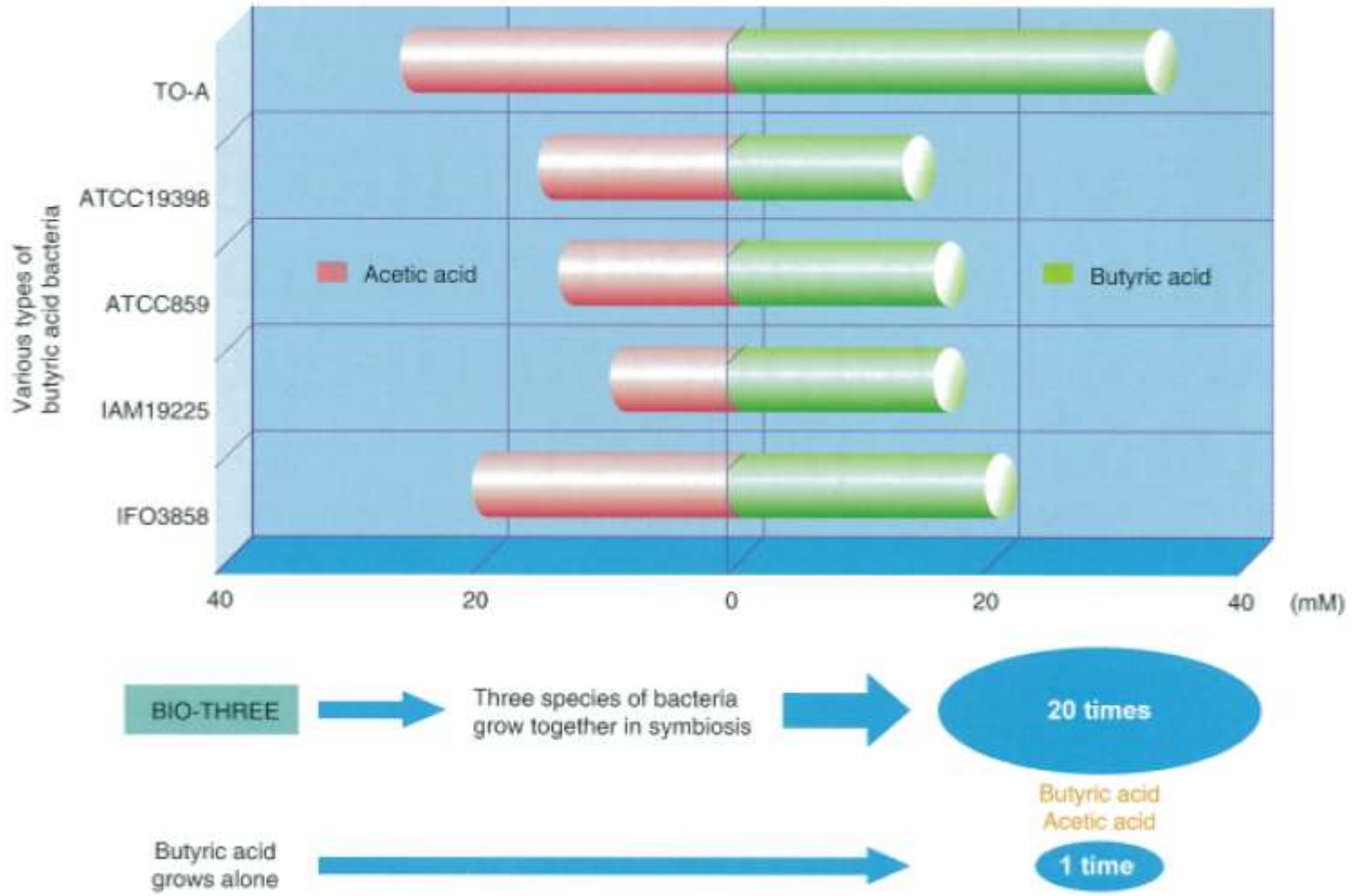


3 Butyrate-producing probiotics: Synergy between C. *butyricum* and PHGG

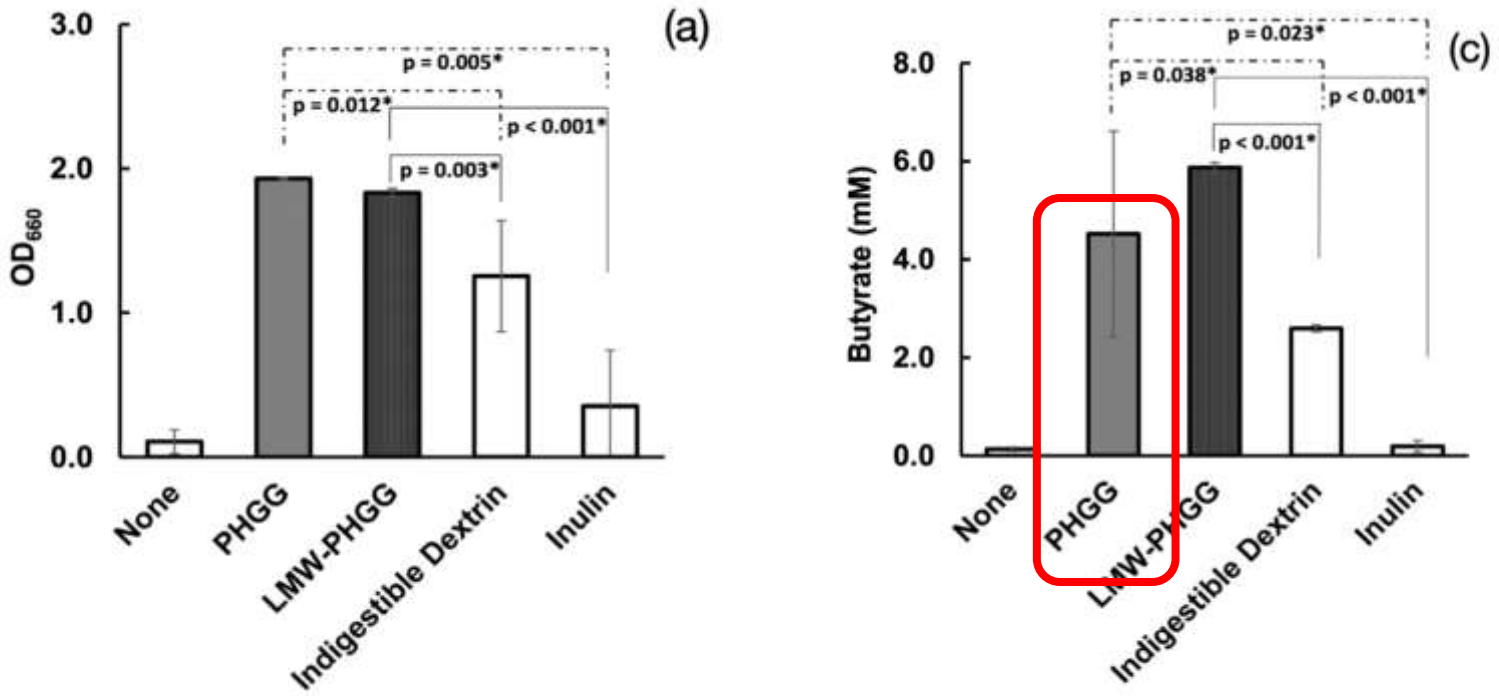
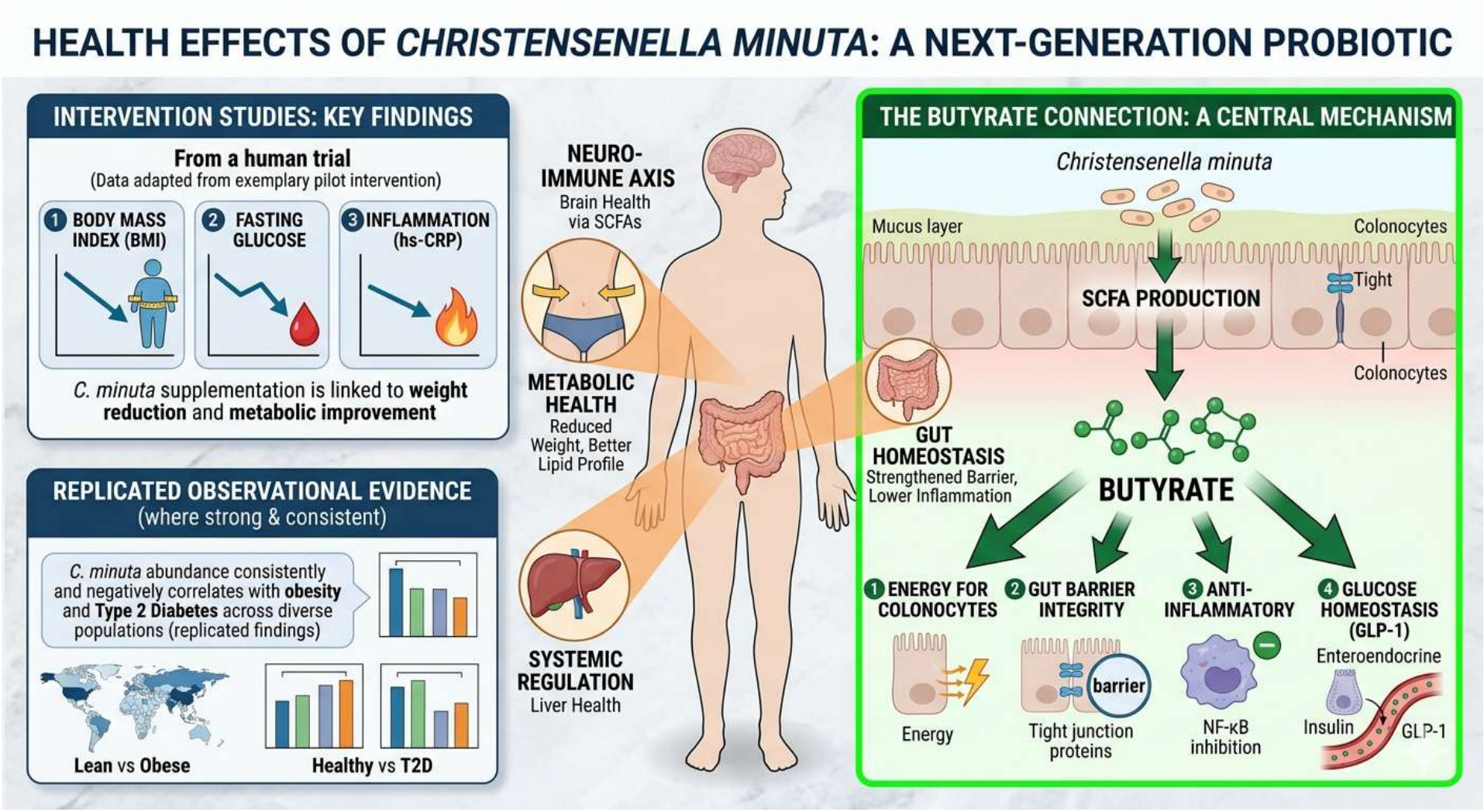


Figure 2. Synergistic effect of different prebiotic dietary fiber supplementation as a carbon source on *Clostridium butyricum* bacterial stain for enhanced butyrate production during in-vitro fermentation. (a) bacterial growth (OD_{660}), (b) variation in pH of basal medium, and (c) butyrate production. [Statistical significance: $p \leq 0.05$]

1. Matsumiya, Y. et al.Functional Foods in Health and Disease - Online ISSN: 2160-3855; Print ISSN: 2378-7007.14,.455–469.(2024)

3 Butyrate-producing probiotics to come: *Christensenella minuta* Lx-03



Example case 3

UTI and low butyrate producers

Case UTIs and low butyrate formers

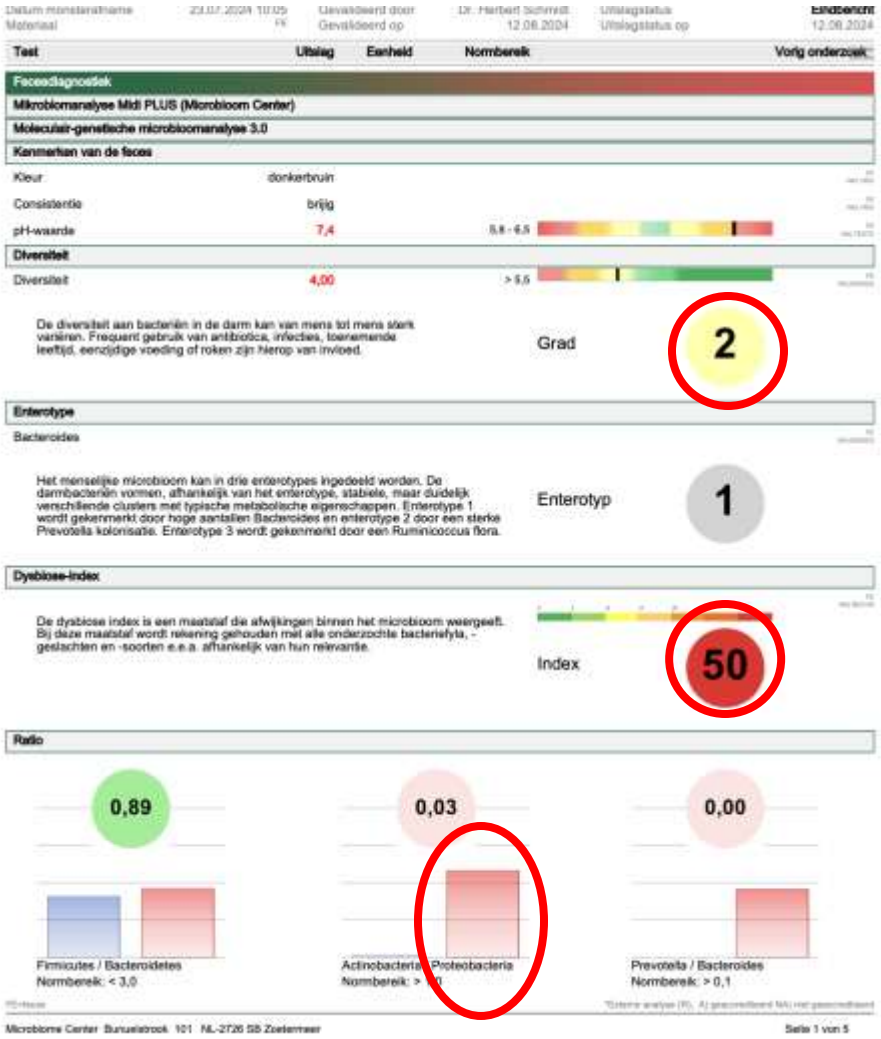
Amber, 1996

- Recurrent UTIs, past 2 years also pyelonephritis, often antibiotics (including probiotics)
- History:
  - Lyme for which different treatments abroad
  - Endometriosis
  - Sinus Tachycardia
- Fam: many autoimmune diseases
- Def: daily, sometimes diarrhea, very bloated and bulging belly.
- Nutrition: been working on it for 12 years, had a holistic natural dietitian, she is clear what she can and cannot eat. Also did an IgG test. Hypersensitive to gluten and milk protein.

- Microbiome analysis Augustus 2024

Case UTIs and low butyrate fo

iome



Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Faecesdiagnostiek				
Mikrobiomanalyse Midi PLUS (Microbioom Center)				
Moleculair-genetische microbioomanalyse 3.0				
Kenmerken van de feces				
Kleur	donkerbruin			
Consistentie	brijig			
pH-waarde	7,4		5,8 - 6,5	
Diversiteit				
Diversiteit	4,00		> 5,5	

De diversiteit aan bacteriën in de darm kan van mens tot mens sterk variëren. Frequent gebruik van antibiotica, infecties, toenemende leeftijd, eenzijdige voeding of roken zijn hierop van invloed.

Grad **2**

Enterotype

Bacteroides

Het menselijke microbioom kan in drie enterotypes ingedeeld worden. De darmbacteriën vormen, afhankelijk van het enterotype, stabiele, maar duidelijk verschillende clusters met typische metabolische eigenschappen. Enterotype 1 wordt gekenmerkt door hoge aantallen Bacteroides en enterotype 2 door een sterke Prevotella kolonisatie. Enterotype 3 wordt gekenmerkt door een Ruminococcus flora.

Enterotyp **1**

Dysbiose-index

De dysbiose index is een maatstaf die afwijkingen binnen het microbioom weergeeft. Bij deze maatstaf wordt rekening gehouden met alle onderzochte bacteriefyla, -geslachten en -soorten e.e.a. afhankelijk van hun relevantie.

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Ratio

Microbiome Center Burusalstraat 101 NL-2726 SB Zoetermeer

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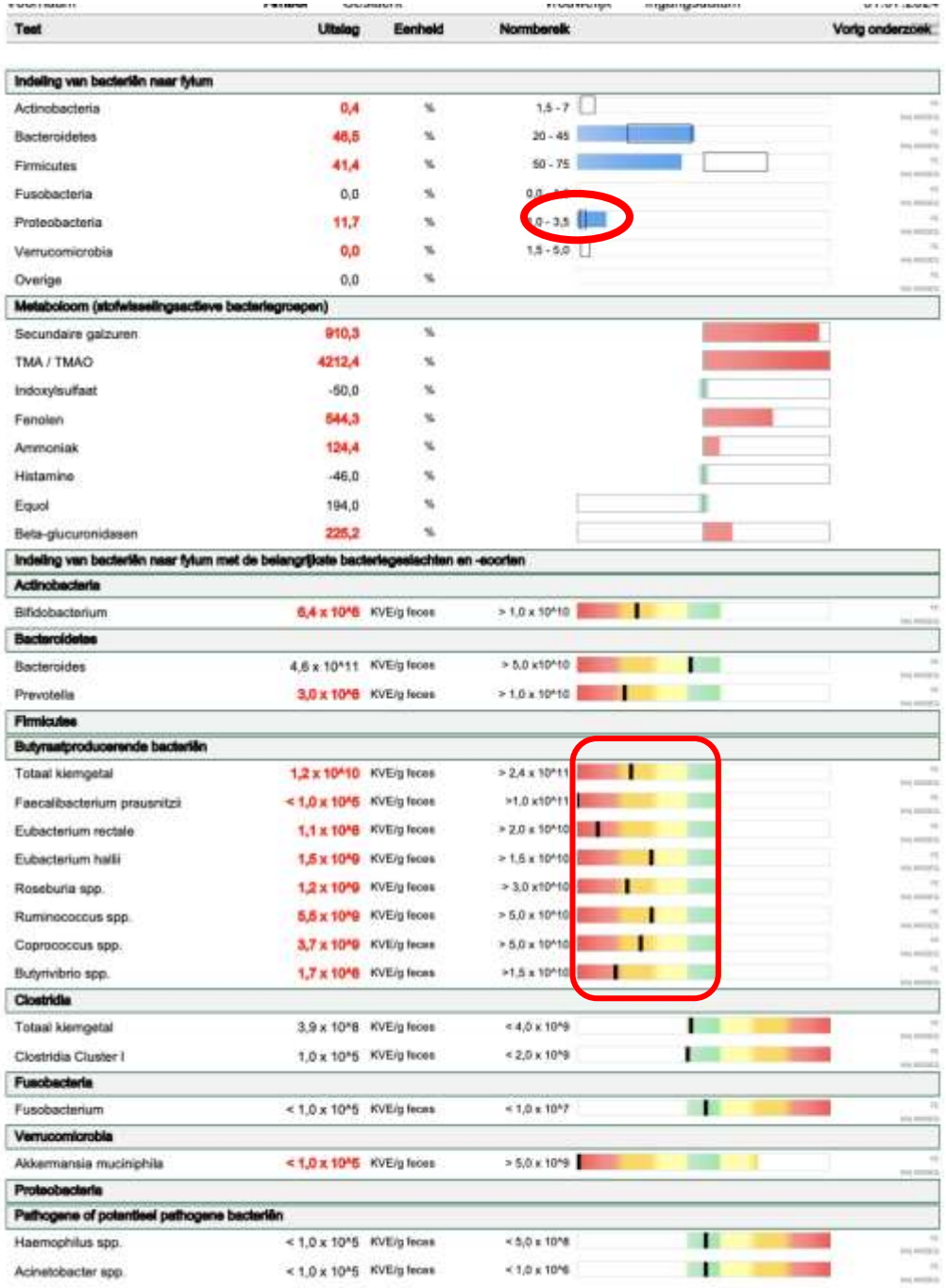
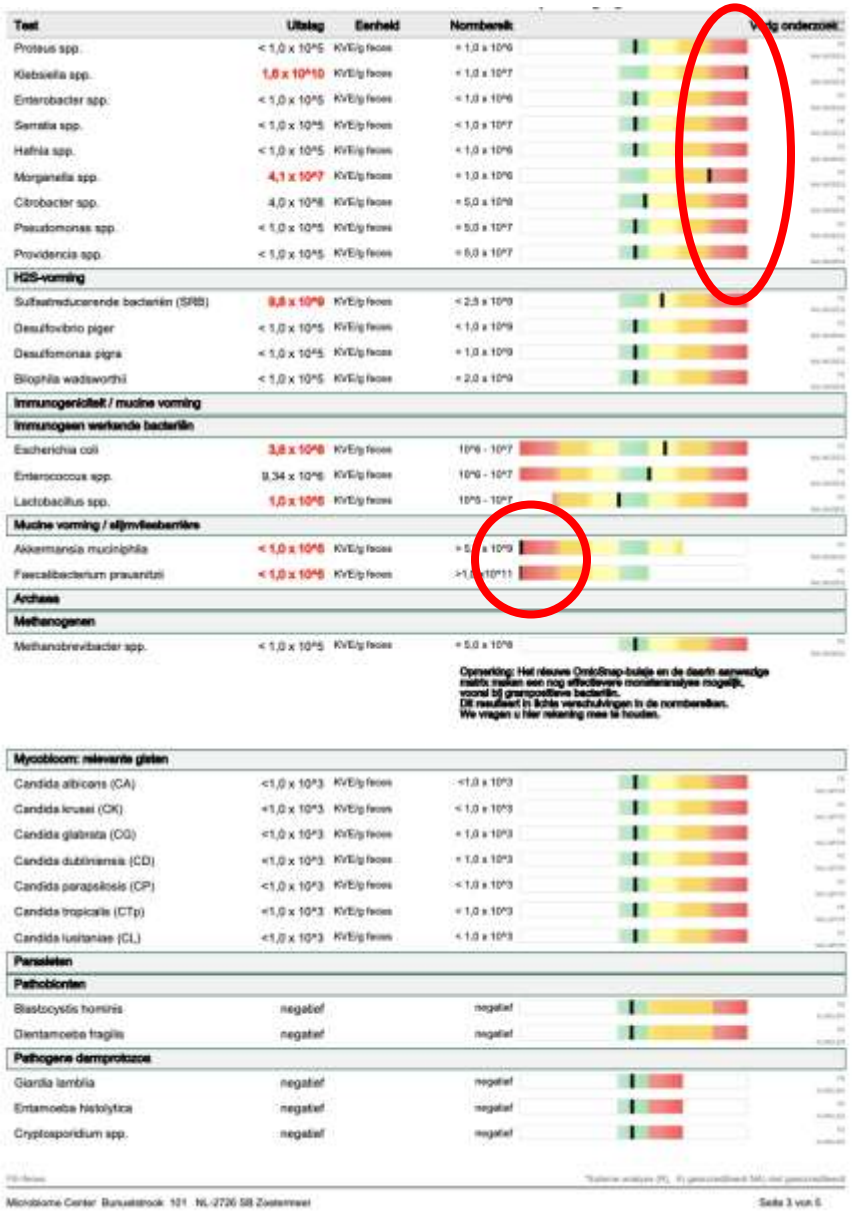


Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Indeling van bacteriën naar fylum				
Actinobacteria	0,4	%	1,5 - 7	
Bacteroidetes	46,5	%	20 - 45	
Firmicutes	41,4	%	50 - 75	
Fusobacteria	0,0	%	0,0 - 1,0	
Proteobacteria	11,7	%	1,0 - 3,5	
Verrucomicrobia	0,0	%	1,5 - 5,0	
Overige	0,0	%		
Metaboloom (stofwisselingsactieve bacteriegroepen)				
Secundaire galzuren	910,3	%		
TMA / TMAO	4212,4	%		
Indoxylsulfaat	-50,0	%		
Fenolen	544,3	%		
Ammoniak	124,4	%		
Histamine	-46,0	%		
Equol	194,0	%		
Beta-glucuronidasen	225,2	%		
Indeling van bacteriën naar fylum met de belangrijkste bacteriegeslachten en -soorten				
Actinobacteria				
Bifidobacterium	6,4 x 10^6	KVE/g feces	> 1,0 x 10^10	
Bacteroidetes				
Bacteroides	4,6 x 10^11	KVE/g feces	> 5,0 x10^10	
Prevotella	3,0 x 10^6	KVE/g feces	> 1,0 x 10^10	
Firmicutes				
Butyraatproducerende bacteriën				
Totaal kiemgetal	1,2 x 10^10	KVE/g feces	> 2,4 x 10^11	
Faecalibacterium prausnitzii	< 1,0 x 10^5	KVE/g feces	>1,0 x10^11	
Eubacterium rectale	1,1 x 10^8	KVE/g feces	> 2,0 x 10^10	
Eubacterium hallii	1,5 x 10^9	KVE/g feces	> 1,5 x 10^10	
Roseburia spp.	1,2 x 10^9	KVE/g feces	> 3,0 x10^10	
Ruminococcus spp.	5,5 x 10^9	KVE/g feces	> 5,0 x 10^10	
Coprococcus spp.	3,7 x 10^9	KVE/g feces	> 5,0 x 10^10	
Butyrivibrio spp.	1,7 x 10^6	KVE/g feces	>1,5 x 10^10	
Clostridia				
Totaal kiemgetal	3,9 x 10^8	KVE/g feces	< 4,0 x 10^9	
Clostridia Cluster I	1,0 x 10^5	KVE/g feces	< 2,0 x 10^9	
Fusobacteria				
Fusobacterium	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7	
Verrucomicrobia				
Akkermansia muciniphila	< 1,0 x 10^5	KVE/g feces	> 5,0 x 10^9	
Proteobacteria				
Pathogene of potentieel pathogene bacteriën				
Haemophilus spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^8	
Acinetobacter spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^8	

Case UTIs and low butyrate formers



Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Proteus spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Klebsiella spp.	1,6 x 10^10	KVE/g feces	< 1,0 x 10^7	
Enterobacter spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Serratia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7	
Hafnia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Morganella spp.	4,1 x 10^7	KVE/g feces	< 1,0 x 10^6	
Citrobacter spp.	4,0 x 10^8	KVE/g feces	< 5,0 x 10^8	
Pseudomonas spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7	
Providencia spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7	
H2S-vorming				
Sulfaatreducerende bacteriën (SRB)	9,8 x 10^9	KVE/g feces	< 2,5 x 10^9	
Desulfovibrio piger	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^9	
Desulfomonas pigra	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^9	
Bilophila wadsworthii	< 1,0 x 10^5	KVE/g feces	< 2,0 x 10^9	
Immunogeniciteit / mucine vorming				
Immunogeen werkende bacteriën				
Escherichia coli	3,8 x 10^8	KVE/g feces	10^6 - 10^7	
Enterococcus spp.	9,34 x 10^6	KVE/g feces	10^6 - 10^7	
Lactobacillus spp.	1,0 x 10^5	KVE/g feces	10^5 - 10^7	
Mucine vorming / slijmvliesbarrière				
Akkermansia muciniphila	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^9	
Faecalibacterium prausnitzii	< 1,0 x 10^5	KVE/g feces	>1,0 x 10^11	
Archaea				
Methanogenen				
Methanobrevibacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^8	

Opmerking: Het nieuwe OmicSnap-buisje en de daarin aanwezige reagentia maken een nog effectievere monsteranalyse mogelijk, vooral bij grampositieve bacteriën.
Dit resulteert in lichte verschuivingen in de normberekken.
We vragen u hier rekening mee te houden.

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Mycobioom: relevante gisten				
Candida albicans (CA)	<1,0 x 10^3	KVE/g feces	<1,0 x 10^3	
Candida krusei (CK)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida glabrata (CG)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida dubliniensis (CD)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida parapsilosis (CP)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida tropicalis (CTp)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida lusitaniae (CL)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Parasieten				
Pathobionten				
Blastocystis hominis	negatief		negatief	
Dientamoeba fragilis	negatief		negatief	
Pathogene darmprotozoa				
Giardia lamblia	negatief		negatief	
Entamoeba histolytica	negatief		negatief	
Cryptosporidium spp.	negatief		negatief	

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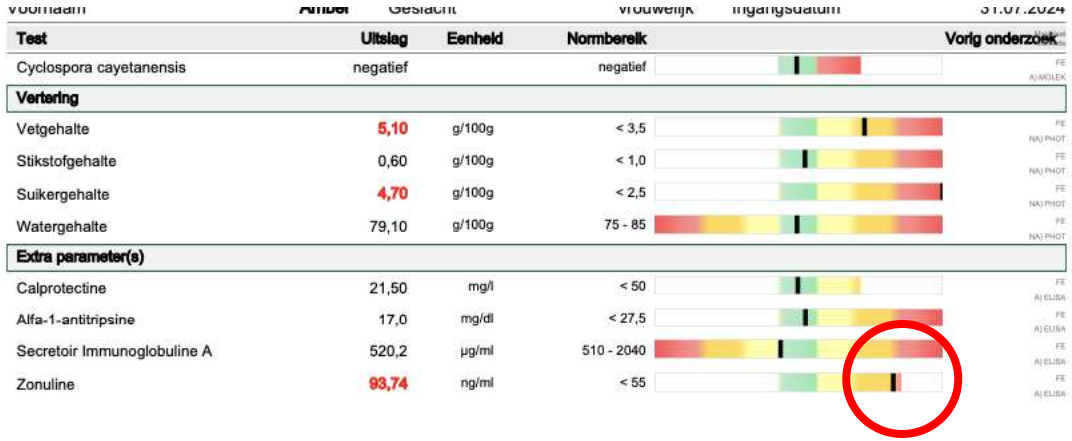

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Cyclospora cayetanensis	negatief		negatief	
Vertering				
Vetgehalte	5,10	g/100g	< 3,5	
Stikstofgehalte	0,60	g/100g	< 1,0	
Suikergehalte	4,70	g/100g	< 2,5	
Watergehalte	79,10	g/100g	75 - 85	
Extra parameter(s)				
Calprotectine	21,50	mg/l	< 50	
Alfa-1-antitripsine	17,0	mg/dl	< 27,5	
Secretoir Immunoglobuline A	520,2	µg/ml	510 - 2040	
Zonuline	93,74	ng/ml	< 55	

Case UTIs and low butyrate formers

MyOwnBlend

DJrepair, iberis complex

MyOwnBlend, magistrale bereiding onderhoudsrecept (oraal)	
2'-Fucosyllactose	3
Bacillus clausii UBBC-07	1
Butyraat generator	2
L fermentum ME-3	2
L. rhamnosus GG	2
PHGG	4
S. Boulardii CNCM-I-1079	1

Case UTIs and low butyrate formers

Result:

- No more bladder infections, is very happy with that.
- Bloated belly is almost gone, sometimes still a little in cycle.
- Final: good and stable.
- Nutrition not adjusted, was already good.

Follow-up:

- MOB maintenance recipe (DJ repair no longer necessary)
- Retest April 2026

Case UTIs and low butyra

Retest: March 2026

Microbiome Center

Datum monsterafname	17.03.2026 18:45	Gevalideerd door	Dr. Herbert Schmidt	Uitslagstatus	Eindbericht
Materiaal	FE	Gevalideerd op	30.03.2026	Uitslagstatus op	30.03.2026

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Feceadiagnostiek				
Microbiomanalyse Mini PLUS (Microbiom Center)				
Moleculair-genetische microbioomanalyse 3.0				
Kenmerken van de feces				
Kleur	bruin			
Consistentie	taaibrijg			
pH-waarde	7,1		5,8 - 6,5	
Diversiteit				
Diversiteit	5,03		> 5,5	

De diversiteit aan bacteriën in de darm kan van mens tot mens sterk variëren. Frequent gebruik van antibiotica, infecties, toenemende leeftijd, eenzijdige voeding of roken zijn hierop van invloed.

Grad **4**

Enterotype

Bacteroides

Het menselijke microbioom kan in drie enterotypes ingedeeld worden. De darmbacteriën vormen, afhankelijk van het enterotype, stabiele, maar duidelijk verschillende clusters met typische metabolische eigenschappen. Enterotype 1 wordt gekenmerkt door hoge aantallen Bacteroides en enterotype 2 door een sterke Prevotella kolonisatie. Enterotype 3 wordt gekenmerkt door een Ruminococcus flora.

Enterotyp **1**

Dysbiose-Index

De dysbiose index is een maatstaf die afwijkingen binnen het microbioom weergeeft. Bij deze maatstaf wordt rekening gehouden met alle onderzochte bacteriefyla, -geslachten en -soorten e.e.a. afhankelijk van hun relevantie.

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Ratio

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Indeling van bacteriën naar fylum*				
Actinobacteria	12,8	%	1,5 - 7	
Bacteroidetes	23,8	%	20 - 45	
Firmicutes	60,6	%	50 - 75	
Fusobacteria	0,0	%	0,0 - 1,0	
Proteobacteria	1,3	%	1,0 - 3,5	
Verrucomicrobia	0,5	%	1,5 - 5,0	
Overige	1,0	%		
Metaboloom (stofwisselingsactieve bacteriegroepen)				
Secundaire galzuren	118,4	%		
TMA / TMAO	209,5	%		
Indoxylsulfaat	-50,0	%		
Fenolen	310,3	%		
Ammoniak	-16,6	%		
Histamine	-50,0	%		
Equol	5442,9	%		
Beta-glucuronidasen	-42,7	%		
Indeling van bacteriën naar fylum met de belangrijkste bacteriegeslachten en -soorten				
Actinobacteria				
Bifidobacterium	7,2 x 10^10	KVE/g feces	> 1,0 x 10^10	
Bacteroidetes				
Bacteroides	2,3 x 10^11	KVE/g feces	> 5,0 x10^10	
Prevotella	9,2 x 10^6	KVE/g feces	> 1,0 x 10^10	
Firmicutes				
Butyraatproducerende bacteriën				
Totaal kiemgetal	1,9 x 10^11	KVE/g feces	> 2,4 x 10^11	
Faecalibacterium prausnitzii	9,3 x 10^10	KVE/g feces	>1,0 x10^11	
Eubacterium rectale**	8,9 x 10^9	KVE/g feces	> 2,0 x 10^10	
Eubacterium hallii***	2,3 x 10^10	KVE/g feces	> 1,5 x 10^10	
Roseburia spp.	9,8 x 10^9	KVE/g feces	> 3,0 x10^10	
Ruminococcus spp.	1,1 x 10^10	KVE/g feces	> 5,0 x 10^10	
Coprococcus spp.	4,4 x 10^10	KVE/g feces	> 5,0 x 10^10	
Butyrivibrio spp.	< 1,0 x 10^5	KVE/g feces	>1,5 x 10^10	
Clostridia				
Totaal kiemgetal	6,5 x 10^8	KVE/g feces	< 4,0 x 10^9	
Clostridia Cluster I	1,0 x 10^5	KVE/g feces	< 2,0 x 10^9	
Fusobacteria				
Fusobacterium	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7	
Verrucomicrobia				
Akkermansia muciniphila	1,5 x 10^9	KVE/g feces	> 5,0 x 10^9	
Proteobacteria				

Case UTIs and low butyrate formers

Microbiome Center

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Proteus spp.	< 1,0 x 10^6	KVE/g feces	< 1,0 x 10^6	
Klebsiella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7	
Enterobacter spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Serratia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^7	
Hafnia spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Morganella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^6	
Citrobacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^6	
Pseudomonas spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7	
Providencia spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^7	
H2S-vorming				
Sulfaatreducerende bacteriën (SRB)	1,9 x 10^9	KVE/g feces	< 2,5 x 10^9	
Desulfovibrio piger	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10^9	
Bilophila wadsworthia	< 1,0 x 10^5	KVE/g feces	< 2,0 x 10^9	
Immunogeniciteit / mucine vorming				
Immunogeen werkende bacteriën				
Escherichia coli	1,5 x 10^7	KVE/g feces	10^6 - 10^7	
Enterococcus spp.	1,75 x 10^7	KVE/g feces	10^6 - 10^7	
Lactobacillus spp.	7,9 x 10^6	KVE/g feces	10^5 - 10^7	
Mucine vorming / slijmvliesbarrière				
Akkermansia muciniphila	1,5 x 10^9	KVE/g feces	> 5,0 x 10^9	
Faecalibacterium prausnitzii	9,3 x 10^10	KVE/g feces	>1,0 x10^11	
Archaea				
Methanogenen				
Methanobrevibacter spp.	< 1,0 x 10^5	KVE/g feces	< 5,0 x 10^6	

Bijgewerkte nomenclatuur/synoniemen:
*** Actinobacteria = Actinomycetota**
Bacteroidetes = Bacteroidota
Firmicutes = Bacillota
Fusobacteria = Fusobacteriota
Proteobacteria = Pseudomonadota
Verrucomicrobia = Verrucomicrobiota

**** Eubacterium rectale = Agathobacter rectalis**
***** Eubacterium hallii = Anaerobutyricum hallii**
****** Clostridium histolyticum = Hathewaya histolytica**

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Mycobioom: relevante gisten				
Candida albicans	<1,0 x 10^3	KVE/g feces	<1,0 x 10^3	
Candida dubliniensis	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida parapsilosis	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida tropicalis	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida lusitaniae	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida krusei (a)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	
Candida glabrata (b)	<1,0 x 10^3	KVE/g feces	< 1,0 x 10^3	

Bijgewerkte nomenclatuur/synoniemen:
(a) Candida krusei = Pichia kudriavzevii
(b) Candida glabrata = Nakaseomyces glabratus

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Vertering				
Vetgehalte	5,00	g/100g	< 3,5	
Stikstofgehalte	0,75	g/100g	< 1,0	
Suikergehalte	4,18	g/100g	< 2,5	
Watergehalte	74,97	g/100g	75 - 85	

Microbiome Center Bureaustrook 101 NL-2726 SB Zoetermeer — Seite 3 von 5

Test	Uitslag	Eenheid	Normbereik	Vorig onderzoek
Extra parameter(s)				
Calprotectine	22,43	mg/l	< 50	FE A) ELISA
Alfa-1-antitripsine	11,3	mg/dl	< 27,5	FE A) ELISA
Secretoir Immunoglobuline A	1116,1	µg/ml	510 - 2040	FE A) ELISA
Zonuline	194,78	ng/ml	< 55	FE NA) ELISA

Summary:

- Butyrate is a bacterial metabolite that is key for our health
- It has both local and systemic effects
- Levels are very low in PAIS patients
- Low levels can be treated with several approaches:
  1. Specific prebiotics/fibers
  2. Influence ecosystem via probiotics
  3. Butyrate-producing probiotics

Thank you for your attention!