

The gut microbiome is an ecology



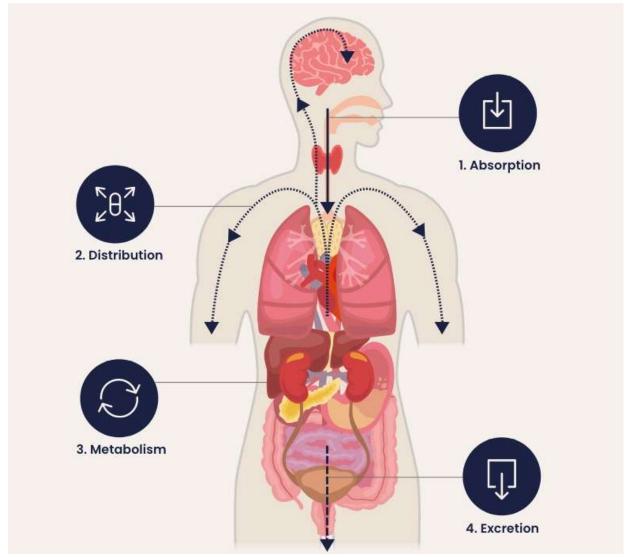


# Classical view vs. ecological perspective

# **Classical pharmacokinetics**



Starts from one organism: human



<sup>1. &</sup>lt;a href="https://www.pharmaceuticalpress.com/resources/article/what-is-pharmacokinetics/">https://www.pharmaceuticalpress.com/resources/article/what-is-pharmacokinetics/</a>

# The microbiome: an ecology



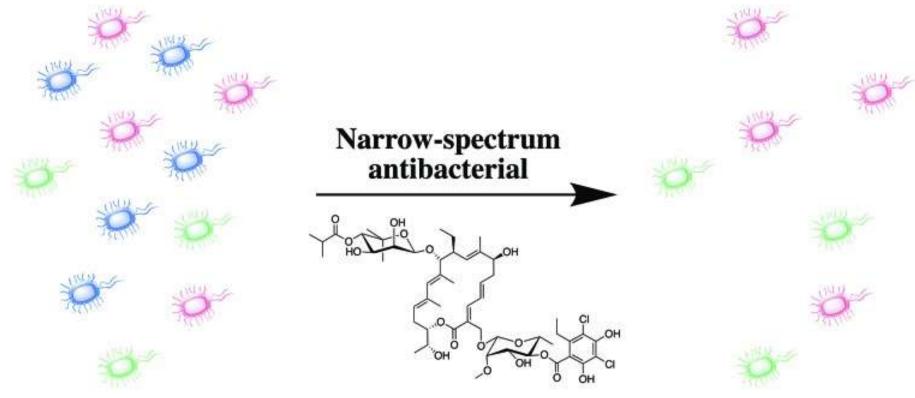


Different organisms that interact with a high degree

### What does this mean for treatments? **Example: narrow-spectrum antibiotics**



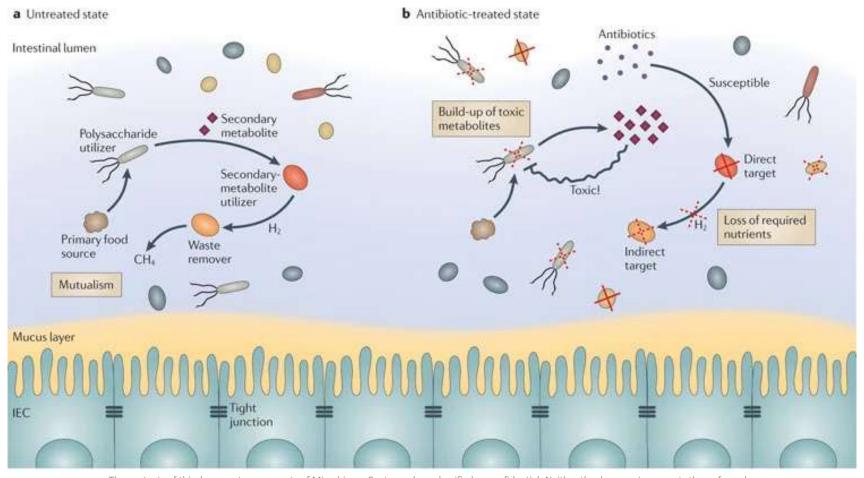
From a classical perspective:



# What does this mean for treatments? Example: narrow-spectrum antibiotics



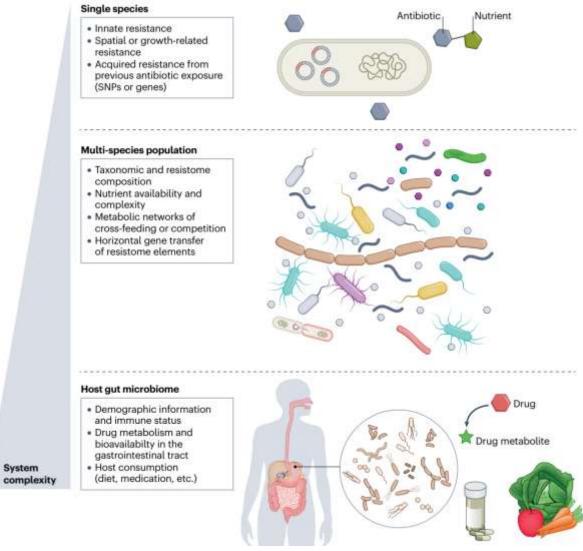
### The ecological reality:



### What does this mean for treatments? **Example:** narrow-spectrum antibiotics<sup>1</sup>

System





# What does this mean for treatments? Example: narrow-spectrum antibiotics

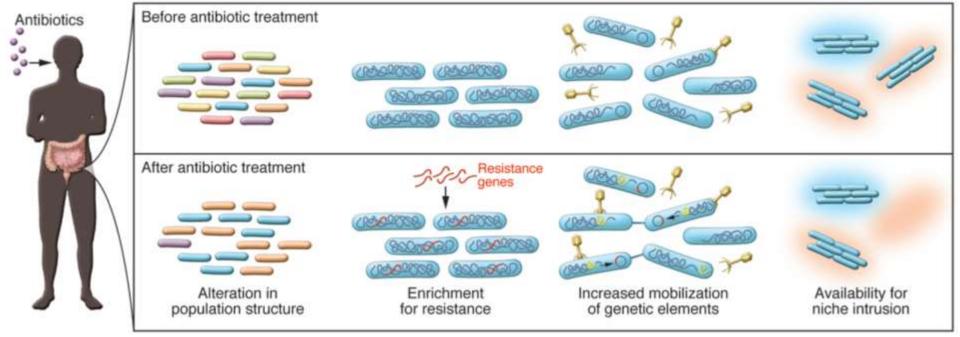


#### Antibiotics cause<sup>1,2</sup>:

- Decrease in alpha diversity
- Decrease in Firmicutes, Bacteroidetes and Actinobacteria
- Less metabolic activity (conversion of bile acids, SCFAs)

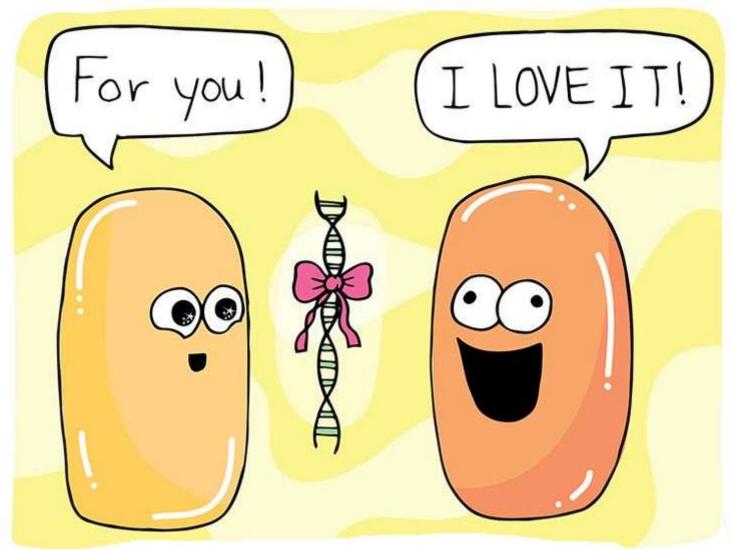
- Increase in resistance and its transmission
- More simple carbohydrates and amino acids opens niches for opportunistic pathogens

NB: narrow-spectrum (and reserve) antibiotic vancomycin has much more negative effects than broad-spectrum amoxicillin<sup>1</sup>.



# Antibiotic-resistant 'gene transfer'





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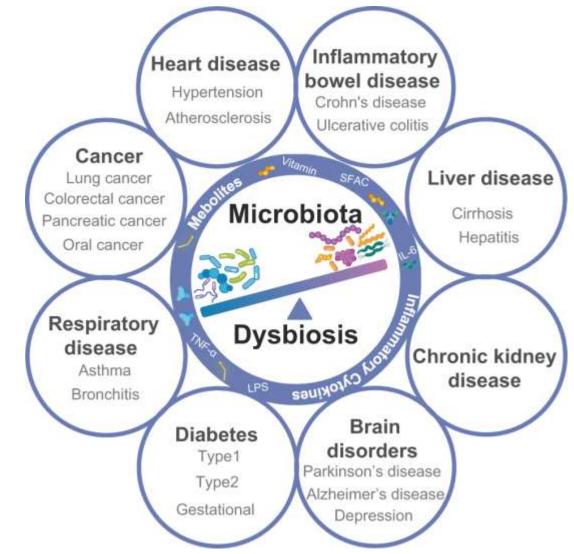
# The gut (microbiome) is at the root of our health

# The gut is at the center of many, if not all, diseases



"We could consider microbiome therapy for patients with GI problems"

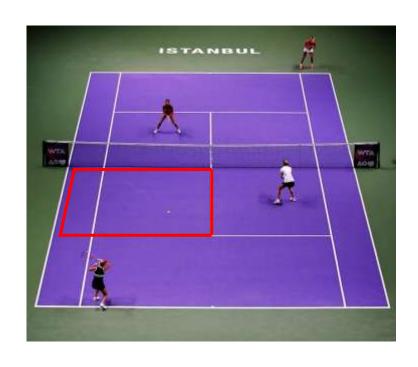
- The gut is often seen as just another organ that needs treatment when problems
- Reality: the gut microbiome is involved in (almost) all diseases<sup>1</sup>



# The large role of the microbiota makes sense...



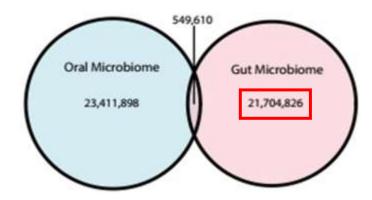
- The **intestines** are the largest area of contact with the outside world: approximately 32 m<sup>2</sup>.<sup>1</sup>
- The microbial density in the gut is very high: we harbor approximately 10<sup>14</sup> bacterial cells in our gut.<sup>2</sup>
  - This is 1.3x more bacterial cells than human cells<sup>2</sup>.



#### Number of human genes<sup>4</sup>:

STATISTICS	T2T-CHM13					
	Summary					
Assembled bases (Gbp)	3.05					
	Gene annotation					
Number of genes	63,494					
Protein coding	19,969					

#### Number of bacterial genes<sup>3</sup>:



<sup>1.</sup> Helander, H. F. et al. Scandinavian Journal of Gastroenterology 49, 681-689 (2014)

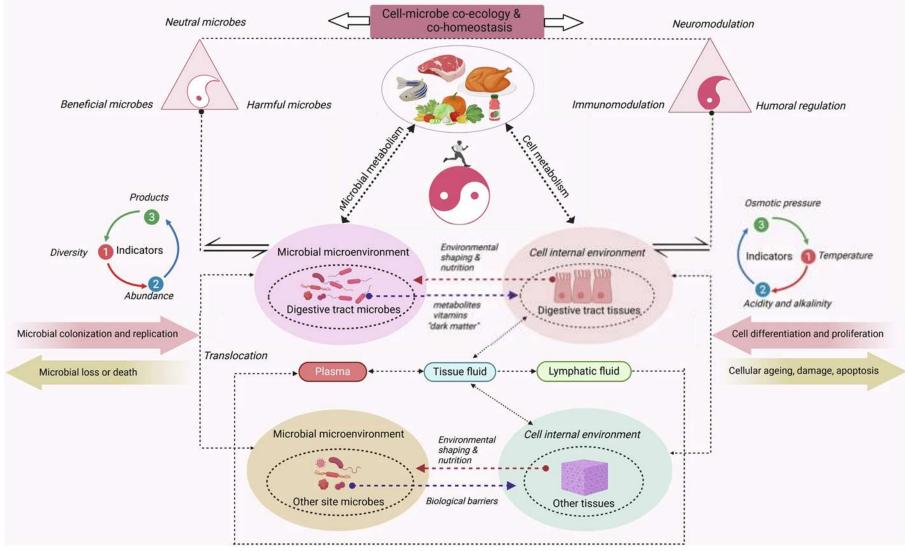
Sender, R. et al. PLoS Biol 14, (2016)

<sup>3.</sup> Tierney, B. T. et al. Cell Host & Microbe 26, 283-295.e8 (2019)

<sup>4.</sup> Nurk, S. et al.Science.376,.44-53.(2022)

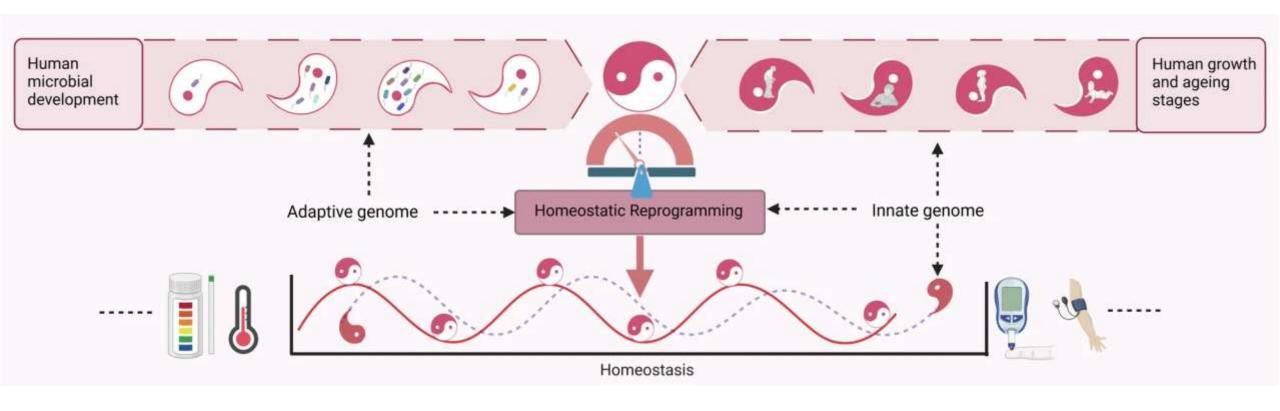
# We are <u>holobionts</u>: human and microbial cells <u>together</u> determine homeostasis<sup>1</sup>





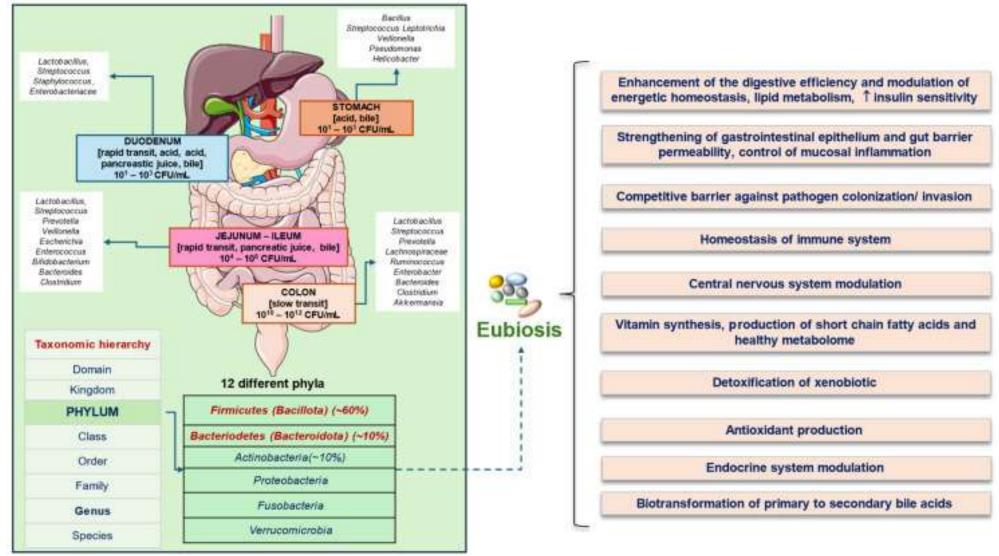
# The commensal microbiota form the *adaptive genome*<sup>1</sup>





# Every aspect of our physiology starts in the gut<sup>1</sup>









# ALL DISEASE BEGINS

IN THE GUT.

-HIPPOCRATES





# Case study: the microbiome as an ecosystem Microbiome

Jes Schalkwijk
Praxis for Integrative Medicine



"To know that you do not know — that is the highest.

Not to know, yet think you know — that is a disease.

Only when you recognize this disease as a disease can you be free from it.

The wise are not sick, because they recognize the sickness as sickness.

Therefore they are not sick."

— Lao Tzu

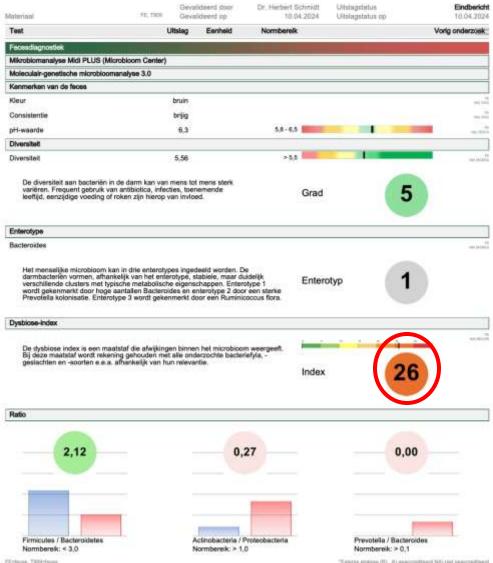
### **General symptom history**



- Under treatment since March 2024
- Three times each morning: loose, yellow, mushy stool
- Bloated stomach and abdomen, foul-smelling flatulence
- Probiotics made the stool slightly firmer
- Additionally: extreme fatigue, nausea (seem to be linked)
- Lots of cramps in the body, pain symptoms spread throughout the body
- Burning sensation in the mouth, diagnosis *Lichen Planus* via dentist

## Microbioom analyse

Microbiome Center Buruelstrook 101 NL-2726 SS Zoetermeer



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Teet	Ultalag	Eenheid	Normberelk		Vorig onderzoe
indeling van becteriën near fylum					
Actinobacteria	2,2	*	1,5-7		94/96
Bacteroidetes	25.8	%	20 - 45		
Firmicules	54.6		50 - 75		1
Fusobacteria	0.0	*	0.0 - 1.0		W. 40
Proteobacteria	8.3	*	1,0-3,5		40.40
Verrucomicrobia	0.6	*	1,5 - 5,0		14,140
	98	*	1,0 - 0,0 - 1,3	1	95.00
Overige Metaboloom (stofwisselingsactieve b	8,6				- Section
	-30.1	*			
Secundaire galzuren					
TMA / TMAO	119,0				
Indoxylsulfaat	-50,0	*			
Fencien	1594,6	*			
Ammoniak	24,9	*		191	
Histamine	-50,0	*			
Equal	68,0	14			
Beta-glucuronidasen	213,1	%			
indeling van becteriën naar fylum me	t de belangrijkste bac	terlegeslachten er	-ecorten		
Actinobacteria					
Bifidobacterium	1,7 x 10^10	KVE/g feces	> 1,0 x 10*10		aces .
Bacteroidetes					
Bacteroides	1,7 x 10^11	KVE/g faces	≥ 5,0 ×10*10		16.60
Prevotella	3,6 x 10^8	KVE/g feces	> 1,0 x 10*10		No. Biol
Firmicutes					
Butyraatproducerende bacteriën					
Totaal kiemgetal	3,5 x 10^11	KVE/g faces	> 2,4 x 10^11		Table 1
Faecalibacterium prausnitzii	9,7 x 10^10	KVE/g feces	>1,0 ×10*11		Alex
Eubacterium rectale	1,6 = 10^10	KVE/g feces	> 2,0 x 10*10		84,940
Eubacterium hallii	3,3 x 10^10	KVE/g feces	> 1,5 x 10^10		NAME OF TAXABLE PARTY.
Roseburia spp.	1,9 x 10^10	KVE/g feces	> 3,0 x10^10	THE RESERVE TO SERVE	100
Ruminococous spp.	8,7 x 10^10	KVE/g faces	> 5,0 x 10*10	E E	
Coprococcus spp.	3,1 x 10^10	KVE/g foces	> 5,0 x 10*10		64) 800
Butyrivibrio spp.	6.9 x 10^10	KVE/g faces	>1,5 x 10*10		
Clostridia					0.00
Totaal kiemgetal	2.3 x 10^10	KVE/g feces	< 4.0 x 10*9		
Clostridia Cluster I		KVE/g faces	< 2.0 × 10*9	io a	NAME OF THE PARTY
Fusobacteria	27.2 17.2		2.755/ATCA		billed
Fusobacterium	1.6 x 10 <sup>4</sup> 7	KVE/g feces	< 1,0 x 10^7		
Verrucomicrobia					
Akkermansia muciniphila	5.6 x 10*6	KVE/g feces	> 5.0 x 10^9		945.0
Proteobacteria	787.07.07	on stansac	10000000000		60.00
Pathogene of potentieel pathogene b	acteriën				
Haemophilus spp.		KVE/g feces	< 5,0 x 10*8	1000	1
Acinetobacter spp.	< 1.0 x 10*5		< 1.0 x 10^6		
					AA MA

Vorig onderzoek:

Tost	Uitslag	Eenheld	Normbereik		Vorig onderzoek				
Proteus spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10*6						
Gebsiella spp.	< 1,0 x 10^5	KVE/g feces	< 1,0 x 0,7	10	1				
Enterobacter app.	5,1 x 10^10	KVE/g feces	< 1,0 x 10°6						
Serratia app.	< 1.0 x 10^5	KVE/g feces	< 1,0 x 10^7						
fafnia 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	111					
Ditrobacter app.	1,1 x 10^9	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						
12S-vorming									
Suifastreducerende bacterién (SRB)	4,2 x 10°9	KVE/g feces	< 2,5 x 10*9						
Desulfavibrio piger	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10*9	10					
Desulfomonas pigra	< 1,0 x 10^5	KVE/g feces	< 1,0 x 10*9						
Blophila wadeworthii	< 1.0 x 10 <sup>4</sup> 5	KVE/g feces	< 2,0 x 10*9	12	-				
mmunogeniciteit / mucine vorming									
mmunogeen werkende bacteriën									
Escherichia coli	2,2 x 1016	KVE/g feces	10^6 - 10^7		-				
Enterococcus app.	1,63 x 10*9	KVE/g feces	10% - 10%	100					
actobacillus spp.	6,9 x 10^5	KVE/g faces	10^5 - 10^7						
Aucine vorning / stijmvliesbarrière									
Vkkermansia muciniphila	5,6 x 10^8	KVE/g faces	> 5,0 x 10*9		-				
aecalibacterium prausnitzii	9,7 x 10^10	KVE/g feces	>1,0 x10*11						
Vrchaea									
Aethanogenen									
Aethanobrevibacter spp.	3,9 x 10^9	KVE/g feces	< 5,0 x 10*8	The state of the s	-				
			Opmerking: Het nieuwe OmidSnap-bulle, en de dan in aanwezige matrix maken een nog effectievere morette ween megelijk, vooral bij gerepoolijkere bedoeffe, Die dan de dan d						

Mycobicom: relevante gisten								
Candida albicans (CA)	<1,0 x 10^3 KVE	E/g feces	<1,0 x 10^3		-			
Candida krusel (CK)	<1,0 x 10^3 KVE	E/g feces	< 1,0 x 10^3		E			
Candida glabrata (CG)	<1,0 x 10^3 KVE	E/g feces	< 1,0 x 10*3		W1 1970			
Candida dubliniensis (CD)	<1,0 x 10^3 KVE	E/g feces	< 1,0 x 10^3					
Candida parapsilosis (CP)	<1,0 x 10°3 KVE	E/g feces	< 1,0 x 10*3					
Candida tropicalis (CTp)	<1,0 x 10^3 KVE	E/g fleces	< 1,0 x 10^9					
Candida lusitaniae (CL)	<1,0 x 10/3 KVE	5/g feces	< 1,0 x 10^3	18				
Parasieten	3 - 1 - 10 - 10 - 10 - 10 - 10 - 10 - 10		F. 1 C4 (1/2) 4/3 4/3					
Pathobionten								
Blastocystis hominis	positief		negatief					
Dientamoeha fragilis	positief		negatief					
Pathogene darmprotozoa	7 3 11 12 2 13 11		-11.7-12.1711					
Giardia lamblia	negatief		negatief	10000	-			
Entamoeba histolytica	negatief		negatief	99 (6	*****			
Cryptosporidium spp.	negatief		Me conte	ents of this document a				
			in the sale was also and a sale as a sale					



Test	Uitslag	Eenheid	Normbereik	Vorig onderz	zoek
Cyclospora cayetanensis	negatief		negatief		FE A) MOLEK
Vertering					
Vetgehalte	5,61	g/100g	< 3,5		NAI PHOT
Stikstofgehalte	0,53	g/100g	< 1,0		FE NA) PHOT
Suikergehalte	2,39	g/100g	< 2,5		FE NA) PHOT
Watergehalte	77,27	g/100g	75 - 85		FE NA) PHOT
Extra parameter(s)	196			,	14471.000
Calprotectine	<17,90	mg/l	< 50		FE A) ELISA
Alfa-1-antitripsine	<1,8	mg/dl	< 27,5		FE A) ELISA
Secretoir Immunoglobuline A	311,0	µg/ml	510 - 2040		A) ELISA
Zonuline	64,89	ng/ml	< 55		FE A) ELISA
Histamine in feces	467,9	ng/ml	< 959		Teos A) ELISA
Maldigestie	9.5				rig salesor
Pancreas elastase in feces	243,24	µg/g	> 200		FE A) ELISA
Galzuren in feces	18,70	µmol/l	< 70		FE (A) PHOTO

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PE-box. T909-None

# **Treatment starten April 2024**



MyOwnBlend initiated without a preceding eradication protocol.

BB058	S. Boulardii	2
BB061	Bifidobacterium lactis HN019	3
BB056	L. rhamnosus GG	2
BB011	Butyrate generator	1
BB020	Bacillus clausii UBB C-07	1
BB027	L. rhamnosus SP1	1
BB054	Akkermansia mucinip hila, pasteurized	1
BB004	DJ repair	4

- In addition, the following supplements were used
- Chryssil, curcumine, ADP(biotisch)
- Pro-Praebioma (Tisso)

#### Results



- Stool consistency improved: became firmer
- Foul-smelling flatulence disappeared
- Overall condition improved
- Upon stopping supplementation: symptoms returned

### Follow-up



- Restarted MyOwnBlend
- HePy treatment via general practitioner:
  - Initially anthroposophic: no effect
  - Then triple therapy
- Symptoms returned after that
- MyOwnBlend repeated again
- December 2024: oral symptoms completely resolved
- Fatigue and nausea both disappeared or significantly improved, with good stool consistency

#### **Additional observations**

Previously frequent cracks in fingers and feet: now greatly reduced

#### P.S.

A follow-up stool analysis is planned for monitoring purposes



# Characteristics of ecologies

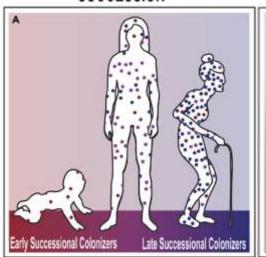
# Characteristics of the microbiome as an ecology<sup>1</sup>

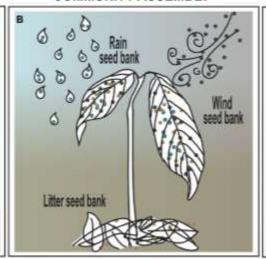


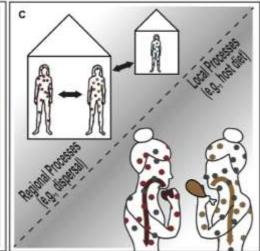
SUCCESSION

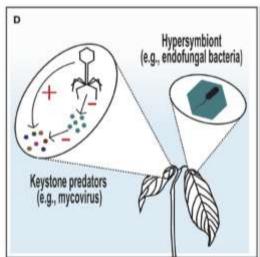
#### COMMUNITY ASSEMBLY

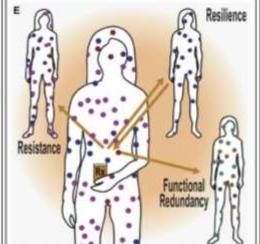


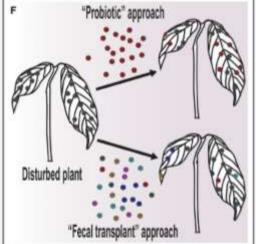






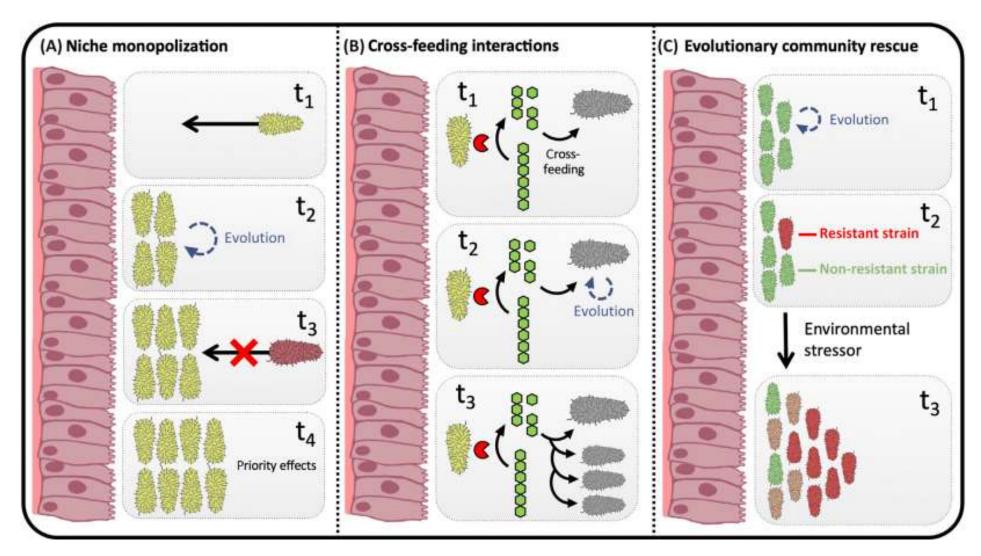






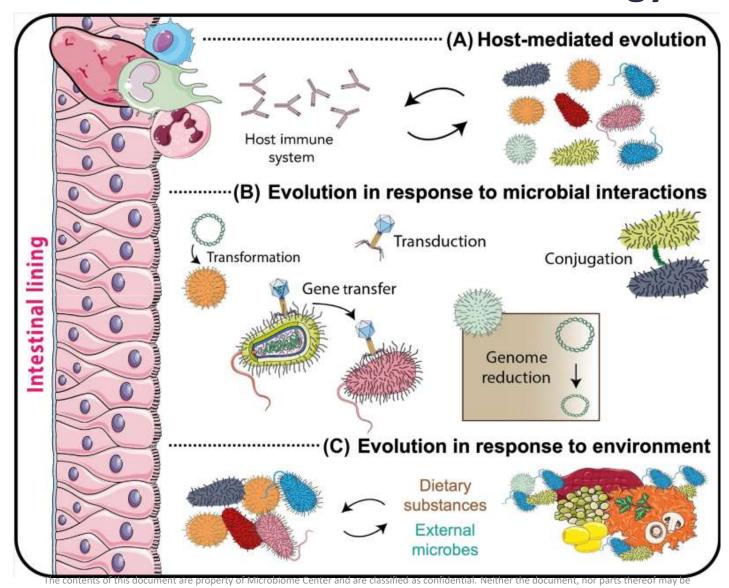
# Characteristics of the microbiome as an ecology<sup>1</sup>





# Characteristics of the microbiome as an ecology<sup>1</sup>

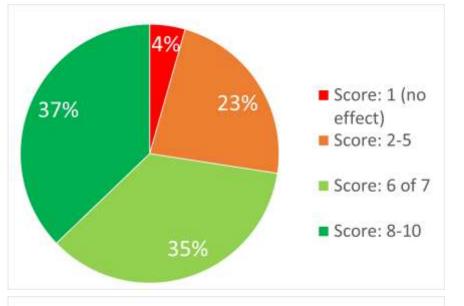




1. 'Gut enricher' Building block

#### Unique building block:

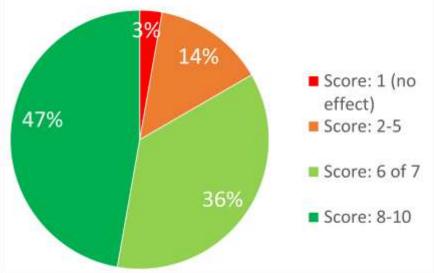
- For use at low diversity:
  - Low diversity and richness of the microbiome is associated with many diseases<sup>1,2</sup>.
- Consists of large number of strains ( $\sim$ 40) in low dosage( $\sim$ 10<sup>6</sup> cfu/g).
- Supports strain selection based on individual ecology and host factors in patients with low diversity(≤4).





Low diversity (n=113)

73% good or excellent



Low diversity+ gut enricher (n=36)

83% good or excellent

<sup>1.</sup> Tuddenham, S. et al. Curr Opin Infect Dis 28, 464–470 (2015)

<sup>2.</sup> Álvarez, J. et al. Gastroenterol Hepatol 44, 519–535 (2021)

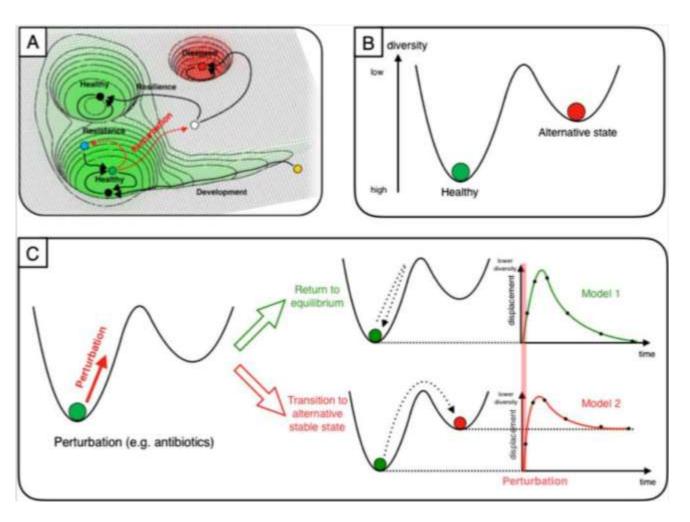
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# What can we do with ecological principles?<sup>1</sup>

#### 2. Understanding the purpose of treatments

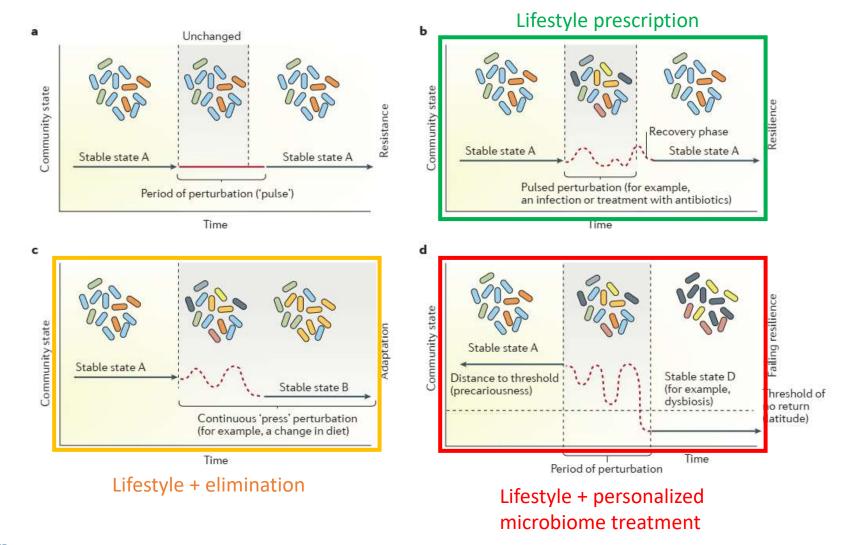


- In a healthy ecosystem, there is 'resilience': resistance to change.
- Goal of microbiome treatment: to move the 'ball' to a stable and desired equilibrium point.
- Personalization helps to 'steer' the direction of change as accurately as possible for the individual patient.



#### 2. Understanding the purpose of treatment





<sup>1.</sup> Fassarella, M., et al., 2020. Gut gutjnl-2020-321747.

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#### 3. Revising the logic behind phased treatment



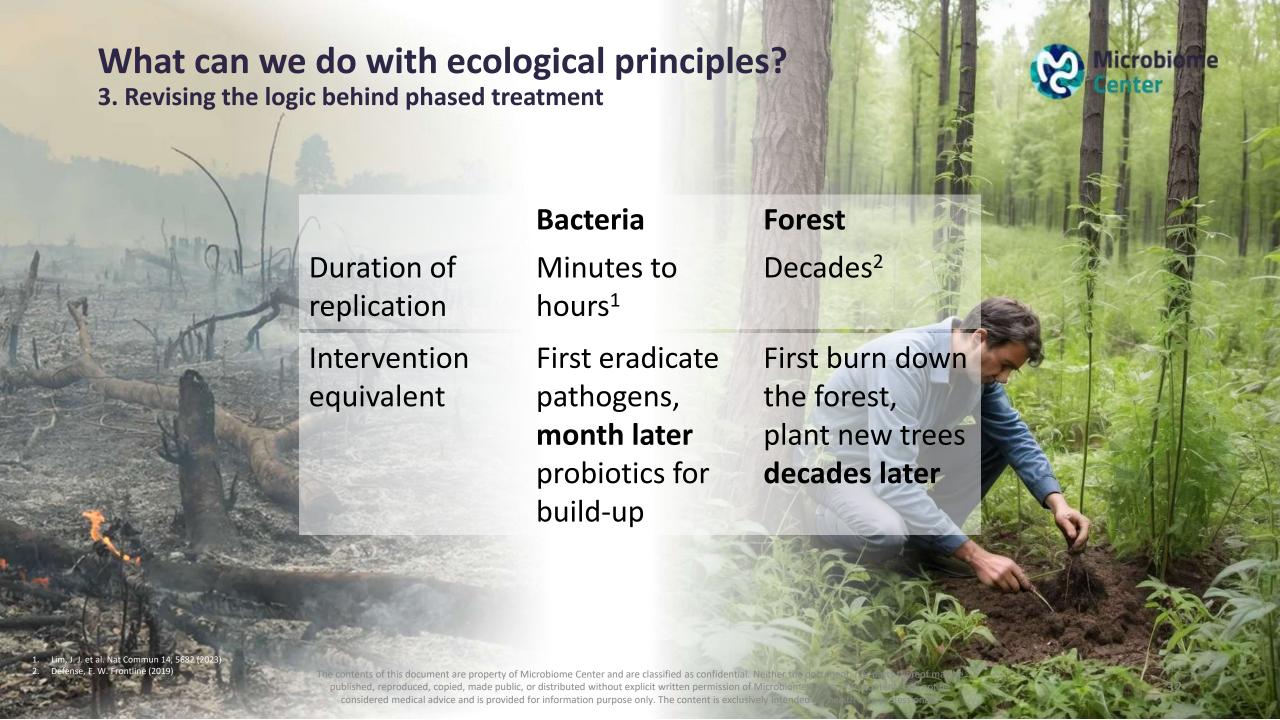
# 5Rs Approach

The functional medicine approach to supporting and healing your digestive tract



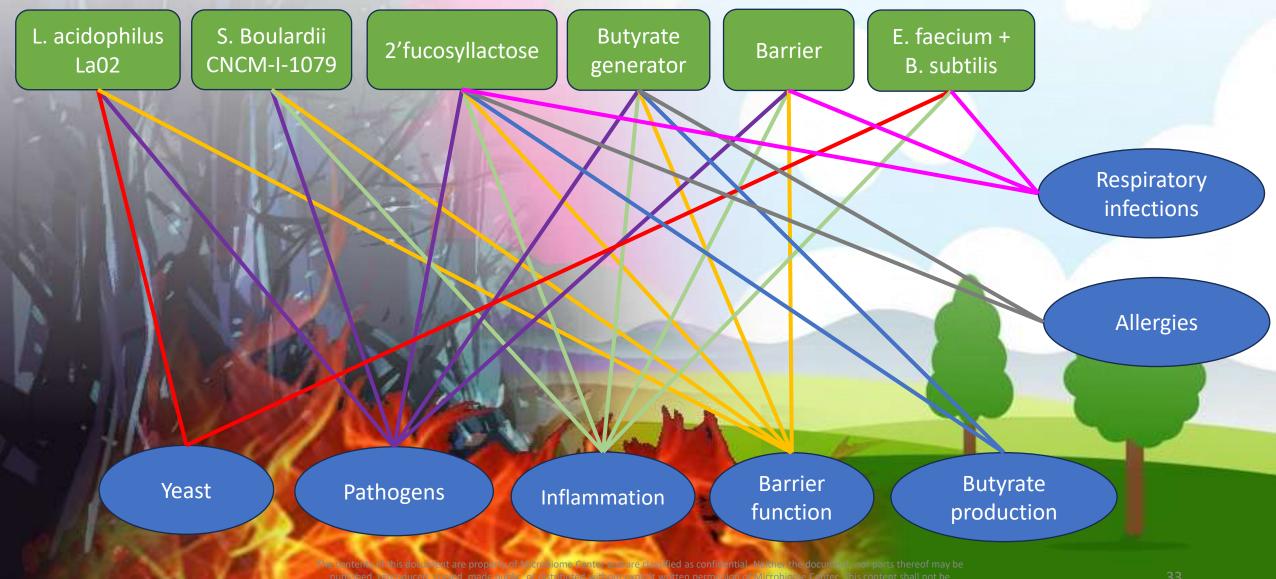








4. In microbiome treatment, everything happens at the same time



#### 4. In microbiome treatment, everything happens at the same time



IL-10

P = 0.222

TNF-α

P = 0.368

Placebo

Post-treatment

Post-treatment

Pretreatment

Pretreatment

Colonic mucosa

20

15

10

2

IL-10

P = 0.000

TNF-α

P = 0.000

Active drug

Post-treatment

Post-treatment

Pretreatment

Pretreatment

2.5

2.0

B 1.0

0.5

0.0

Example probiotic: Saccharomyces cerevisiae var boulardii CNCM-I-1079

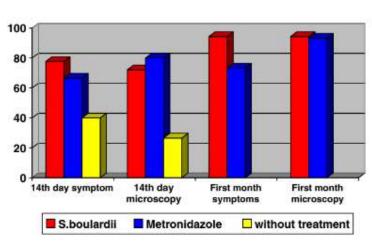
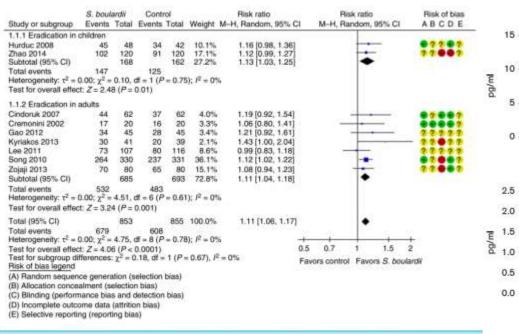


Fig. 1 Cure rate for clinical findings and parasitological examinations between study groups on the 14th day and first month





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

Inhibits *Helicobacter pylori*<sup>4</sup>

Anti-inflammatory and intestinal barrier functionenhancing effects<sup>5,6</sup>

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Dinleyici, E. C. et al. Am. J. Trop. Med. Hyg. 80, 953-955 (2009) Dinlevici, E. C. et al. Parasitol, Res. 108, 541-545 (2011)

Besirbellioglu, B. A. et al. Scandinavian Journal of Infectious Diseases 38, 479-

Szajewska, H. et al. Alimentary Pharmacology & Therapeutics 41, 1237–1245

<sup>5.</sup> Abbas, Z. et al. European Journal of Gastroenterology & Hepatology 1 (2014)

Garcia Vilela, E. et al. Scandinavian Journal of Gastroenterology. 43,.842-

#### 4. In microbiome treatment, everything happens at the same time

Example prebiotic: 2'fucosyllactose

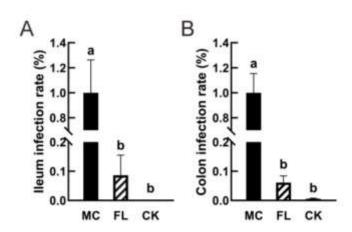
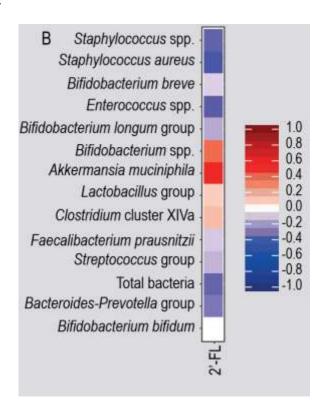
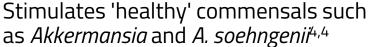
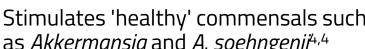


Figure 1. Escherichia coli O157 colonization and pathological section of ileum. (A) The colonization in ileum; (B) colonization in colon;









Sprenger, N. et al. Eur J Nutr 56, 1293-1301 (2017)

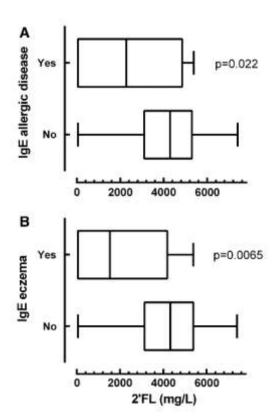


Fig. 2 Breast milk consumed by C-section-born infants who did not show IgE-associated allergic disease and IgE-associated eczema contained higher levels of 2'-fucosyllactose a proxy for FUT2-dependent oligosaccharides. 2'-Fucosyllactose (2'FL) levels in early breast milk (2.6 ± 1.1 days postpartum) that was consumed by C-section-born infants who showed IgE-associated allergic disease (a) or IgE-associated eczema (b) at 2 years or not. Box and whisker plots are shown with median and minimal and maximal values. Two-tailed p values from unpaired t test are indicated

#### Beneficial effect on allergies<sup>5,6</sup>

Wang, Y. et al. Nutrients 12, (2020)

Castillo-Courtade, L. et al. Allergy 70, 1091-1102 (2015)

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Aakko, J. et al. Beneficial Microbes 8, 563-567 (2017) Kostopoulos, I. et al. Scientific Reports 10, 14330 (2020)

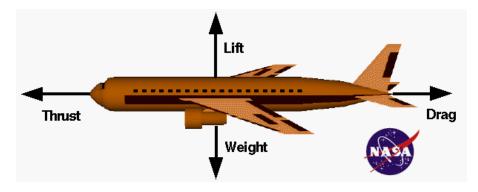


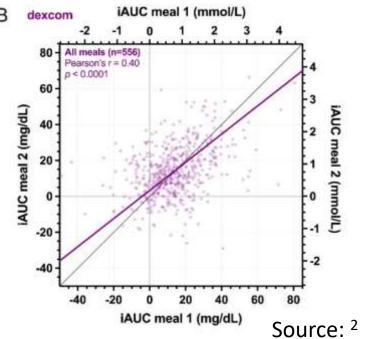
# Our biology is 'complex'

# Reductionism doesn't work in complex systems



- Many life science studies have a pitfall:
  - Reductionism: study separate factors to understand the whole.
  - Borrowed from physics. There, it works because the superposition principle applies<sup>1</sup>.
- Superposition does not apply if a system is either:
  - non-linear
  - Regulated
  - Interactive
- In physiology all three apply!



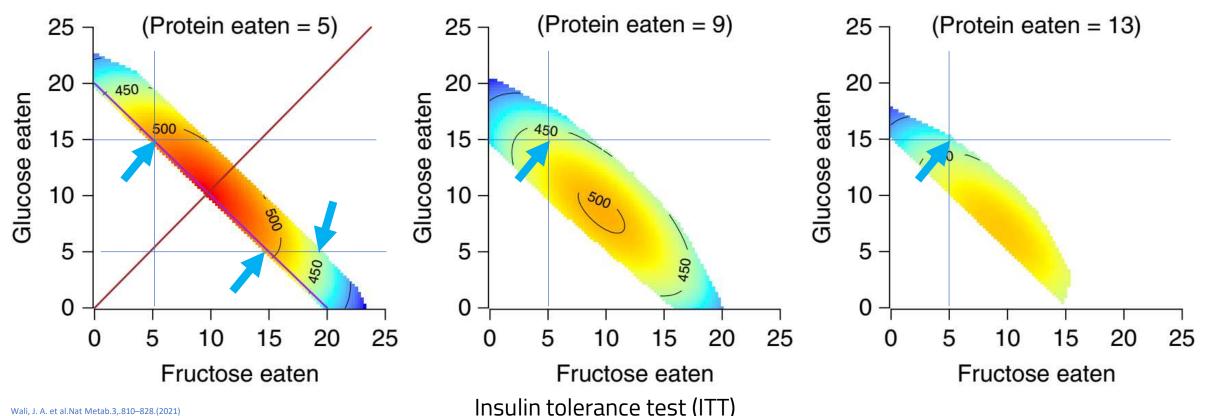


# In a complex system context is key!



But if I prescribe everything at once, I don't know what effect has what effect....

...True, but in a complex biological system you can't know that anyway.



### How to work with a complex/chaotic system?

→ Cynefin framework



# Complex

the relationship between cause and effect can only be perceived in retrospect

probe – sense - respond

emergent practice

## **Complicated**

the relationship between cause and effect requires analysis or some other form of investigation and/or the application of expert knowledge

sense – analyze - respond good practice

Confusion

# novel practice

no relationship between cause and effect at systems level

act – sense -respond

Chaotic

# best practice

the relationship between cause and effect is obvious to all

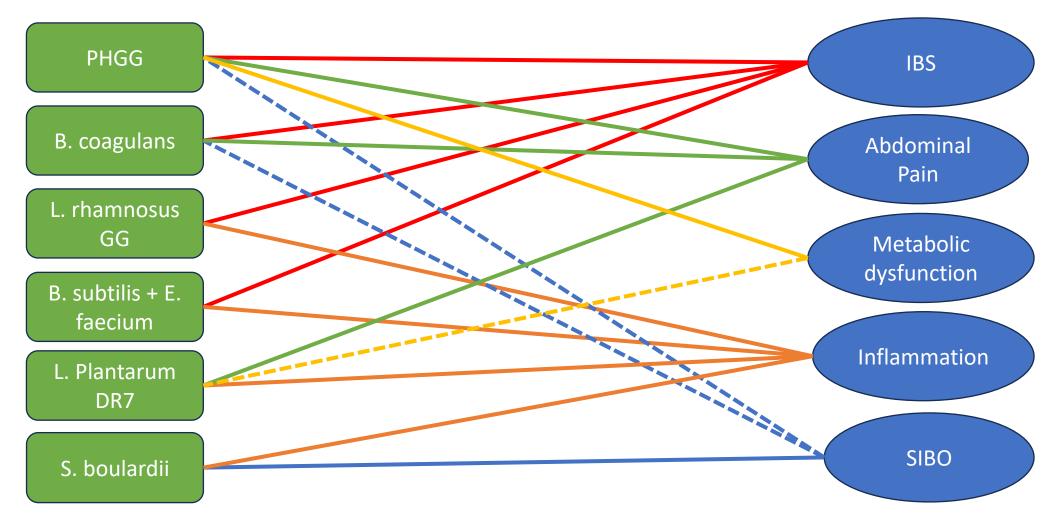
sense – categorize - respond

**Simple** 

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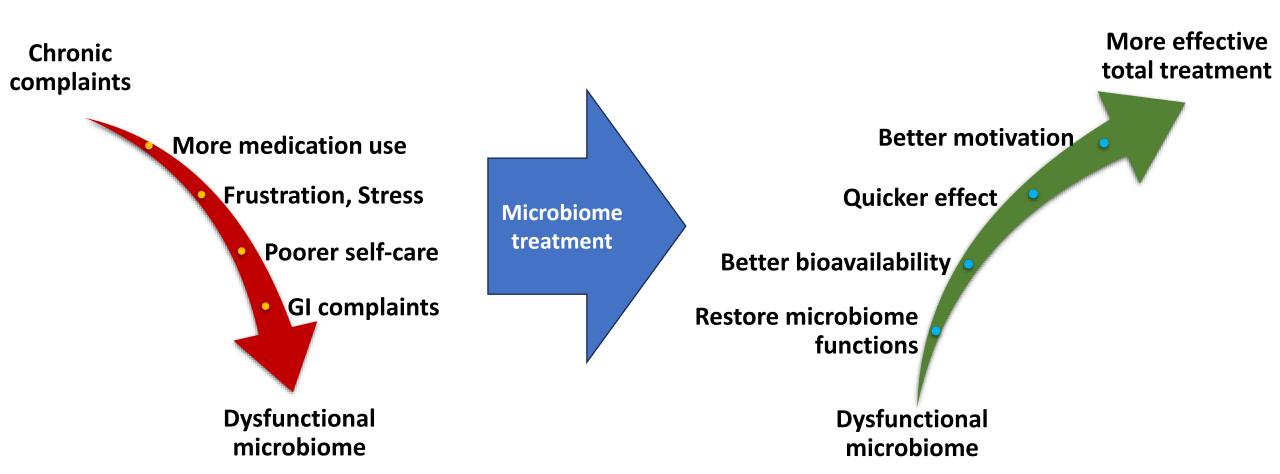
# Start with acting: using the best conceivable intervention





# Why start with gut treatment?





# Example 1: more effective treatment of urinary tract infections



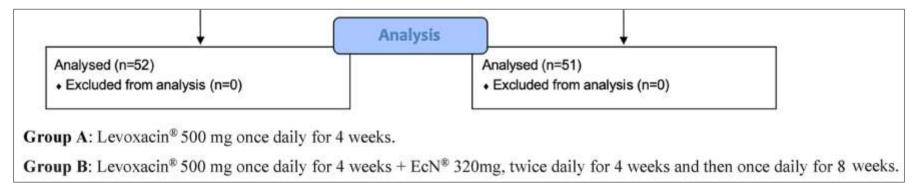
Meta-analyses of RCTs of antibiotic treatment of UTIs<sup>1</sup>:

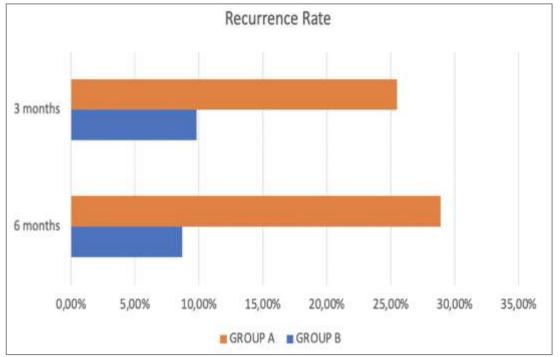
→ more effective with probiotics

	Probio	Probiotics Placebo			Risk Ratio		Risk Ratio				
Study or Subgroup	Events	Total	Events	Total	Weight	M-H, Random, 95% C		M-H, Ran	dom, 95% C	1	
Cohen 2020	87	133	30	64	20.3%	1.40 [1.05, 1.86]		7796M165676	•	0.00	
Happel 2020	6	18	7	11	9.5%	0.52 [0.24, 1.16]			+		
Laue 2017	17	17	11	17	18.6%	1.52 [1.07, 2.17]			-		
Russo 2019	20	24	9	24	14.0%	2.22 [1.29, 3.84]			-		
Sgibnev 2019	39	44	18	42	18.4%	2.07 [1.44, 2.98]			-		
Zhang 2021	30	52	28	47	19.2%	0.97 [0.70, 1.35]		- 1	+		
Total (95% CI)		288		205	100.0%	1.38 [1.01, 1.89]			•		
Total events	199		103								
Heterogeneity: Tau <sup>2</sup>	= 0.10; Chi <sup>2</sup>	= 18.0	3, df = 5 (	P = 0.0	$(03)$ ; $I^2 = 7$	2%	0.04	1	!	10	400
Test for overall effect	Z = 2.03 (	P = 0.0	4)				0.01	0.1 Favors placebo	Favors pro	10 obiotics	100

# Example 2: more effective treatment of chronic bacterial prostatitis<sup>1</sup>: *E. coli* MC231

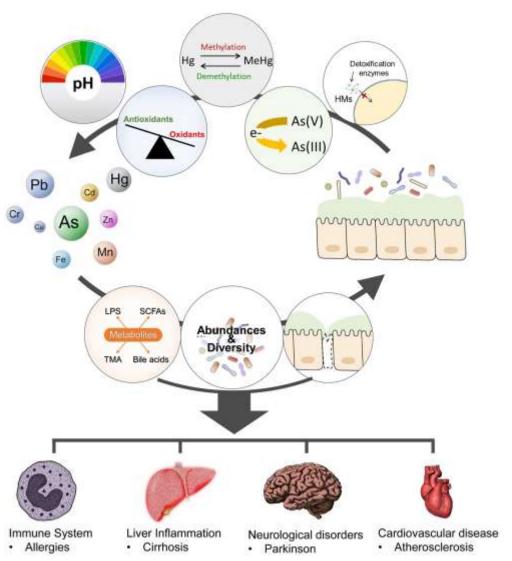


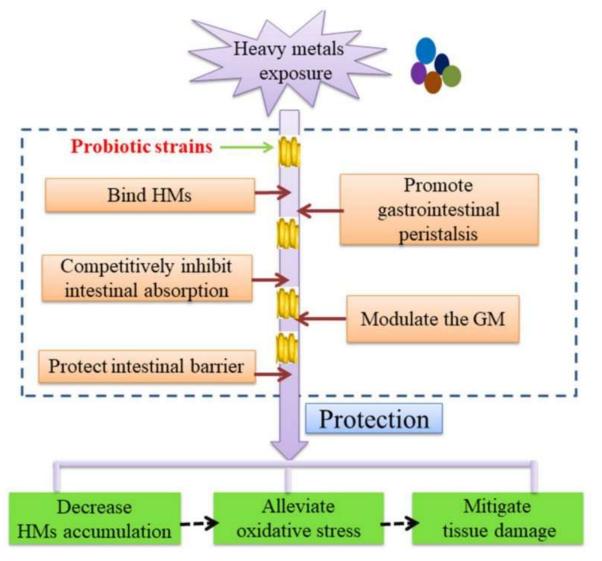




## Example 3: detoxification: the microbiome helps<sup>1,2</sup>









# Take home messages

In an ecology, everything happens at the same time

...there is cross-feeding, niche competition, evolutionary adaptation, exchange, etc.

...there are rarely direct cause-and-effect relationships: complex/chaotic

Treatment is about shifting the balance



"You don't strike me as being complicated"



... phased construction contradicts biological reality

... is the use of niche selection useful in case of low diversity

... pre- and probiotics have a multitude of effects

... all diseases / treatments **start in the gut** 

