# The human microbiome and physiological microbiota

Jakub Hurych

Department of Medical Microbiology, Second Faculty of Medicine, Charles University and Motol University Hospital

Microbiology II (3rd year)
2025/2026

# Outline

- **The gut microbiome**
  - General introduction and current state of knowledge
  - **Commercial testing** – is it worthwhile or not?
  - **How to care for the microbiome**: fibre and its impact on health
  - **Antibiotics** and their negative impact on the microbiome
- **Physiological microbiota**

# Interest is growing

RESEARCH ARTICLE

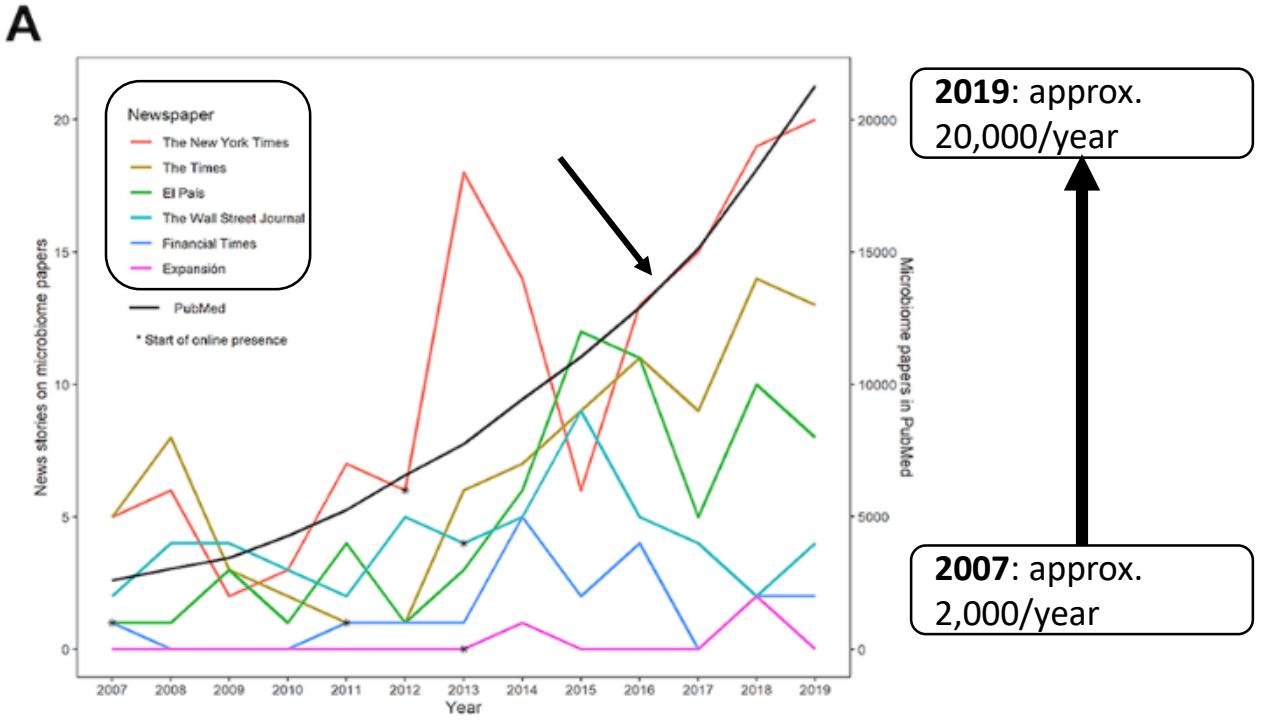
## Microbiome research in general and business newspapers: How many microbiome articles are published and which study designs make the news the most?

**Andreu Prados-Bo**[1,2]*, **Gonzalo Casino**[1,3]*

**1** Department of Communication, Pompeu Fabra University, Barcelona, Spain, **2** Blanquerna School of Health Sciences, Ramon Llull University, Barcelona, Spain, **3** Iberoamerican Cochrane Centre, Biomedical Research Institute Sant Pau (IIB Sant Pau), Barcelona, Spain

- The professional community takes note
- The general public is taking notice

**You should too!**




Prados, Casino: Microbiome research in general and business newspapers: How many microbiome articles are published and which study designs make the news the most? *PLOS One*. 2019. 10.1371/journal.pone.0249835

FN MOTOL 2 LFUK

FN MOTOL 2. LF UK

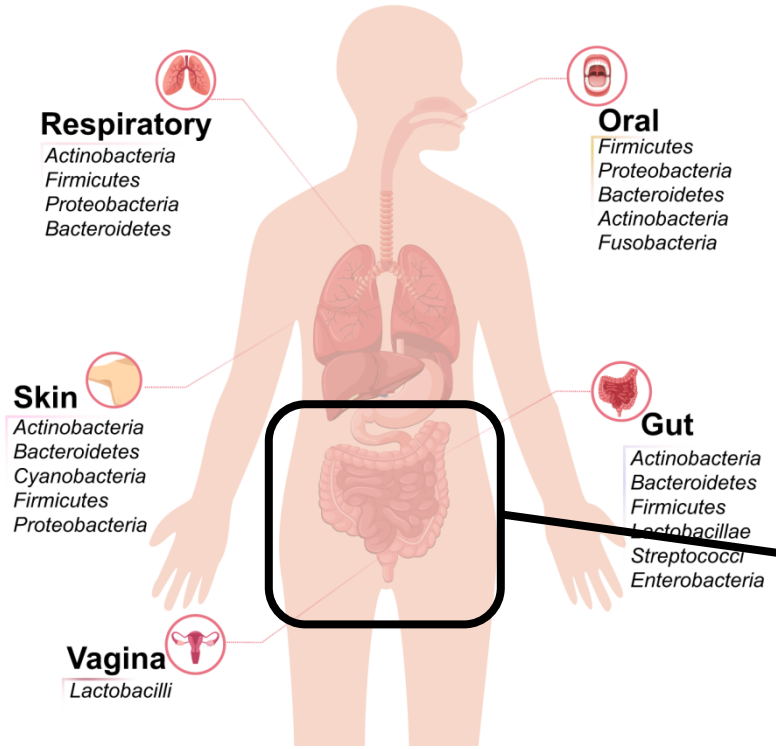
# A necessary introduction to the gut microbiome

What it is, what it consists of, and what influences it

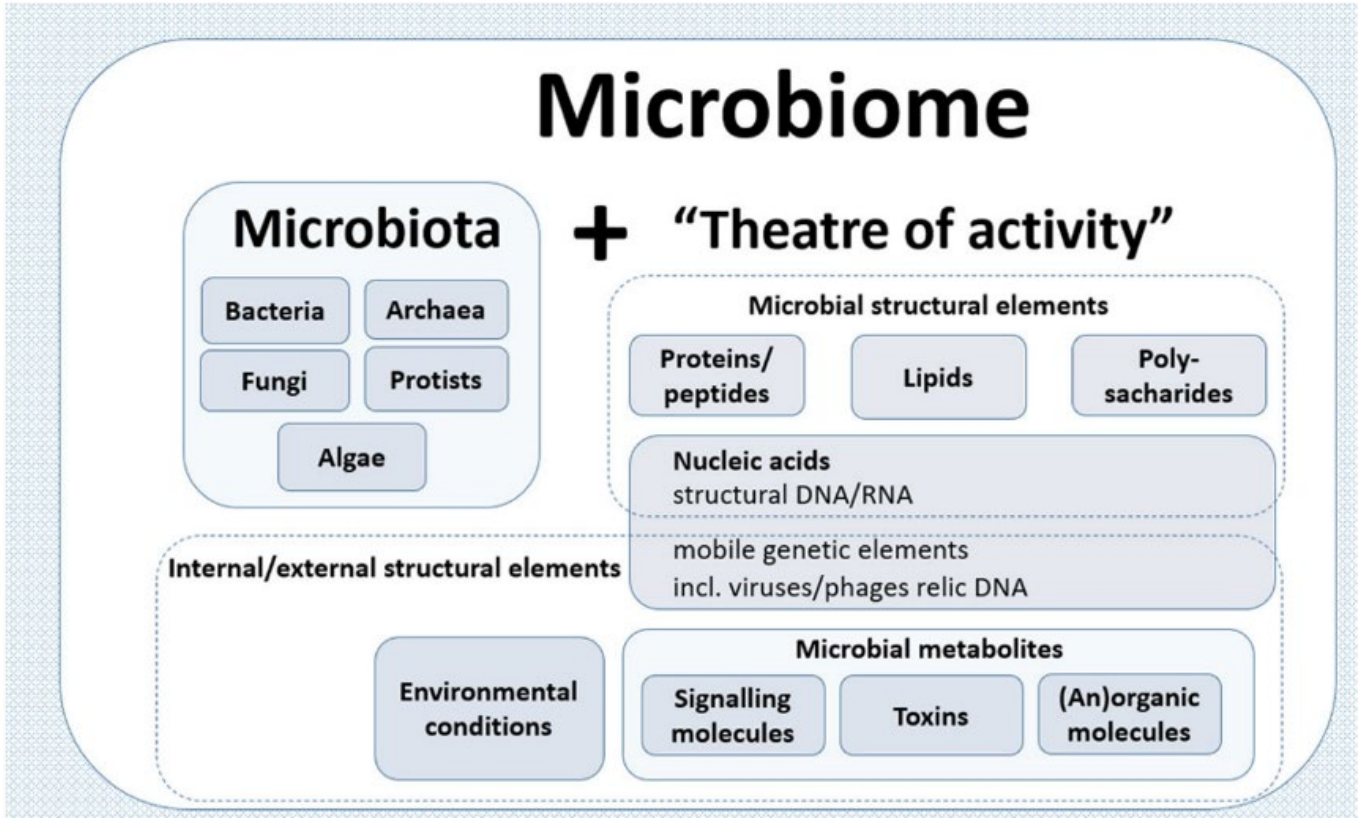
# Microbiome

**Microbiome** = a characteristic microbial community that inhabits a specific, rationally defined habitat with typical physical and chemical conditions

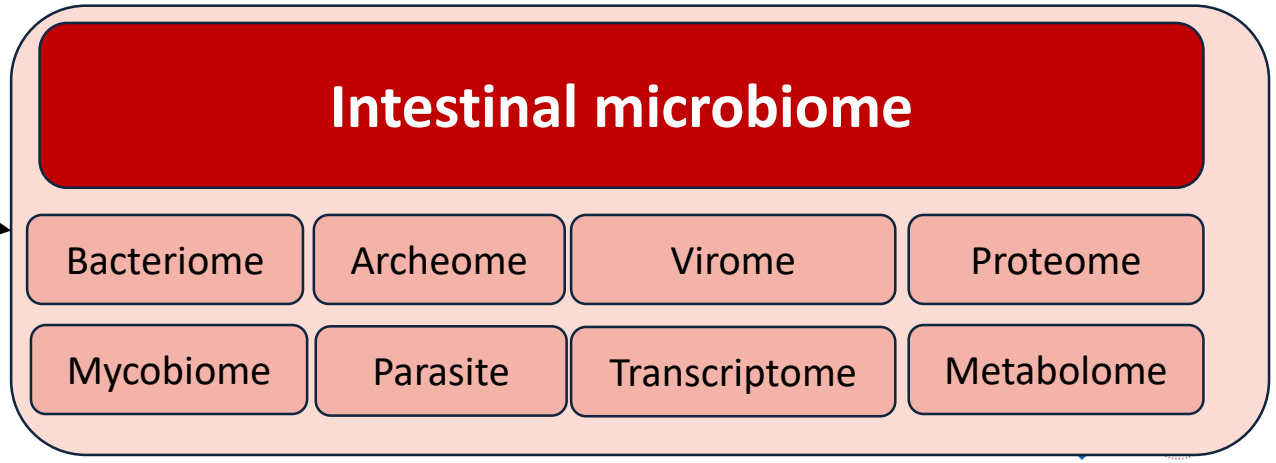
Berg et al, *Microbiome*, 2020




Hou et al, *Sig Transduct Target The, 2022*



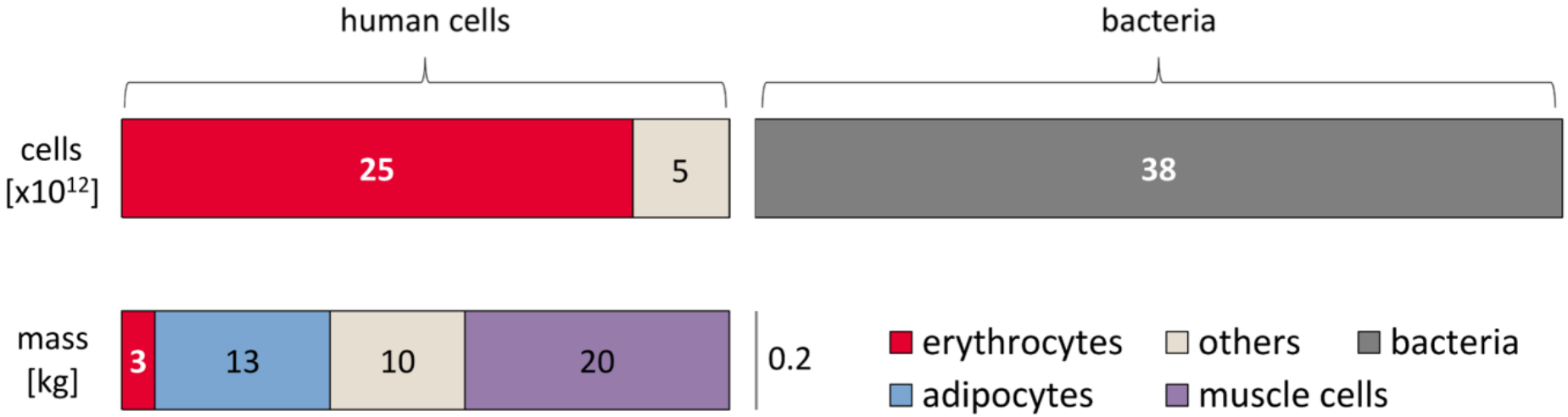

Berg et al, *Microbiome*, 2020



# Terminology

| Term | Definition |
|---|---|
| **Microbiome** | A characteristic microbial community that inhabits a specific, rationally defined habitat with typical physical and chemical conditions. |
| **Microbiota** | A collection of living microorganisms within a given microbiome |
| **Probiotics** | Living microorganisms that, when administered in sufficient quantities, confer a health benefit on the host. |
| **Prebiotics** | Food components that serve as "energy sources" for beneficial intestinal bacteria. |
| **Synbiotics** | Food supplements containing a combination of probiotics and prebiotics. |

# Are we more humans or microbes (bacteria)?




Sender et al, PLOS, 2016

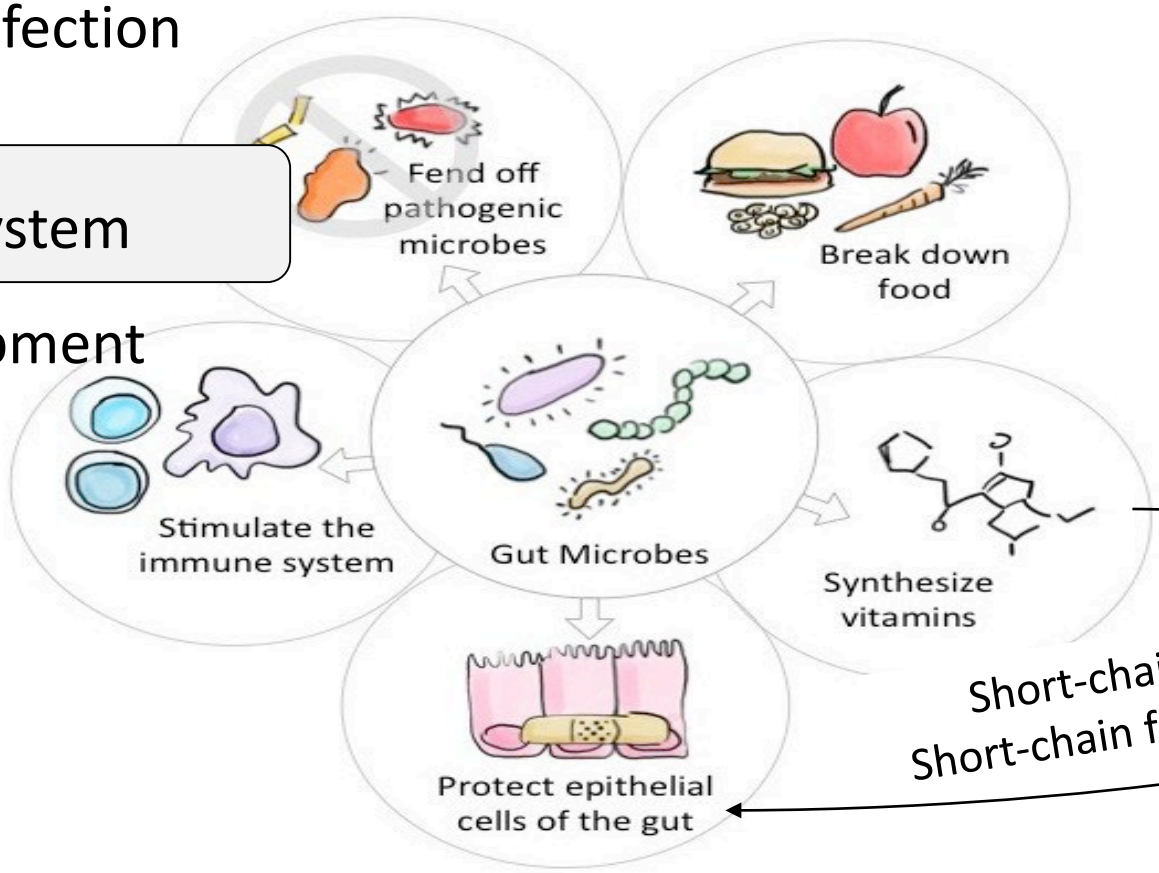
| | Number of cells | Number of genes | Mass |
|---|---|---|---|
| Human | 30 trillion ($3.0 \times 10^{13}$) | 20-25 thousand ($2.0 \times 10^{4}$) | 70-100 kg |
| Microbes | 38 trillion ($3.8 \times 10^{13}$) | 2-20 million ($2.0 \times 10^{6}$ –$2.0 \times 10^{7}$) | 0.2 kg |
| | 1.3 times more bacteria | 100 times more bacteria | **350-500 times more human** |

# Physiological functions of the gut microbiome

Defence against infection

Digestion

Immune system development




**EUBIOSIS**

= balance in the composition and function of the gut microbiome

Metabolism

Short-chain fatty acids
Short-chain fatty acids (SCFA)

Intestinal wall integrity

Sommer & Bäckhend, *Nat Rev Microbiology*, 2013

FN MOTOL 2 LFUK

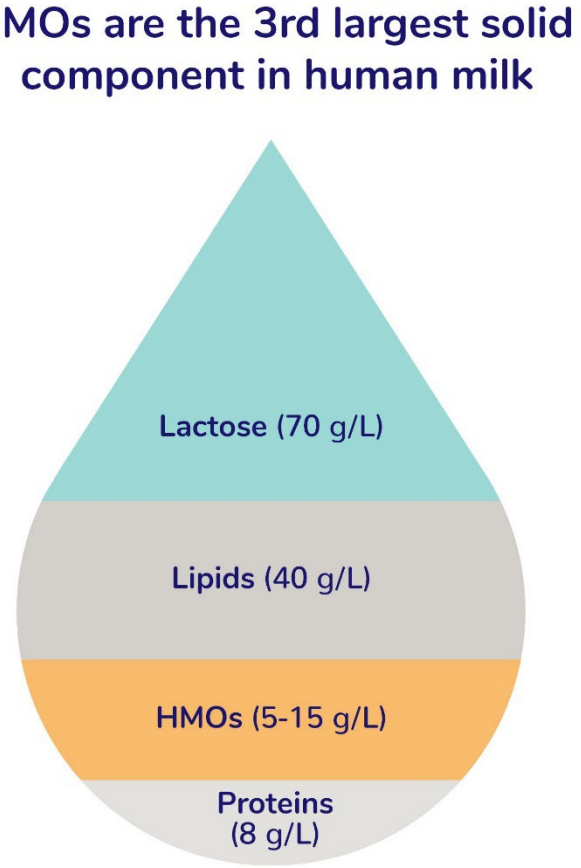
# Breast milk and microbiome nutrition

**The crucial importance of HMO** (human milk oligosaccharides)

- The third most common component, indigestible for infants but **an important food** source **for bacteria:**

1) **Bifidobacteria**. They prevent colonisation by other pathogenic microbes from the mother's nipple, such as *Staphylococcus.*

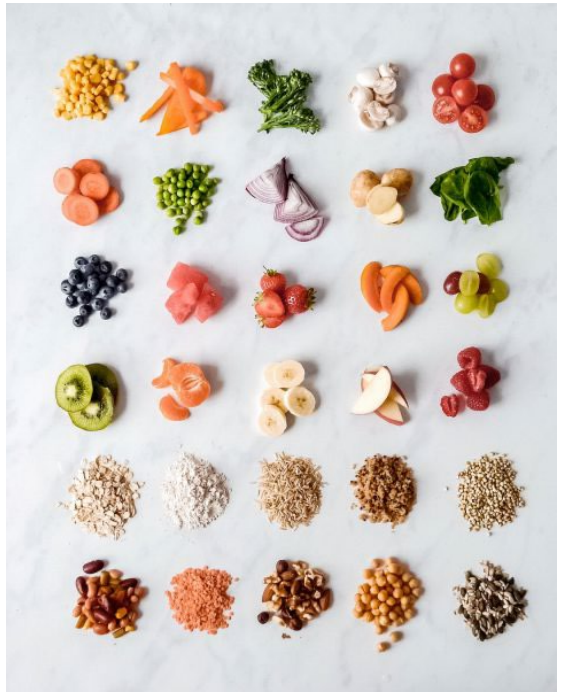
2) **Lactobacilli**. These are able to break down sugars in HMO, which can then be used by the infant as a source of energy.



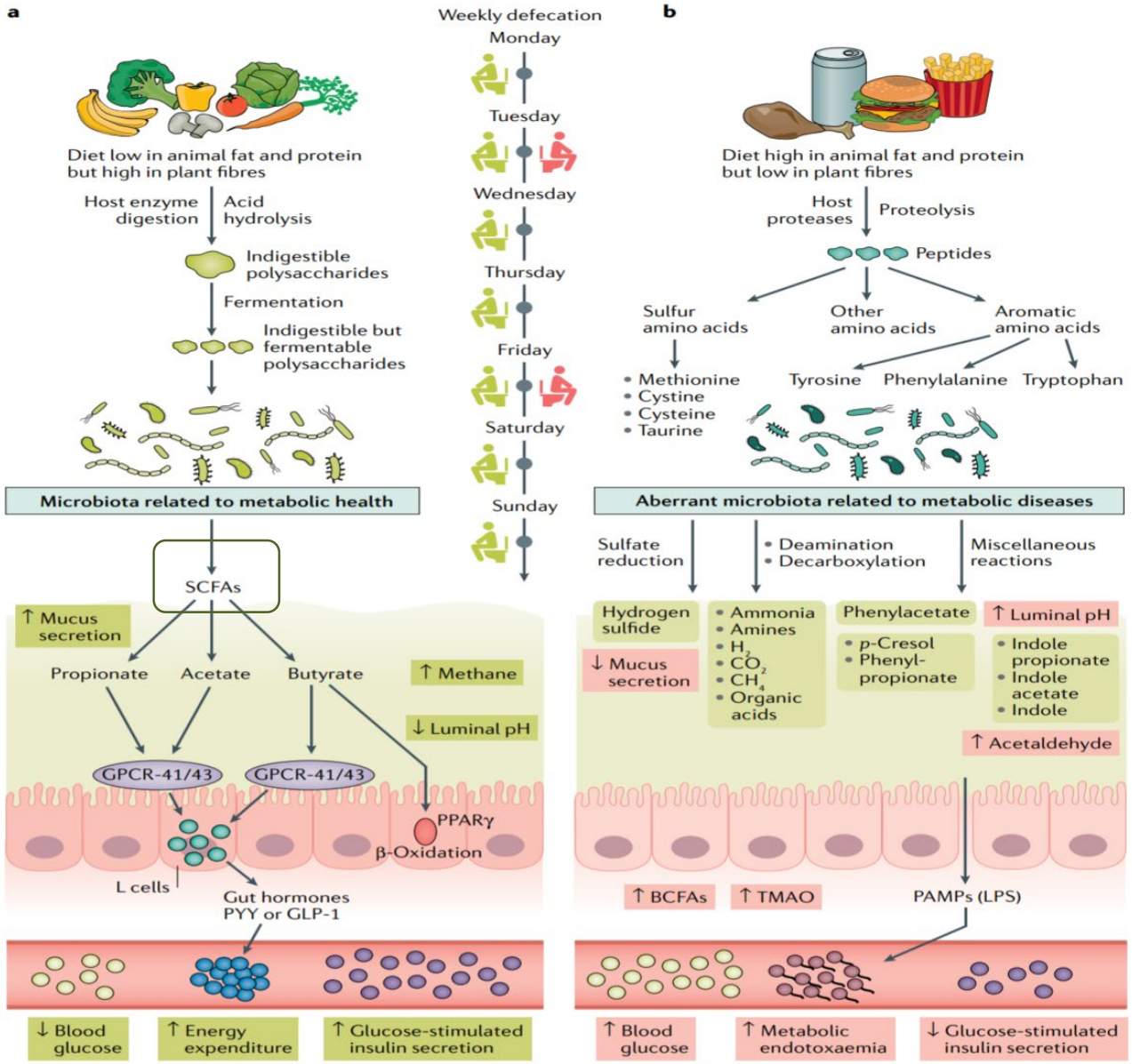

nestle.com

FN MOTOL 2 LFUK

# What exactly is a high-fibre diet?



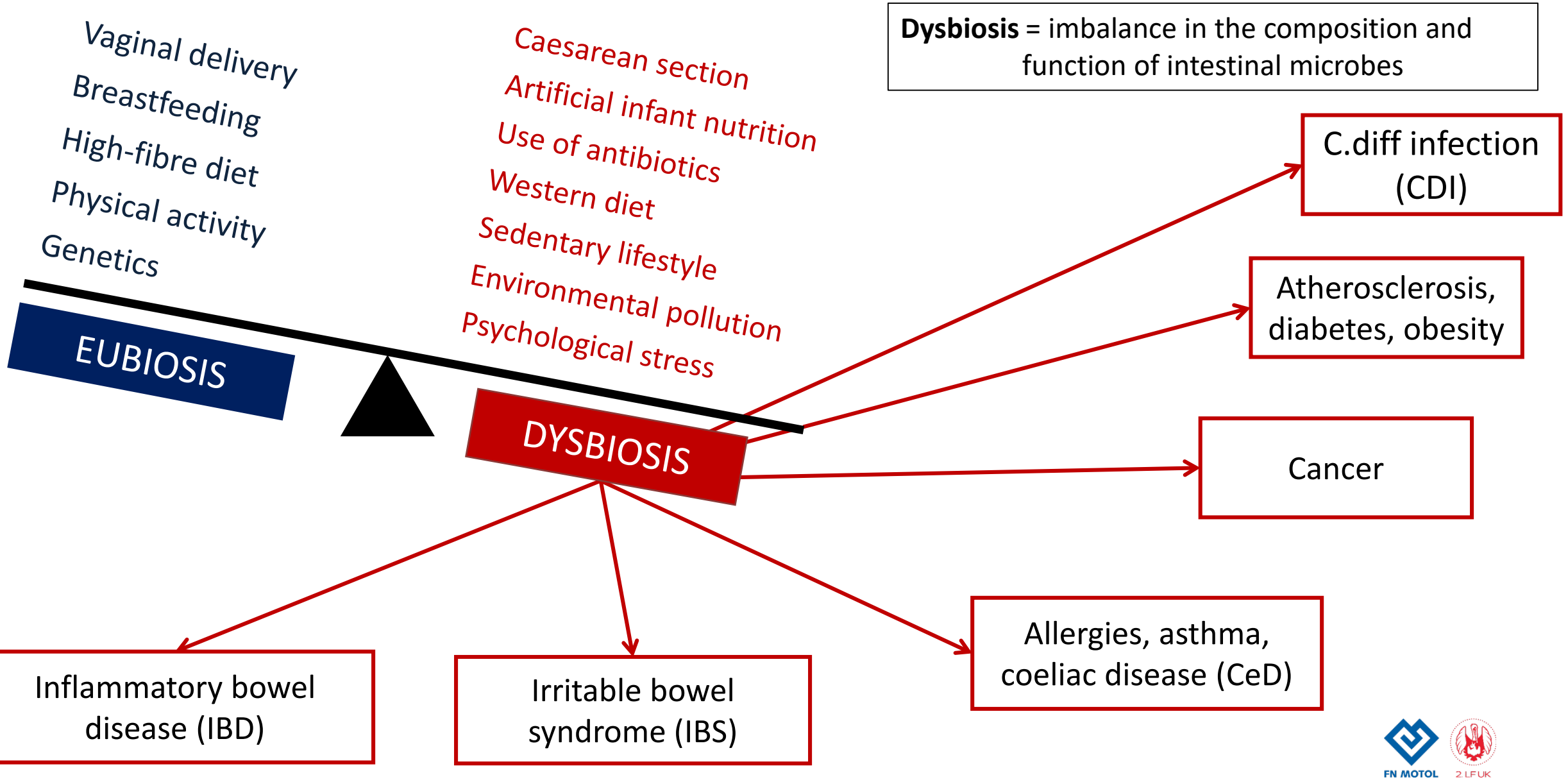
"Thirty different plants per week"
(Knight et al, **American Gut Project**, 2012)



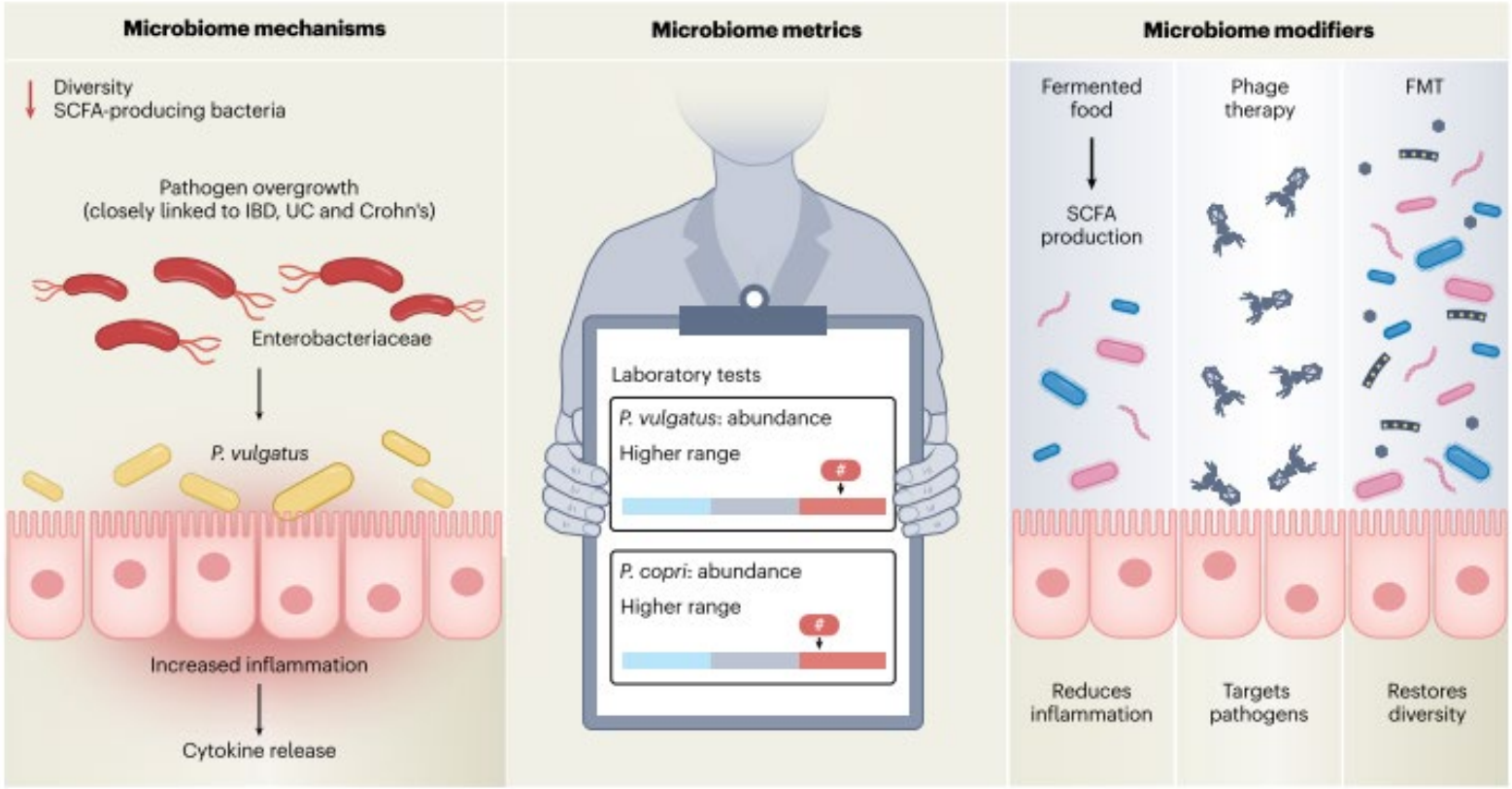

Fan & Pedersen; *Nature Reviews Microbiology,* 2020

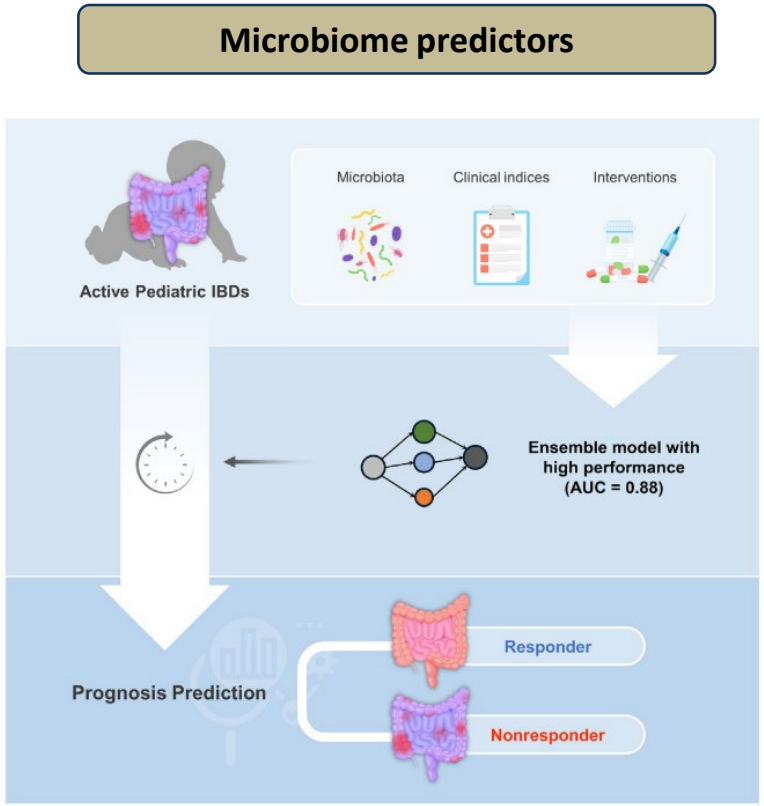
FN MOTOL
2 LF UK

# Influence on the composition of the gut microbiome



# How this translates into practice – an example on IBD




**Understanding the mechanism**
Reduced diversity and proportion of SCFA producers

**Finding measurable metrics**
Representation of *Phocaeicola vulgatus* (neg) and *Prevotella copri* (pos**)**

**Find therapeutic tools**
Diet, phage therapy or FMT

**Predict anything**
Response to treatment based on composition

Gilbert et al., Nature, 2025; Lee et al. iScience, 2025

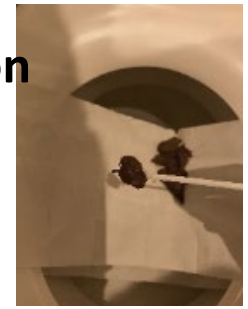
FN MOTOL 2 LF UK

# How the microbiome is analysed

A bit boring, but it helps to understand the whole thing

# Methods for studying the gut microbiome

**Stool sample collection**
At patients' homes
Storage:
- short term at -18°C
- long-term at -80°C



**DNA extraction**

## 16S/18S rDNA profiling

PCR for 16S/18S rDNA

Massively parallel amplicon sequencing

Comparison of ASV/OTU with reference database

Evaluation of **taxonomy**

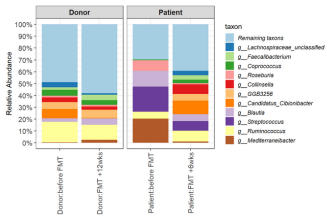
## Metagenomic sequencing

Random fragments, **ALL DNA**

Sequencing
Genome assembly

Evaluation of both taxonomy (more in-depth) and prediction of **functional capabilities of the microbiome**

Comprehensive bioinformatic analysis and evaluation of outputs




More cool!

FN MOTOL
2 LF UK

# What the result might look like

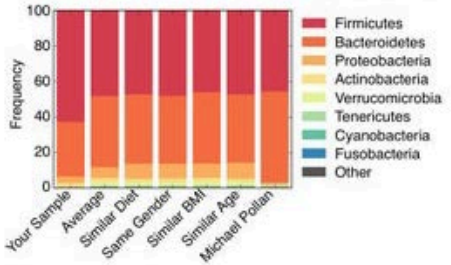
British Gut Project — microbio.me/BritishGut/authed/download/?barcode=000038289&filetype=result-pdf

1 of 1

american gut

## YOUR AMERICAN GUT SAMPLE

### What's in your American Gut sample?




Your most abundant microbes:

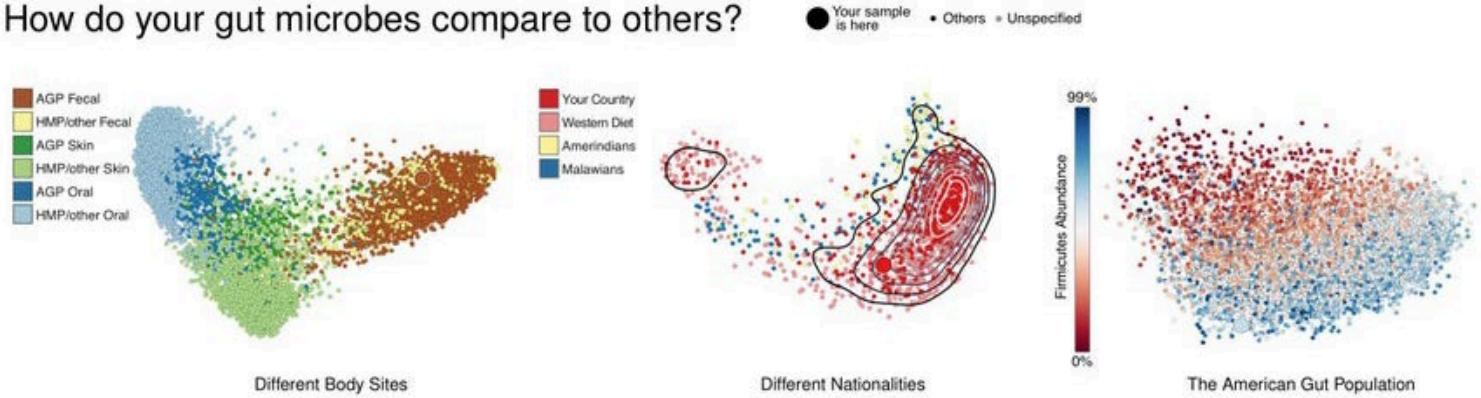
| Taxonomy | Sample |
|---|---|
| Genus *Bacteroides* | 26.6% |
| Genus *Faecalibacterium* | 15.8% |
| Family Lachnospiraceae | 10.5% |
| Genus *Lachnospira* | 7.3% |

Your most enriched microbes:

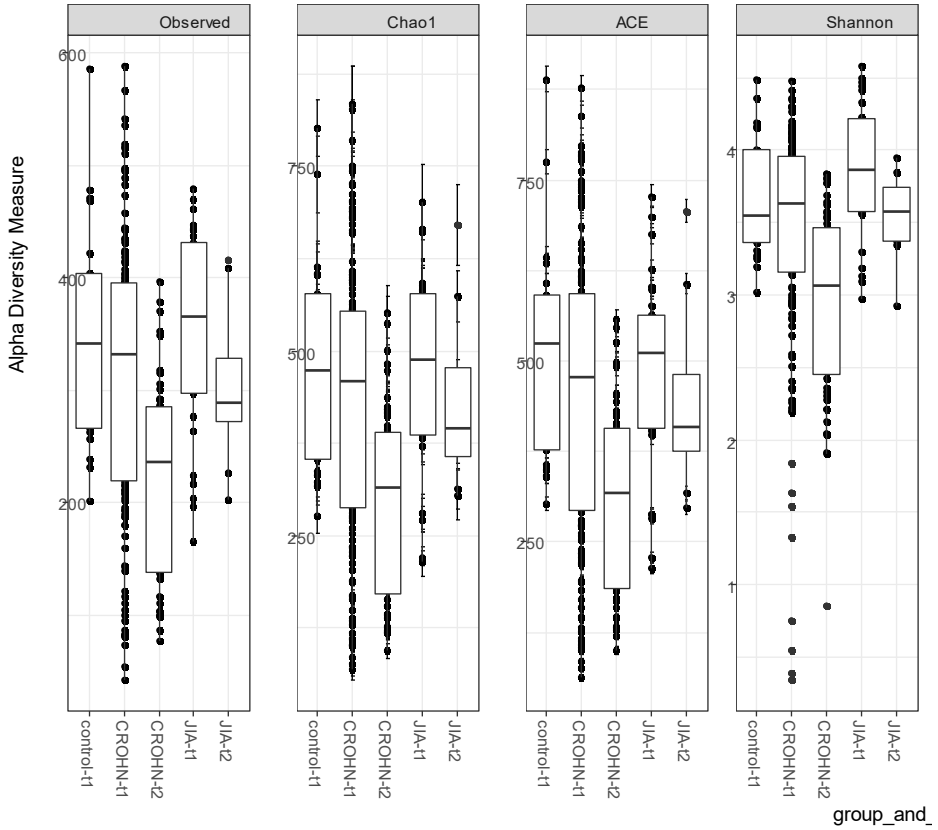
| Taxonomy | Sample | Population | Fold |
|---|---|---|---|
| Genus *Peptoniphilus* | 1.21% | 0.11% | 11x |
| Genus *Lachnospira* | 7.29% | 0.88% | 8x |
| cont. Genus *Ruminococcus* | 1.78% | 0.71% | 3x |
| Genus *Pyramidobacter* | 0.07% | 0.00% | 37x |

Your sample contained 8 rare taxa, including the following: Genus *Actinobaculum*, Genus *Arcanobacterium*, Genus *Anaerofustis*, Genus *Selenomonas*, Genus *Succiniclasticum*.

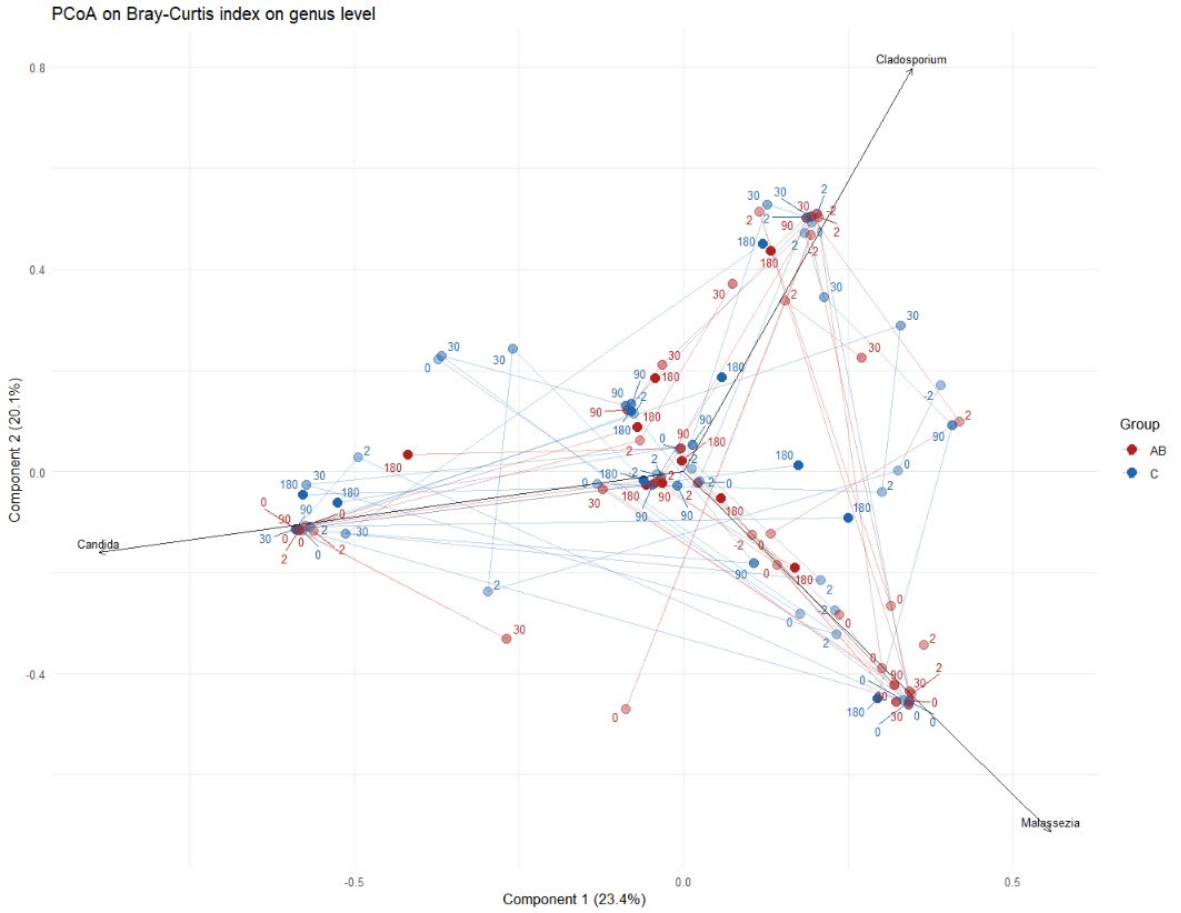
### How do your gut microbes compare to others?



# Diversity - alpha and beta




Alpha = within one sample

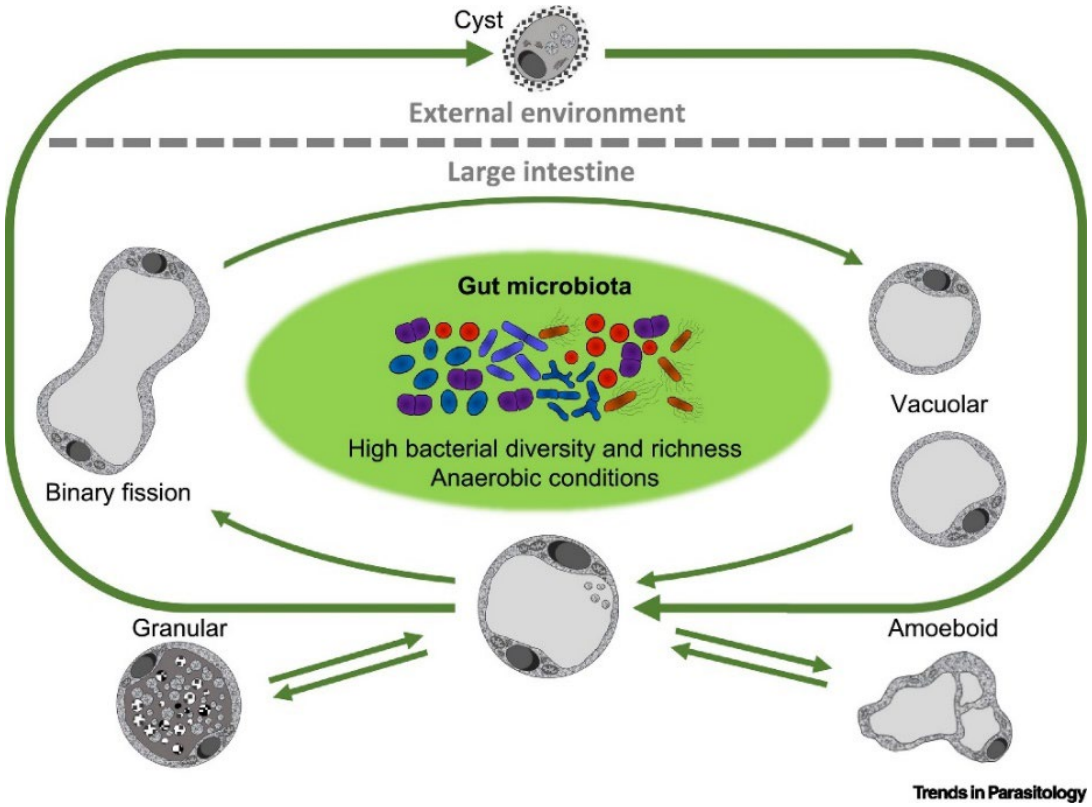



Beta = between samples

FN MOTOL 2 LFUK

# Non-bacteria: *Blastocystis*

- The most abundant eukaryote in the human gut [1-3]
- **Marker of high bacterial diversity** [4,5]
- Prevalence varies
  - Higher in developing countries (40-100%) [6-8]
  - Lower in industrialised countries (7-50%) and intestinal diseases (up to 5%) [9-12]
- Marker **of cardiometabolic health**, more common in people on a plant-based diet [13]




Stensvold, Trends in Parasitology, 2020

1)Tito. *Gut.* 2019; 2) Andersen. *FEMS Microbiol Ecol.* 2015; 3) Rostami. *Parasitol Res.* 2017; 4) Clark. *Adv Parasitol.* 2013; 5) Cinek. *Parasit Vectors.* 2021; 6) Poulsen. *Am J Trop Med Hyg*. *2016; 7*) Mohammad. *Asian Pac J Trop Med.* 2017; 8) Oliveira-Arbex; *Infect Genet Evol.* 2018; 9)Wawrzyniak. *Ther Adv Infect Dis.* 2013; 10) Stensvold. *Parasitol Int.* 2016; 10) Bart. BMC Infect Dis. 2013; 11) El Safadi. *BMC Infect Dis.* 2016; 11) *Scanlan. Infect Genet Evol.* 2016. 11) Scanlan. *FEMS Microbiol Ecol.* 2014. 12) Lhotska. *Front Cell Infect Microbiol.* 2020; 13) Piperni et al. Cell. 2024

# What is a "good and bad" composition?

## GOOD

High alpha diversity (300-1000 species)

Anaerobic environment (e.g. very few *Proteobacteria*)

More SCFA producers

*Blastocystis* positive

Healthy microbiome?

## BAD

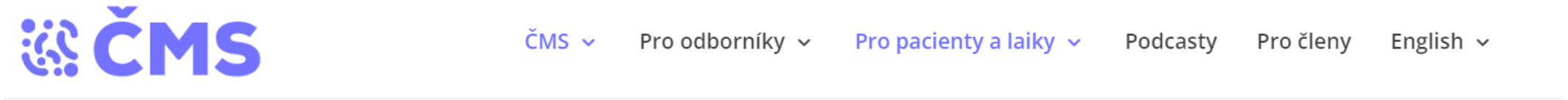
Low alpha diversity (less than 100 genera)

Many facultative anaerobes (e.g. more *Proteobacteria*)

Few SCFA producers

*Blastocystis* negative

# The concept of a healthy microbiome does not yet exist




## A jaké by tedy měl mít zdravý člověk složení mikrobiomu?

**NEVÍME** – a neví to zatím nikdo, ani komerční subjekty, které nabízejí, že Vám mikrobiom opraví!

Vědci mají jistě všeobecnou představu o složení mikrobiomu, ale pro konkrétního člověka v konkrétní životní situaci to definovat zatím nelze.

Vezmeme-li v potaz, že počet genů mikroorganismů ve střevním traktu je 100-150x větší, než počet genů v genomu člověka, a zároveň je genetická informace mikroorganismů vysoce individuální a variabilní, odpovídá to na otázku, proč je tak těžké mikrobiom studovat a proč nejsou výsledky více uplatňované v praxi. Zatím je prozkoumána pouze část mikroorganizmů, u nichž víme, jaké živiny spotřebovávají a jaké látky produkují. Mnohé jsou prospěšné, některé mohou za určitých podmínek organismu škodit, o jiných zatím nevíme téměř nic.

V některých případech lze skutečně říct, že konkrétní složení mikrobiomu je nezdravé (např. převaha patogenních kmenů bakterie *Clostridioides difficile* způsobujících úporné průjmy), ale nikdo dosud nedokázal přesně definovat „zdravé“ nebo „správné“ složení mikrobiomu.

www.mikrobiom-cms.cz

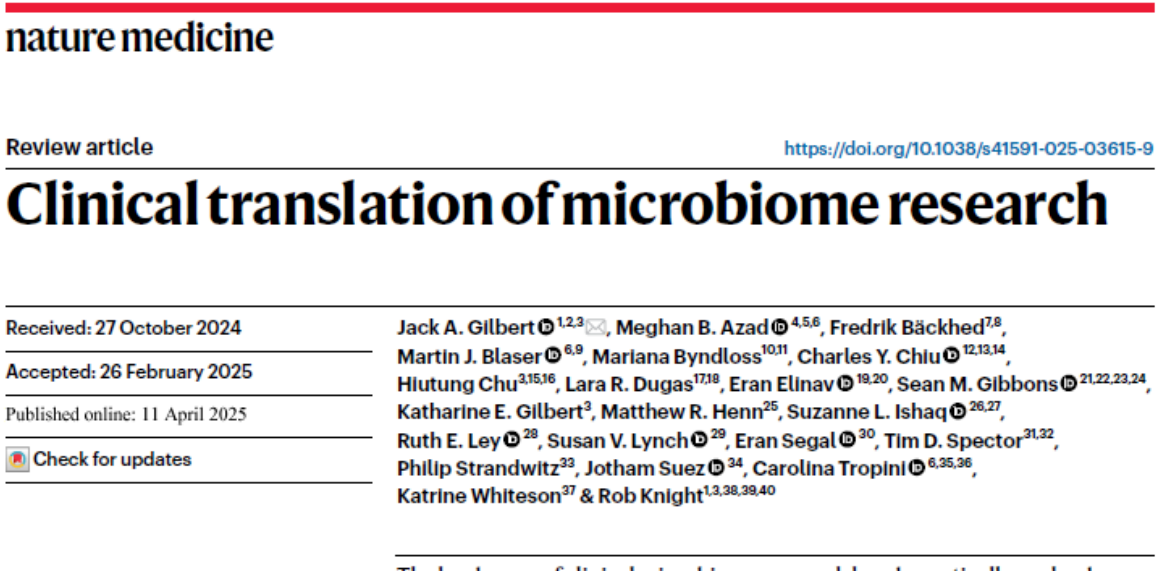
FN MOTOL 2 LF UK

# Where is the knowledge about the microbiome?

- **It is getting closer and closer to practical application.** We can point to:
  - microbial metrics that can help diagnose diseases [1]
  - or indicate the success of treatment (currently only for FMT) [2]

Not yet in common use, large studies are still ongoing (see below)

"The future use of personalised microbiome interventions that take into account individual microbiome composition and realistic lifestyle changes **will help** bridge the gap between research and practice **in the future**." – Gilbert et al., *Nature Medicine*, 2025



nature medicine

Review article

https://doi.org/10.1038/s41591-025-03615-9

**Clinical translation of microbiome research**

Received: 27 October 2024

Accepted: 26 February 2025

Published online: 11 April 2025

Check for updates

Jack A. Gilbert[1,2,3], Meghan B. Azad[4,5,6], Fredrik Bäckhed[7,8], Martin J. Blaser[6,9], Mariana Byndloss[10,11], Charles Y. Chiu[12,13,14], Hiutung Chu[3,15,16], Lara R. Dugas[17,18], Eran Elinav[19,20], Sean M. Gibbons[21,22,23,24], Katharine E. Gilbert[3], Matthew R. Henn[25], Suzanne L. Ishaq[26,27], Ruth E. Ley[28], Susan V. Lynch[29], Eran Segal[30], Tim D. Spector[31,32], Philip Strandwitz[33], Jotham Suez[34], Carolina Tropini[6,35,36], Katrine Whiteson[37] & Rob Knight[1,3,38,39,40]

1) Schmartz, G. P. et al. Nat. Commun. 2024
2) Weingarden, A. et al. Microbiome. 2015.

FN MOTOL 2 LFUK

"The microbiome is the key to health," and the key to health is the diversity of plant foods.


**The question is:** "Can I have my microbiome tested commercially?"

**The answer:** YES!

**Question:** "Can I test my microbiome and obtain valid information that will help me?"

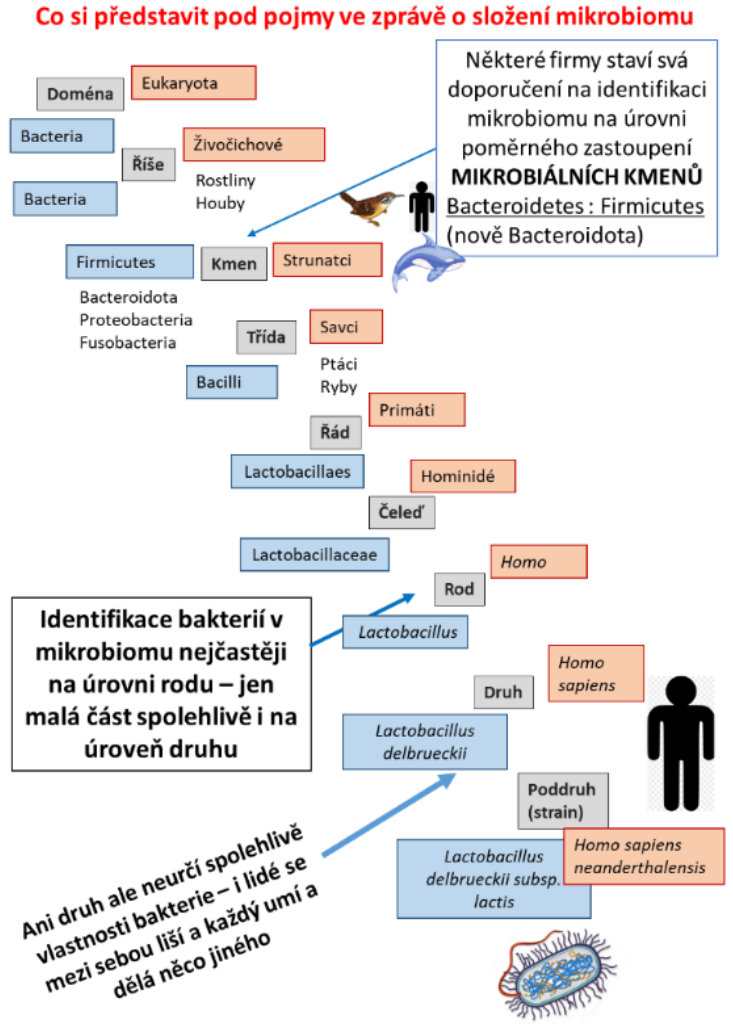
**Answer:** No.

And why?

# What are the problems? I.

## Insufficient depth of taxon identification

- Information about the representation of the main "groups" – usually phyla and their ratios (Firmicutes/Bacteroidetes)
- **The Firmicutes/Bacteroidota (F/B)** ratio has long been considered a simple indicator of health or dysbiosis, but **the current scientific consensus strongly questions** this indicator.




*Obr. 1 Co si představit pod pojmy ve zprávě o složení mikrobiomu*

# What are the problems II.

**Potentially incorrect interpretation of the function of the microbiome**

- Insufficient depth – see point 1.
- The mere presence of a certain bacterium does not imply specific abilities, and these in turn do not imply that a process, e.g. the production of certain substances, is actually taking place (see Fig.).

Multiomics – **the need for metabolomics**

Dysbiózu ve střevě si lze představit jako dům po zásahu tornáda

**Jak dům opravit?**

**Bude potřeba mnoho řemeslníků, např. zedník.**

**Zedník = člověk (*Homo sapiens*)**

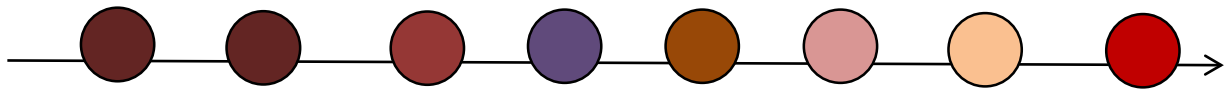
ALE Ne každý *Homo sapiens* je ale zedník


Stejně tak např. ne každá bakterie *Lactobacillus reuteri* má potřebné schopnosti právě pro vaše střevo, a i když ty schopnosti bude mít, za určitých podmínek je nemusí projevit.

# What are the problems III.

**Conclusions based on a single sample**

- Although the gut microbiome is very stable in the long term, its specific composition **can fluctuate considerably in the short term.**



Changes in composition over time

FN MOTOL 2 LFUK

# How variable is the microbiome?

- **In the short term** (hours to days)
  - Changes after eating, defecation, change of environment, stress, use of medication (e.g. antibiotics)
  - Fluctuations in the relative abundance of certain species
    - e.g. anaerobes such as *Bacteroides* or *Clostridium*

Article | Open access | Published: 18 November 2021

**Temporal variability in quantitative human gut microbiome profiles and implications for clinical research**

Doris Vandeputte, Lindsey De Commer, Raul Y. Tito, Gunter Kathagen, João Sabino, Séverine Vermeire, Karoline Faust & Jeroen Raes

*Nature Communications* **12**, Article number: 6740 (2021) | Cite this article



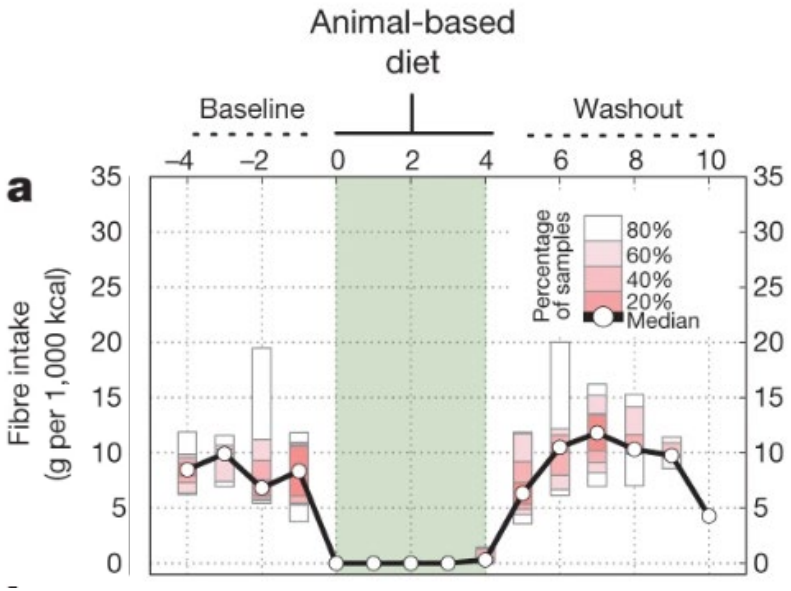
High variability – but the overall composition quickly returns to its original state – **the** so-called **resilience of the gut microbiome ***

* Vandeputte et al. *Nat Commun.* 2021

FN MOTOL 2 LFUK

# How variable is the microbiome?

- **Short term** (hours to days)
  - Dietary intervention (n=10): high-fat diet (animal-based)




Fibre intake

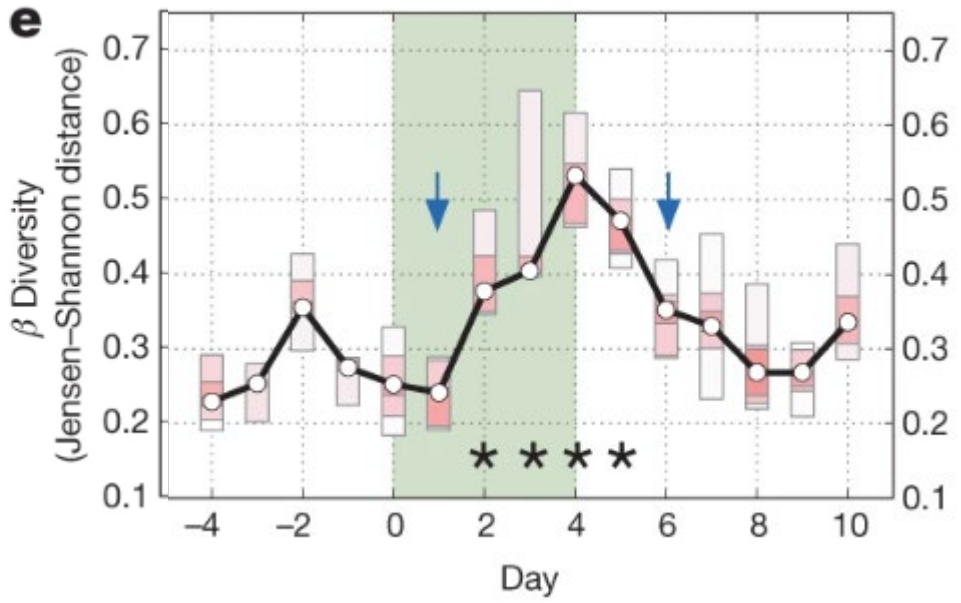
Letter | Published: 11 December 2013

**Diet rapidly and reproducibly alters the human gut microbiome**

Lawrence A. David, Corinne F. Maurice, Rachel N. Carmody, David B. Gootenberg, Julie E. Button, Benjamin E. Wolfe, Alisha V. Ling, A. Sloan Devlin, Yug Varma, Michael A. Fischbach, Sudha B. Biddinger, Rachel J. Dutton & Peter J. Turnbaugh

*Nature* **505**, 559–563 (2014) | Cite this article

**198k** Accesses | **1953** Altmetric | Metrics




**Dramatic changes within 48** hours with extreme dietary change, but return to original state within another 48 hours

# Factors influencing variability

- **Long term** (months to years)
  - In adults, the microbiome tends to be relatively stable unless there are major interventions (e.g., antibiotics, FMT).
  - In childhood and old age, the microbiome is generally more dynamic and less stable
  - Stability is supported by a consistent lifestyle, diet, and absence of antibiotics

| Factor | Effect on variability |
|---|---|
| Antibiotics | Very strong, often causing disruption for months |
| Diet | moderate to significant (especially with extreme changes) |
| Travel | temporary changes (e.g. traveller's diarrhoea) |
| Age | The microbiome of children and seniors is more variable |
| Chronic diseases | e.g. IBD or metabolic syndrome alter stability |

Freely adapted from Vandeputte et al. *Nat Commun.* 2021

FN MOTOL 2 LFUK

# What are the problems IV.

**Potentially incorrect interpretation of microbiome health/dysfunction**

- The host-microbiome relationship is **highly individual**, and the (un)beneficial nature of a particular microbiome composition always depends on the current context.
- With the exception of clear pathogens**, it is impossible to say with certainty which specific bacteria are beneficial to a given host and which are not.**

Notable exceptions (it seems): *Faecalibacterium prausnitzii* and a protozoan called *Blastocystis*

FN MOTOL 2 LFUK

# What are the problems V.

## Offer of personalised food supplements

The current state of scientific knowledge and our technical capabilities **do not** currently **allow us** to predict the exact "behaviour" of the microbiome or, based on an analysis of its composition, **to prepare an individualised probiotic or prebiotic preparation** that will lead to a predefined, specific, long-term and sustainable change.

# SUMMARY

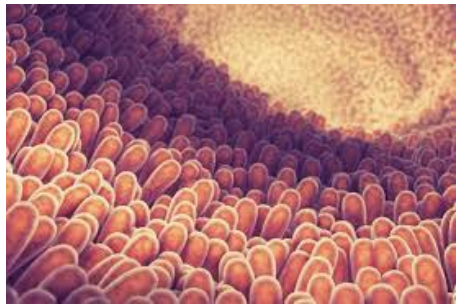
- Commercial analyses (so far):
  - **They cannot provide targeted advice**
  - **Cannot** be used to prepare individualised meal plans or tailor-made probiotics
  - **It is therefore important to consider carefully whether it is worth spending so much money on them**

FN MOTOL 2. LF UK

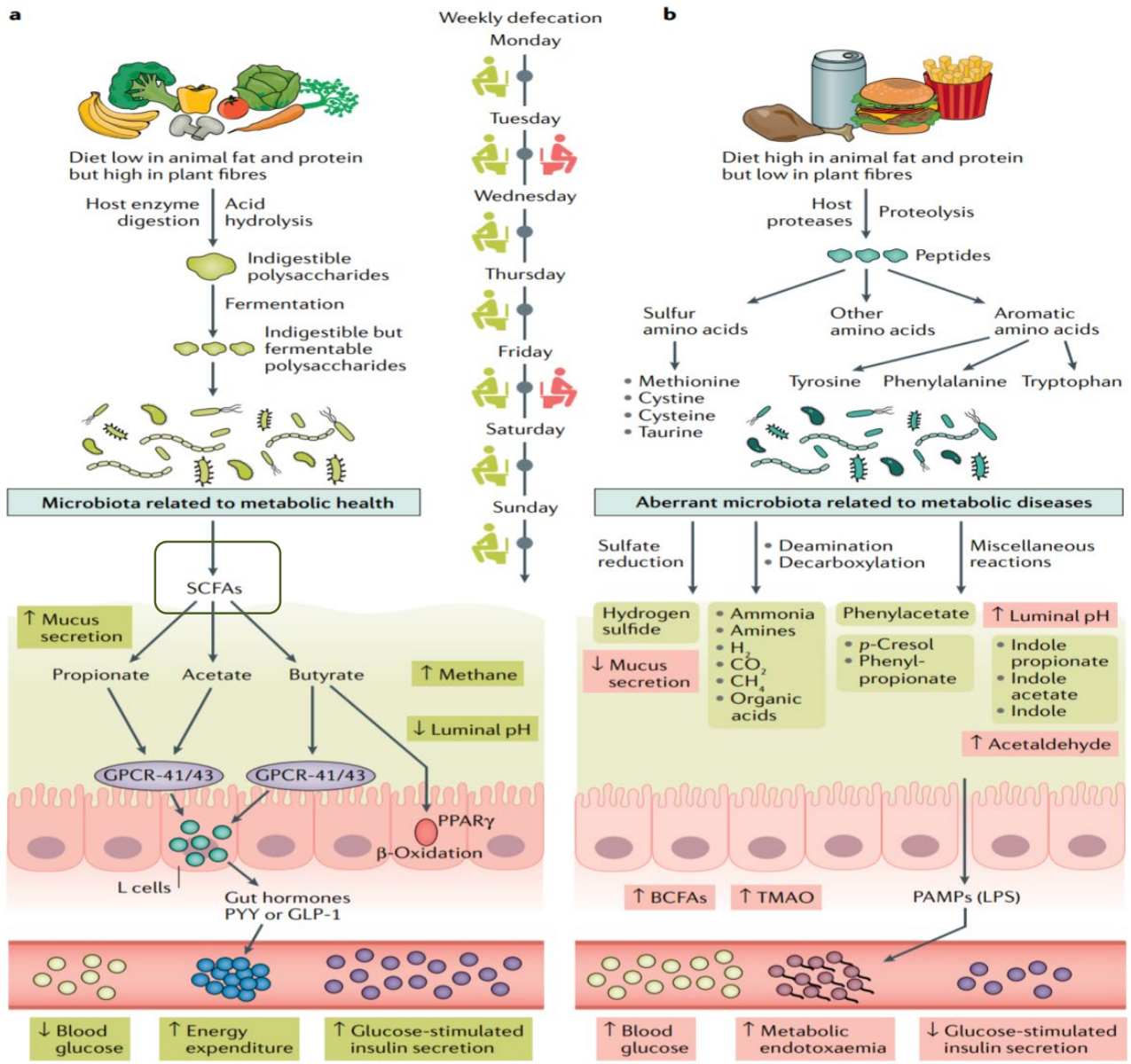
# How to take care of your microbiome

Fibre

Adequate fibre intake (especially soluble fibre) **promotes SCFA production**



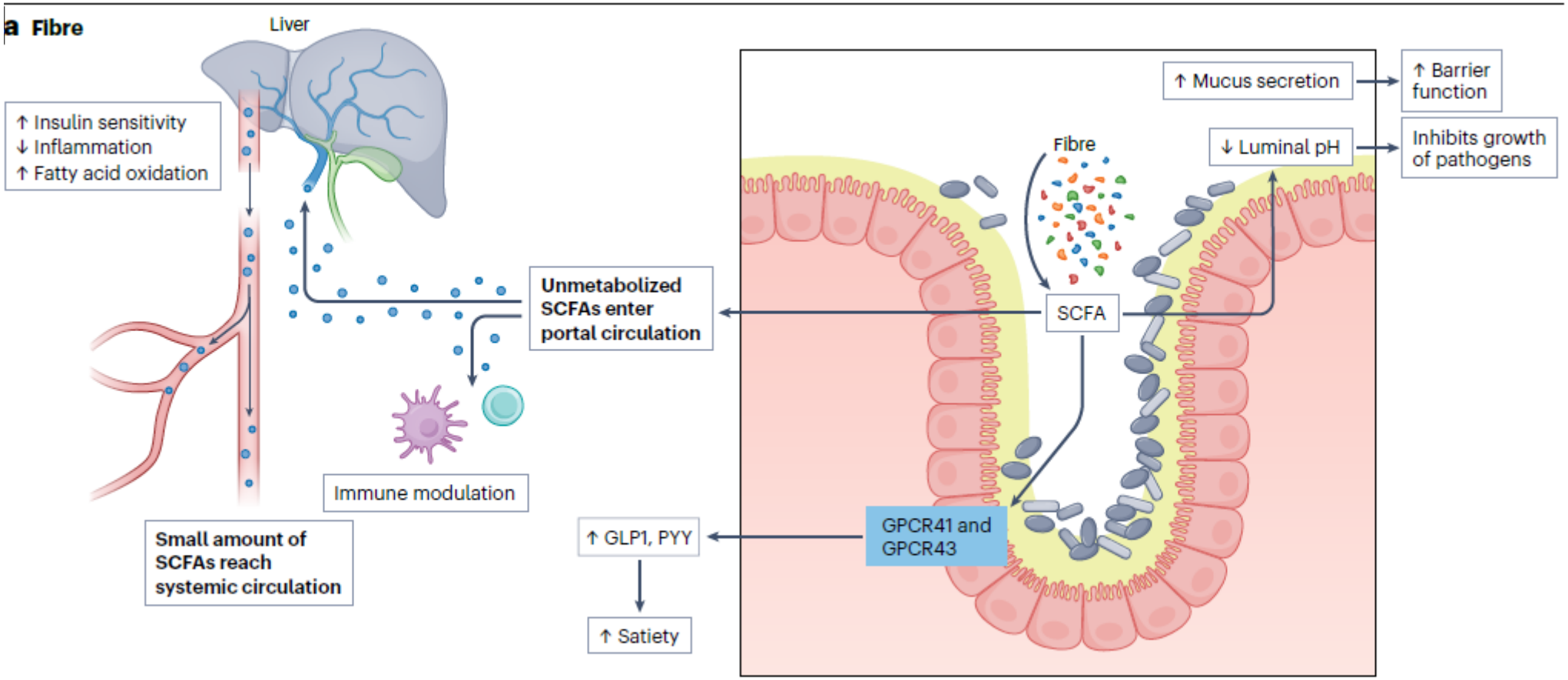
Supports intestinal epithelial function




Fan & Pedersen; *Nature Reviews Microbiology,* 2020

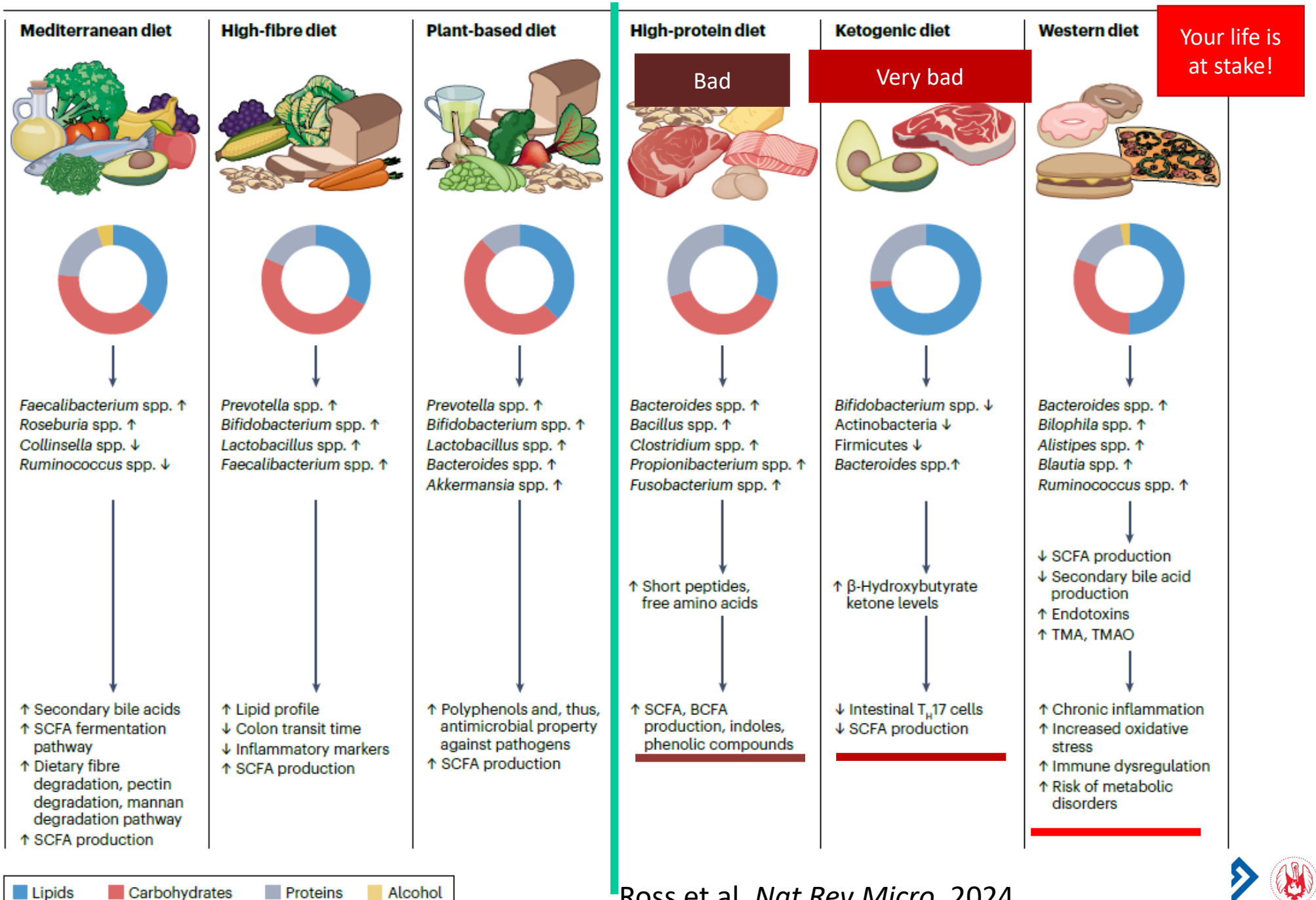
FN MOTOL 2 LFUK

**And not just food for the intestinal epithelium.** It increases sensitivity to INS, reduces the production of pro-inflammatory molecules and increases MK oxidation



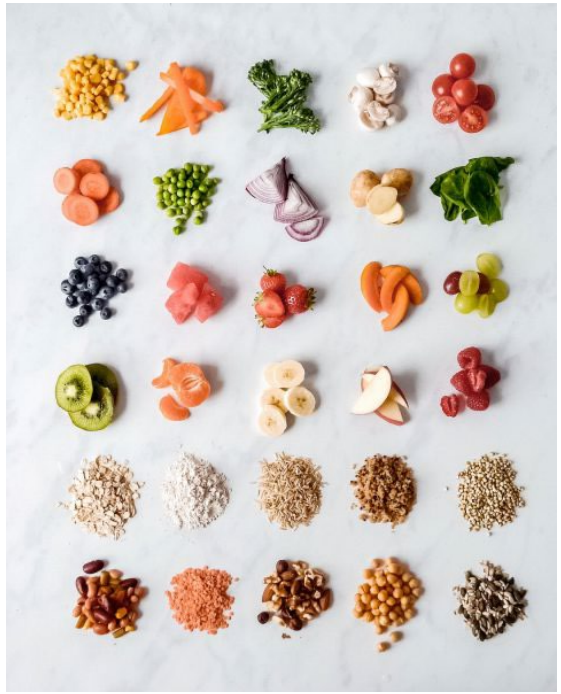

Ross et al. *Nat Rev Micro*. 2024

**We are what we eat**

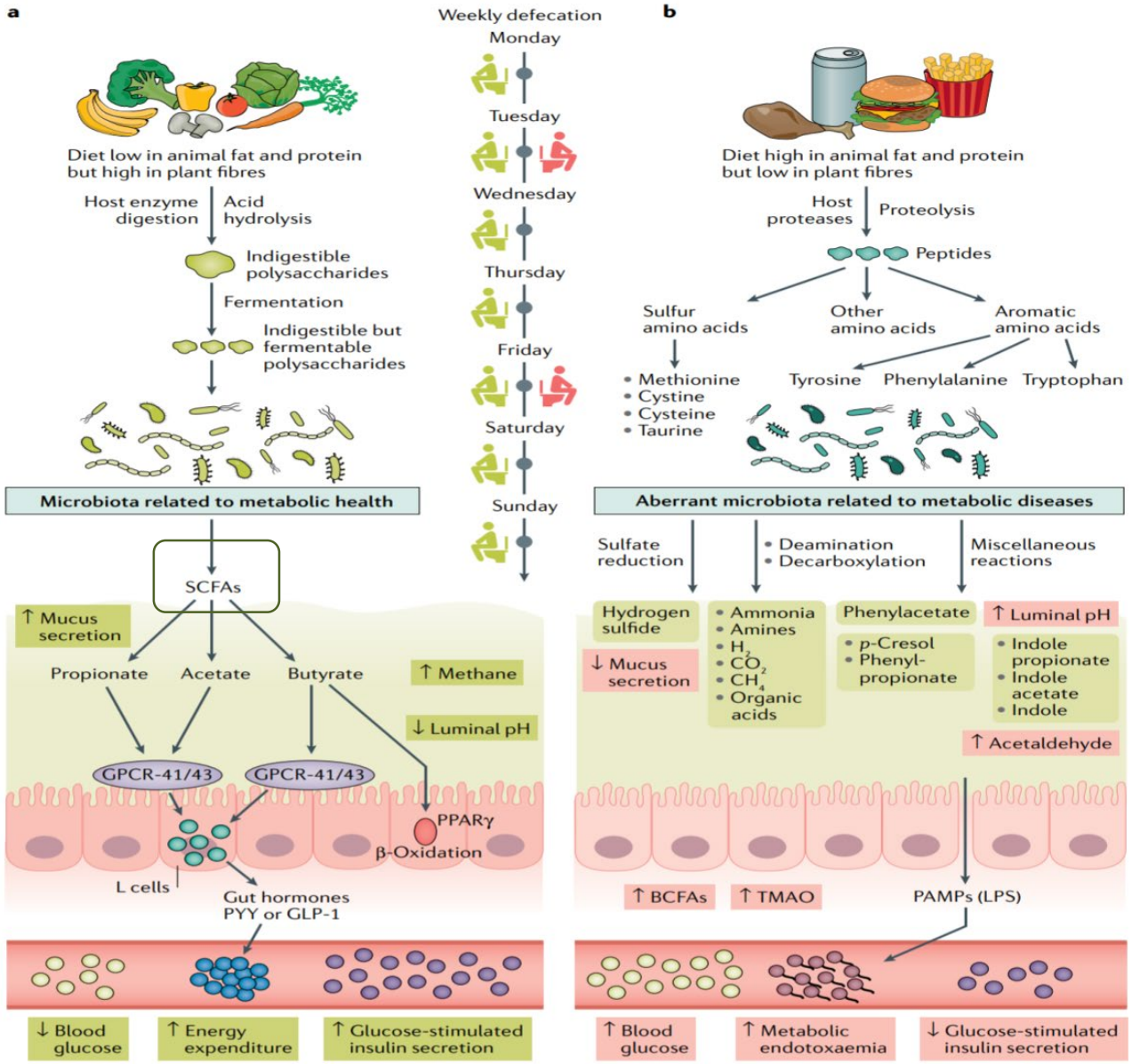



Ross et al. *Nat Rev Micro*. 2024

# Confirmation of what was already known...



"Thirty different plants per week"
(Knight et al, **American Gut Project**, 2012)




Fan & Pedersen; *Nature Reviews Microbiology,* 2020

FN MOTOL
2 LFUK

# Practical recommendations

- **≥30 different plant-based foods per week** [1,2]
  - Regularly three servings of fermented foods per day (different types) [3]
  - Main source of protein: less meat, more legumes and whole grain sources [1,2]
  - Limit ultra-processed foods that promote "bad" bacteria [2]
- **Diversity > uniformity** – no single food or bacterium is a panacea; a balanced and varied diet is key

1) Knight et al, American Gut Project, 2012.
2) Fackelman et al. Nat Microbiology. 2024
3) Asnicar et al. 2021. Cell

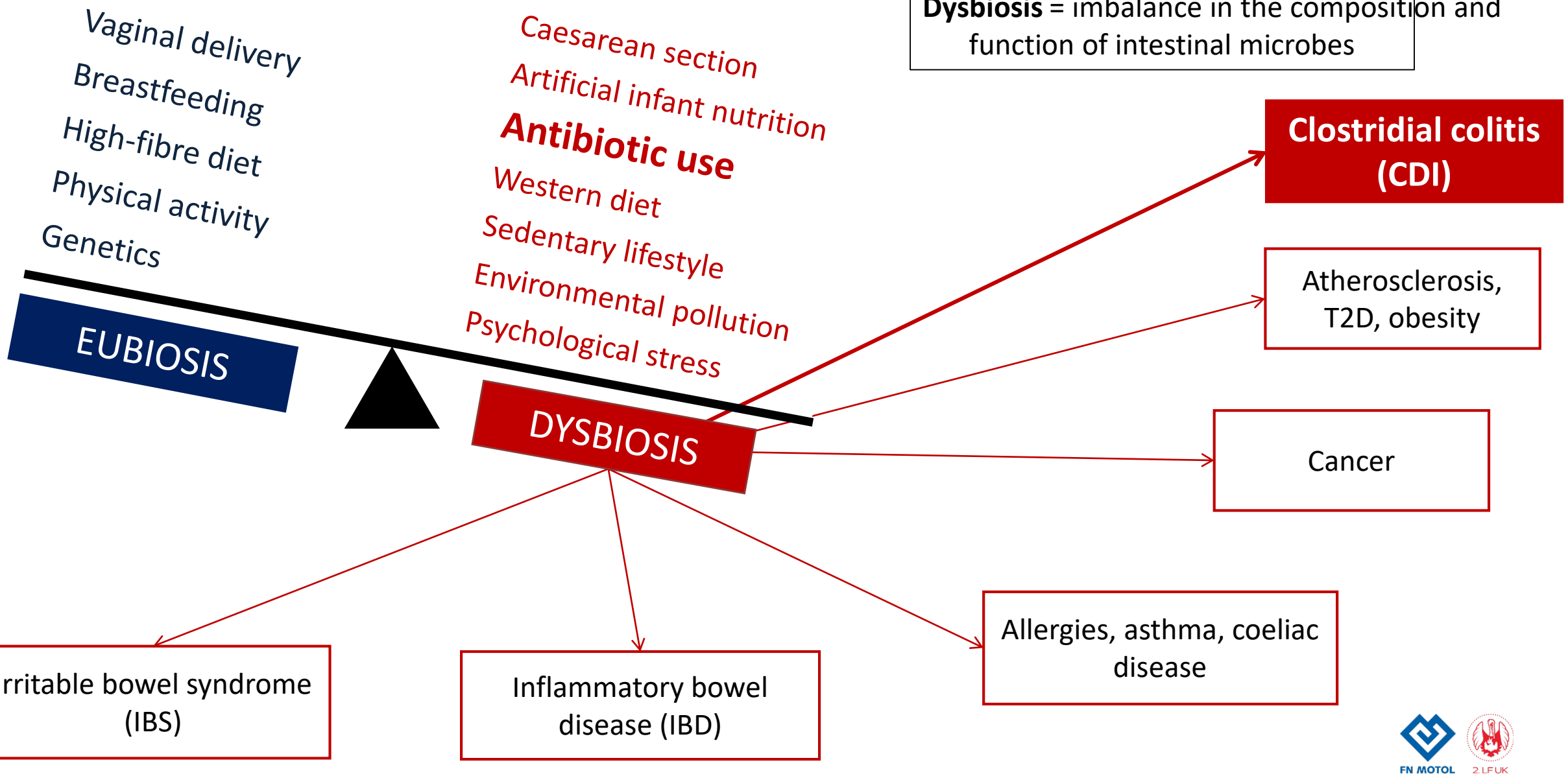
FN MOTOL 2. LF UK

# ATBs and their role in dysbiosis

The dysbiosis model and the effect of ATB treatment on the gut microbiome

# Intestinal microbiome dysbiosis

**Dysbiosis** = imbalance in the composition and function of intestinal microbes



# Difficilogenic ATB

- ATBs whose use is associated with a higher risk of **clostridial colitis**

4 "C"

**Clindamycin**

**Cephalosporins**

**Co-aminopenicillins**

**Ciprofloxacin (+other FQs)**

Štefan, Antibiotics, 2024

*Open Forum Infectious Diseases*

MAJOR ARTICLE

Comparison of Different Antibiotics and the Risk for Community-Associated *Clostridioides difficile* Infection: A Case–Control Study

**Aaron C. Miller,[1,©] Alan T. Arakkal,[2] Daniel K. Sewell,[2] Alberto M. Segre,[3] Joseph Tholany,[1,©] and Philip M. Polgreen,[1] CDC MInD-Healthcare Group**

[1]University of Iowa, Carver College of Medicine, Iowa City, Iowa, USA, [2]University of Iowa, College of Public Health, Iowa City, Iowa, USA, and [3]Department of Computer Science, University of Iowa, Iowa City, Iowa, USA

FN MOTOL 2 LFUK

# FMT outside the main indications

THE ONLY APPROVED INDICATION IS STILL
**rCDI**

Not this!


https://www.youtube.com/watch?v=VMFSwMvac8I

FN MOTOL 2 LFUK

# Overview of studies on FMT in direct treatment for non-CDI diagnoses

| Diagnosis | Number of RCTs | Summary of FMT use |
|---|---|---|
| **Ulcerative colitis** | 13 | Potential for inducing remission in ulcerative colitis; further research needed for long-term results. |
| **ARB carriage** | 1 | Single RCT with non-significant conclusion, cohort studies show potential for decolonisation. |
| **Crohn's disease** | 2 | Promising results in Crohn's disease; stronger evidence needed for wider application. |
| **Irritable bowel syndrome (IBS)** | 9 | Some suggest improvement in IBS symptoms, but results are mixed; larger studies needed. |
| Metabolic syndrome | 4 | Evidence of effect on metabolic parameters (insulin sensitivity, lipids); requires combination with other interventions. |
| Hepatic encephalopathy | 3 | Results suggest that FMT may reduce the frequency of hepatic encephalopathy recurrence and improve patients' quality of life by modulating the gut microbiota and reducing systemic inflammation. |
| Chronic fatigue syndrome (CFS) | 1 | Possible effect on alleviating CFS symptoms by restoring the balance of the gut microbiota. However, the results are limited so far and further studies are needed. |
| Autism | 0 | Observational studies, some of which suggest alleviation of autism symptoms and improvement in gastrointestinal problems. However, no randomised controlled trials have been conducted to date, limiting the evidence to support this therapy for ASD. |
| Parkinson's disease | 2 | Promising initial results in influencing GI symptoms and possibly neurological outcomes; need for confirmation. |
| Obesity | 3 | Some studies show an effect on weight and metabolic health in obese patients. Results are mixed, |

# Statement on FMT

- FMT may be accompanied by mild side effects (diarrhoea, cramps or abdominal pain, fever, bloating, flatulence and/or constipation), but some can be very serious or even fatal (however, these are usually the result of inadequate donor screening and the subsequent transplantation of pathogenic microorganisms).
- **FMT must therefore always be performed under strict medical supervision.** The Czech Medical Association strongly warns against unprofessional attempts at home FMT – this could endanger the health and even the life of the recipient! This is due to the need for thorough screening for the presence of pathogenic microorganisms in donated stool and the prevention of serious intestinal infections. Not to mention injuries resulting from self-administration or contamination during processing at home.

https://www.mikrobiom-cms.cz/stanoviska-cms/fekalni-mikrobialni-transplantace/

FN MOTOL 2 LFUK

# SUMMARY

- Irrational use of antibiotics leads to dysbiosis and thus to the risk of other diseases, not only CDI
- The most difficult antibiotic is clindamycin, but cephalosporins, potentiated aminopenicillins and fluoroquinolones are also high-risk.
- FMT is only approved for the treatment of recurrent *C. difficile* infection.

# Is it the real key to health or a commercial illusion?

# What is its real impact on health and what are the limits of current knowledge?

- From a microbiome perspective, the saying **"we are what we eat"** applies**.**

- **Limits**: is it the cause or the effect? We do not know.

- **Variability over time:** Need to monitor dynamics, not test once.

- **Resistance:** Antibiotics have a negative effect (but perhaps not permanently).

# Can nutritional recommendations be personalised based on microbiome analysis?

- **Not yet.** We can see what the microbiome characteristics of healthier people are.

- The recommendations are still the same and relatively simple – **"eat more than 30 plant-based foods a day"** (and these are not tailor-made diets or probiotics).

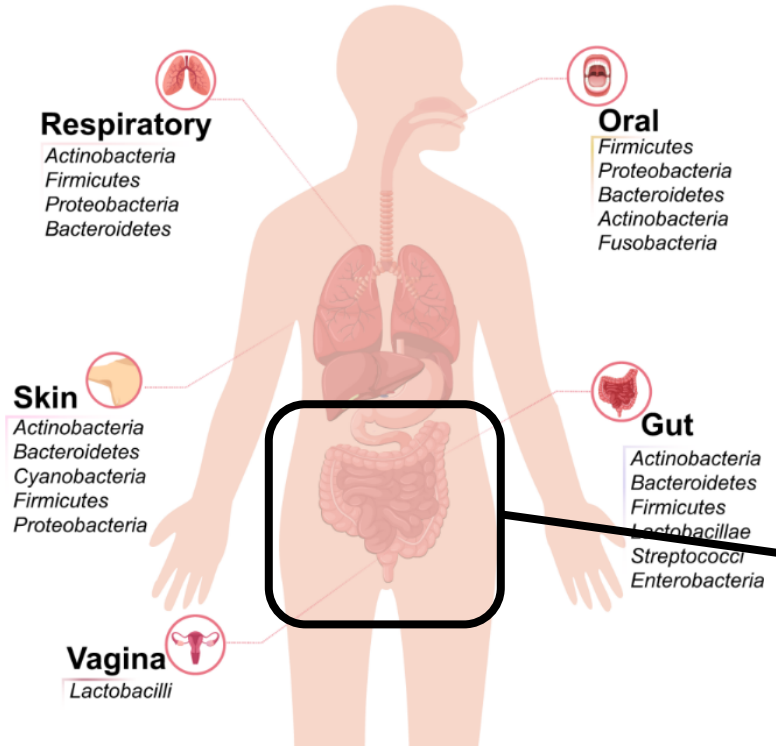
FN MOTOL 2. LF UK

# Physiological microbiota

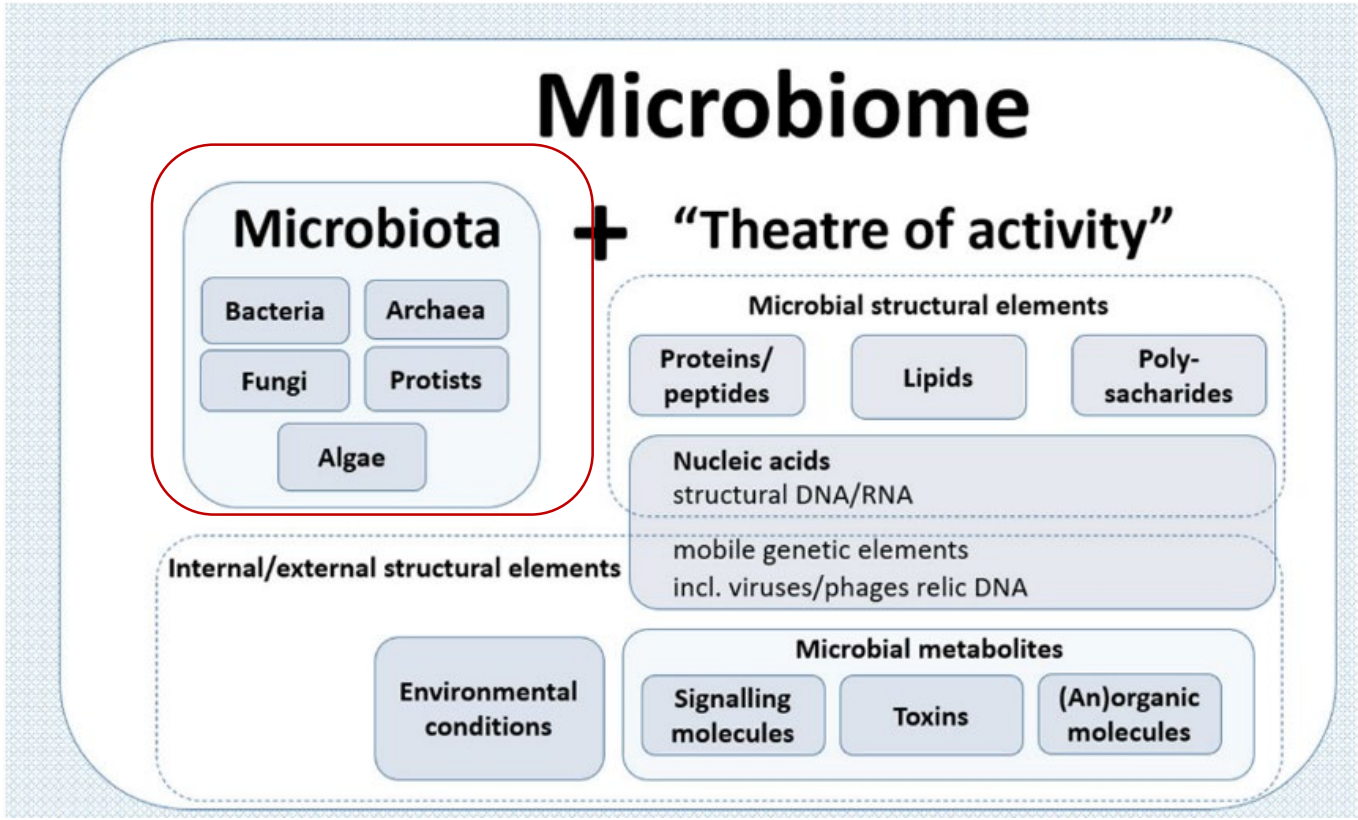
# Microbiome

**Microbiome** = a characteristic microbial community that inhabits a specific, rationally defined habitat with typical physical and chemical conditions

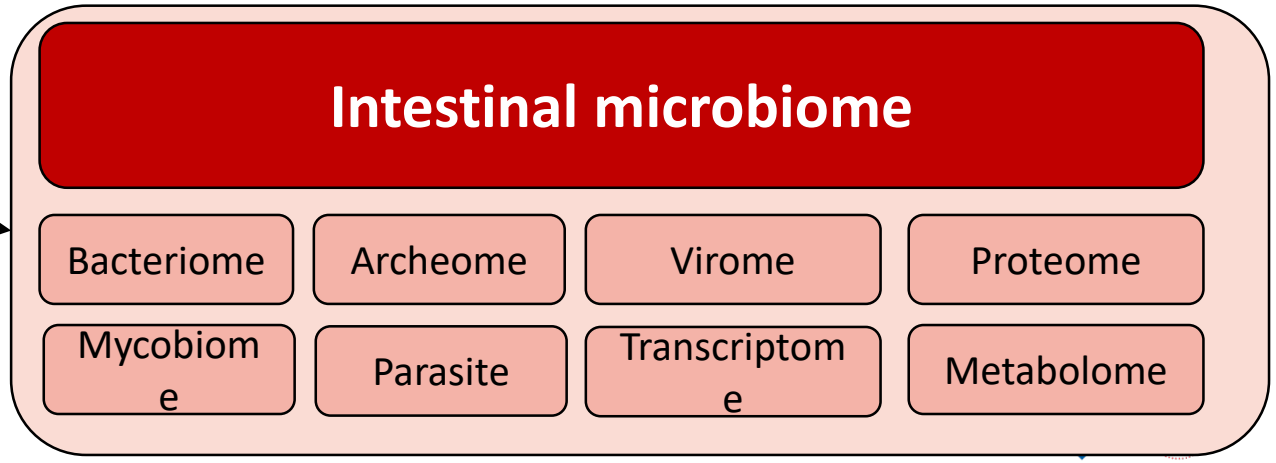
Berg et al, *Microbiome*, 2020




Hou et al, *Sig Transduct Target The, 2022*




Berg et al, *Microbiome*, 2020



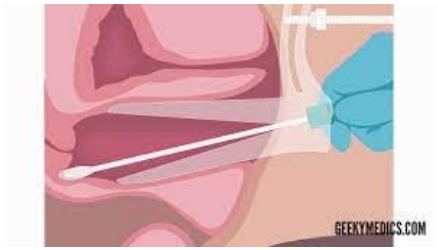
# PHYSIOLOGICAL MICROBIOTA

Coagulase-negative staphylococci, diphtheroids

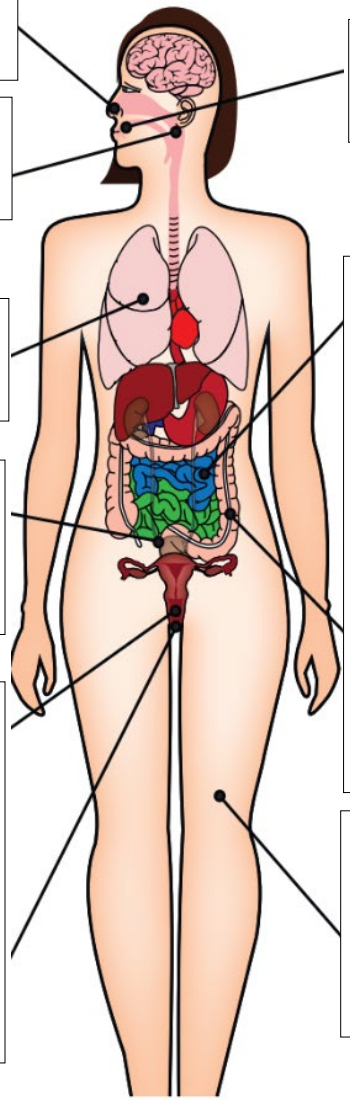
Viridans streptococci, oral neisseria, diphtheroids

Viridial streptococci (swallowed)

CoN staphylococci, diphtheroids, enterococci ($10^3$ and less in urine)

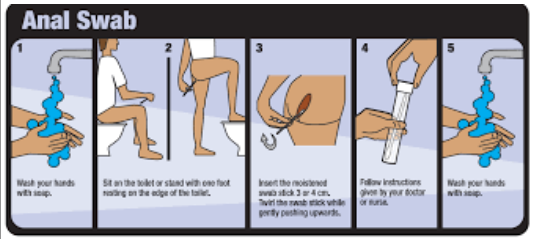



Lactobacilli, diphtheroids CoN staphylococci, viridal streptococci

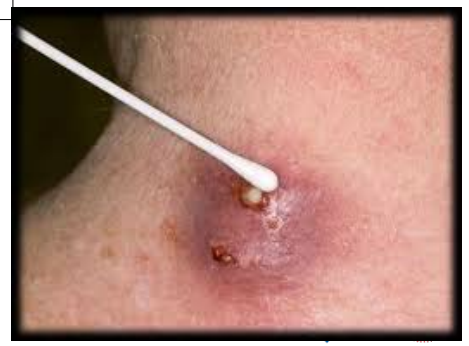


Viridans streptococci, oral neisseria, diphtheroids

Almost everything:
- except GI infections (Campylobacter, Salmonella, Yersinia)
- Toxigenic *C. difficile* and *H. pylori* (in stool)
- Parasites (*Cryptosporidium*, *Entamoeba histolytica* etc.*)* but not *Blastocystis* unless symptoms are present




Coagulase-negative staphylococci, diphtheroids, micrococci (*Cutibacterium acnes*)

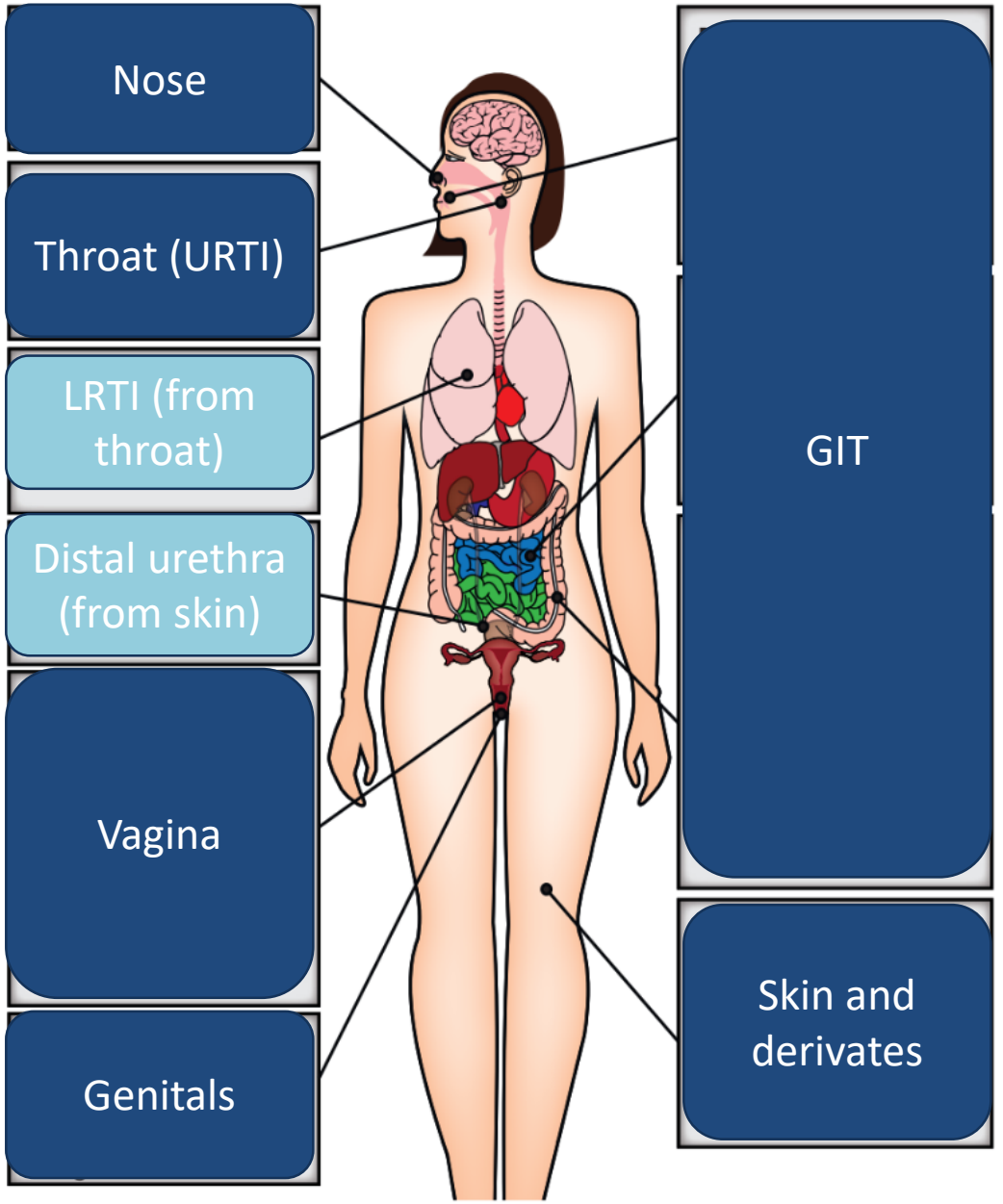


# PHYSIOLOGICAL MICROBIOTA

**Most common materials with physical microbiota**

- Skin swabs
- Nasal and nasopharyngeal swabs
- Throat swab
- Vaginal swab
- Rectal and stool swabs

(Sputum and aspirates from DCD – but this is contamination from HCD)



| Material | Physiological findings |
| --- | --- |
| Skin swab | Coagulase-negative staphylococci, diphtheroids |
| Nasal and nasopharyngeal swabs | Coagulase-negative staphylococci, diphtheroids, *S. aureus* carriage |
| Throat swab | Viridans streptococci and Neisseria, anaerobes |
| Sputum and aspirates from DCD | Almost "sterile" |
| Vaginal swab | Lactobacilli, coagulase-negative staphylococci |
| Rectal swab and stool | Enterobacteria, enterococci, coagulase-negative staphylococci |

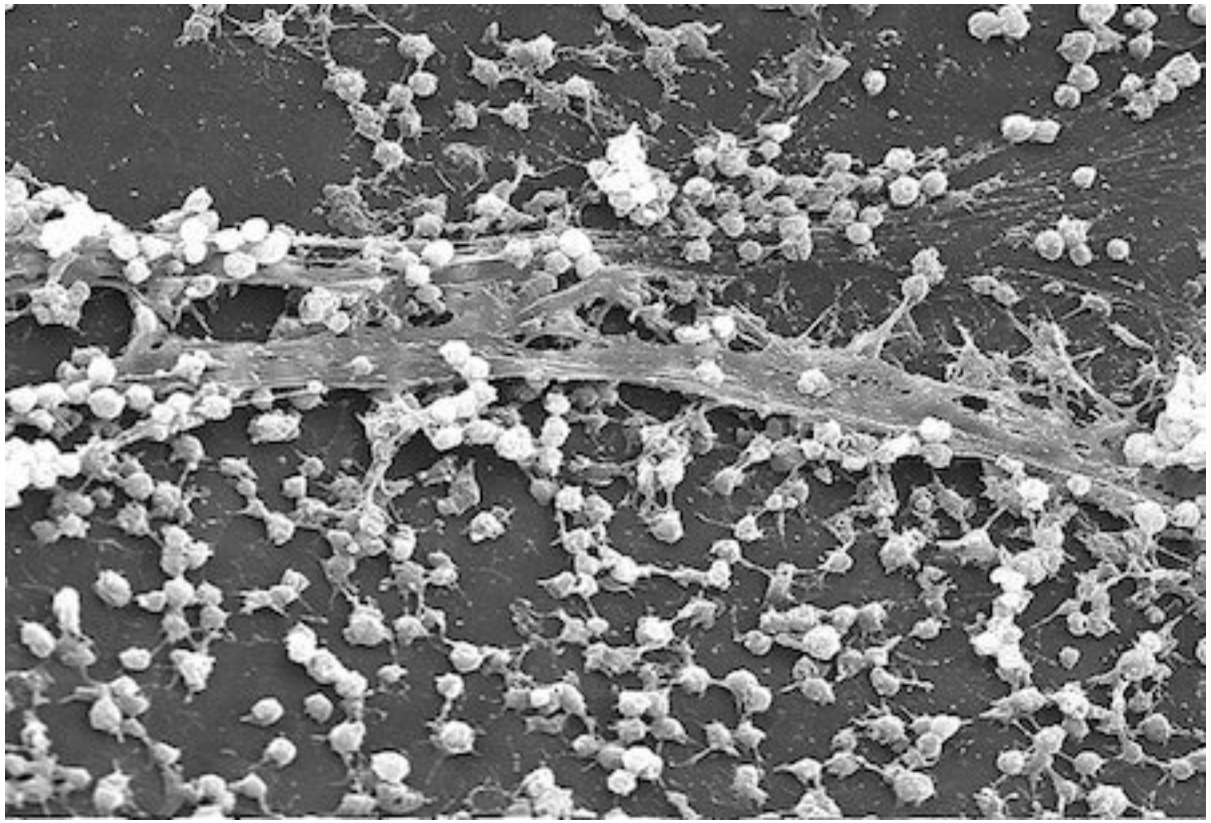
| Material | Physiological findings |
| --- | --- |
| Skin swab | Coagulase-negative staphylococci, diphtheroids |
| Nasal and nasopharyngeal swabs | Coagulase-negative staphylococci, diphtheroids, *S. aureus* carriage |
| Throat swab | Viridans streptococci and Neisseria, anaerobes |
| Sputum and aspirates from DCD | Almost "sterile" |
| Vaginal swab | Lactobacilli, coagulase-negative staphylococci |
| Rectal swab and stool | Enterobacteria, enterococci, coagulase-negative staphylococci |

| Name | Haemolysis on KA | Pathogenicity | |
|---|---|---|---|
| ***S. aureus*** | Yes | +++ | Physiologically in the nose (approx. 20%);<br>Pathogenic potential:<br>- Soft tissues, orthopaedic, pneumonia (! PVL+), UTI, BSI,<br>- Enterotoxicosis, STSS, SSSS |
| ***S. capitis*** | Yes | + | **Physiologically on the skin**;<br>Colonisation of catheters, prostheses and valves |
| ***S. epidermidis*** | No | + | |
| ***S. hominis*** | No | + | |
| ***S. haemolyticus*** | Yes | + | |
| ***S. lugdunensis*** | Yes | ++ | **Physiologically on the skin**;<br>Soft tissues, orthopaedics, endocarditis, BSI |
| ***S. saphrophticus*** | No | ++ | Physiologically on the skin;<br>UTI |

CoNS are not just *S. epidermidis and S. saphrophticus*

# Coagulase-negative staphylococci

- Where does it make sense to address this? In all materials with a risk of **biofilm** formation
  - Blood cultures*
  - Catheters with significant quantities*
  - Orthopaedic materials (tissues, swabs, punctures)
  - Wound swabs from spinal surgery patients
  - Deep wounds with signs of infection



*Staphylococcus aureus* biofilm collected from an infected indwelling catheter *(The Role of Bacterial Biofilms in Antimicrobial Resistance*, ASM, 2023)

# BEWARE OF THESE FINDINGS with physiological microbiota

**Everything in a sterile sample:**

- ❑ Tissues
- ❑ Heart valves
- ❑ Blood cultures (except for one of several bottles, where CoNS – suspected contamination)
- ❑ Joint aspirate
- ❑ CSF

**Among others:**

- ❑ More than $10^3$ CFU from suprapubic puncture
- ❑ STDs pathogens in children
- ❑ *E. coli* from stool sample in children under 2 years of age

FN MOTOL 2 LFUK

# THANK YOU FOR YOUR ATTENTION


Jakub Hurych

Dept of Medical Microbiology, Second Faculty of Medicine, Charles University and Motol University Hospital

jakub.hurych@lfmotol.cuni.cz


2. LÉKAŘSKÁ FAKULTA
UNIVERZITA KARLOVA

FN MOTOL

Univerzita Karlova

Národní institut virologie a bakteriologie