Christian Brechot, MD, PhD

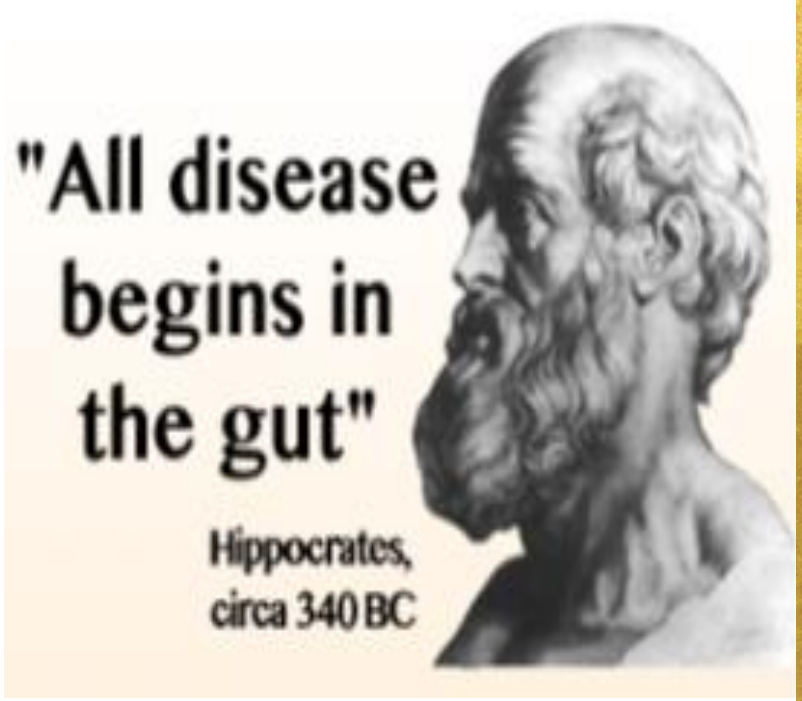
Professor Dept Internal Medicine
Senior Associate Dean for Research in Global Affairs
Associate Vice President for International Partnerships and Innovation
University of South Florida, USA

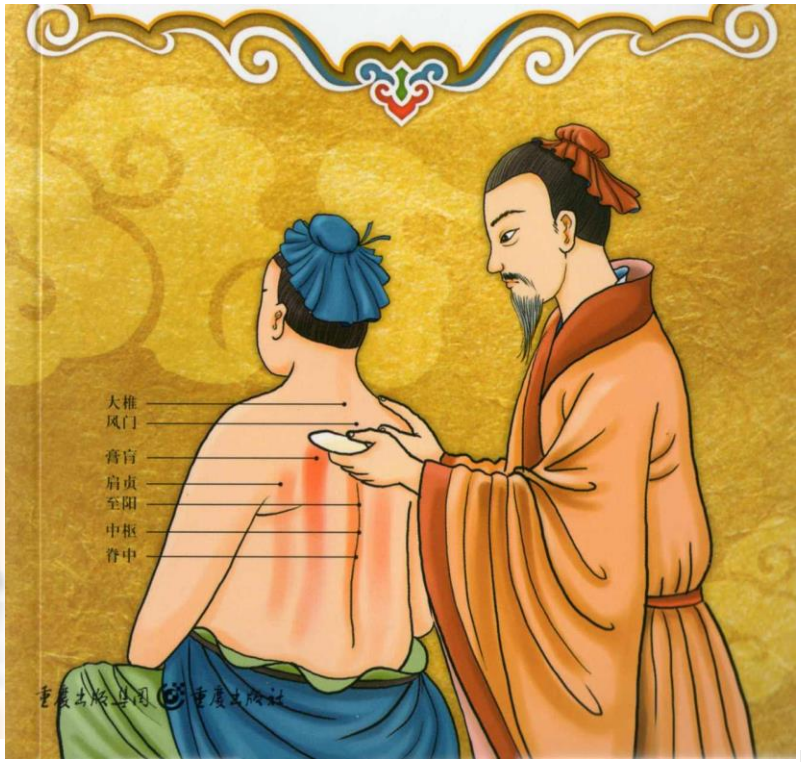
Emeritus President and Board Vice-Chair , Global Virus Network

Disclosures

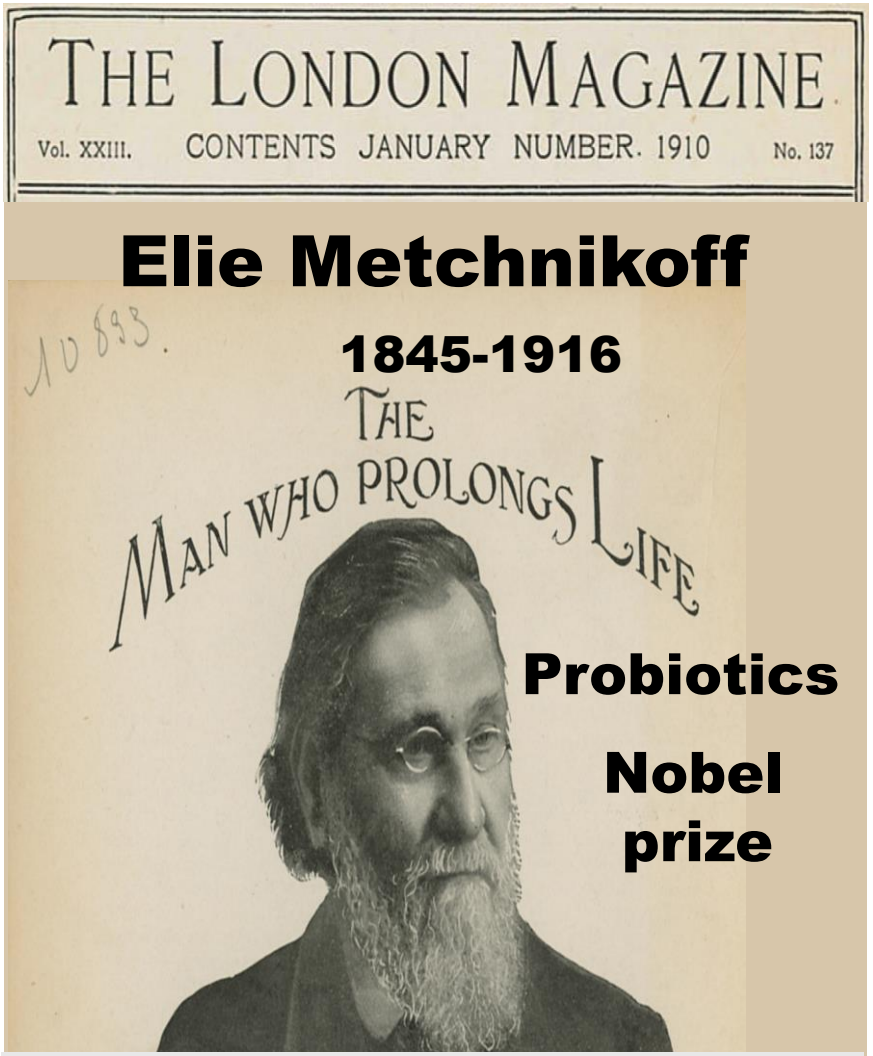
- Chairman and founder: The Healthy Aging Company;
- Medical Director; Theravectys
- Consultant: Geobiomics
- Boards: RareCells, The Healthy Aging Company, Theravectys

The Microbiome: a legacy of medicine and research

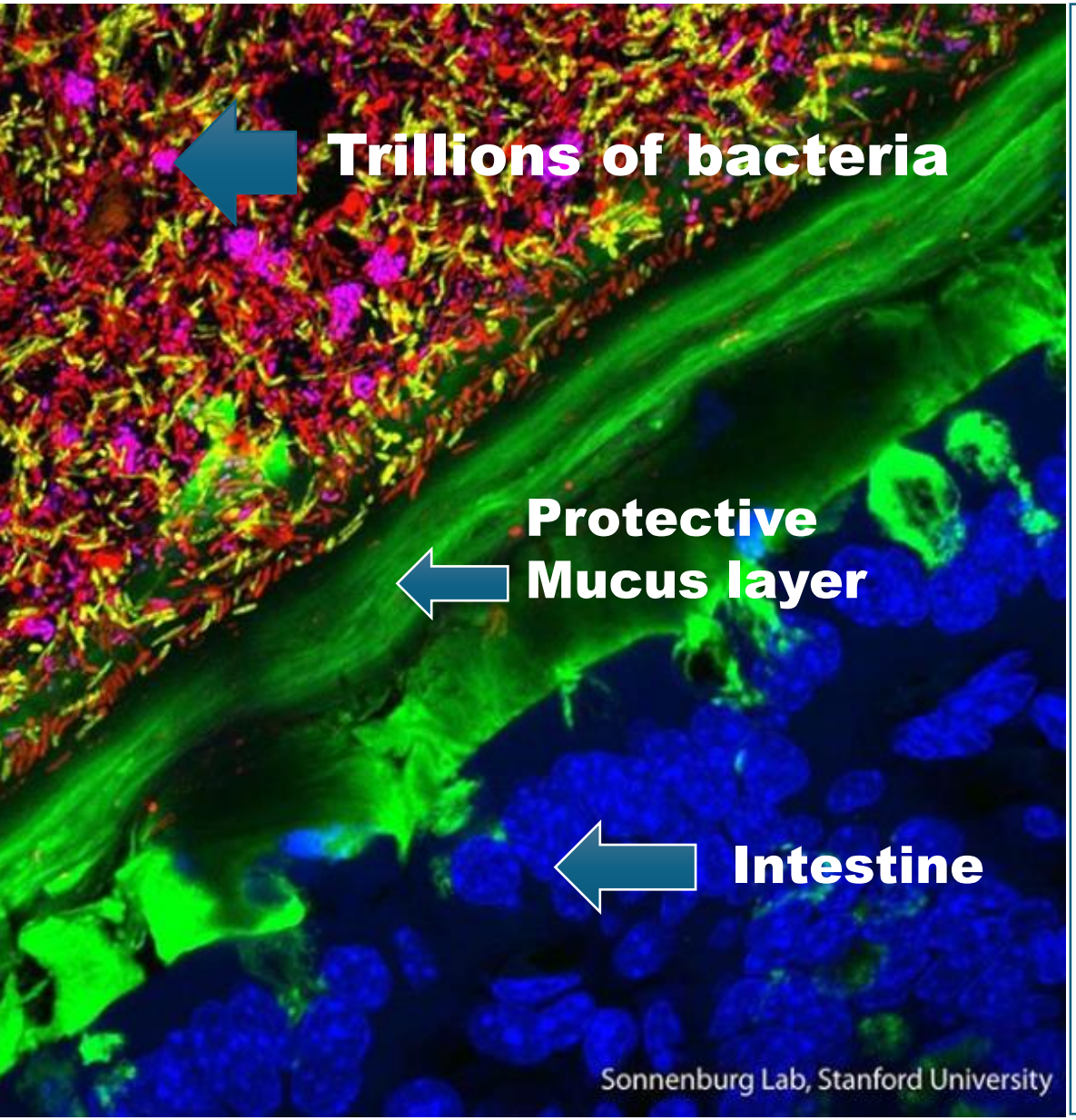




4th century; China:
Ge Hong: “yellow soup.”



We feed in our digestive tract what is causing our chronic poisoning [...]. There is a link between the intestinal flora and senile degeneration



GENETICS
HUMAN GENOME

Symbiotic Evolution

Commensals

Symbionts:

Pathobionts:

Anti-inflammatory

Pro-inflammatory

BACTERIAL and VIRAL
GENOMES: MICROBIOMES

ENVIROMENT

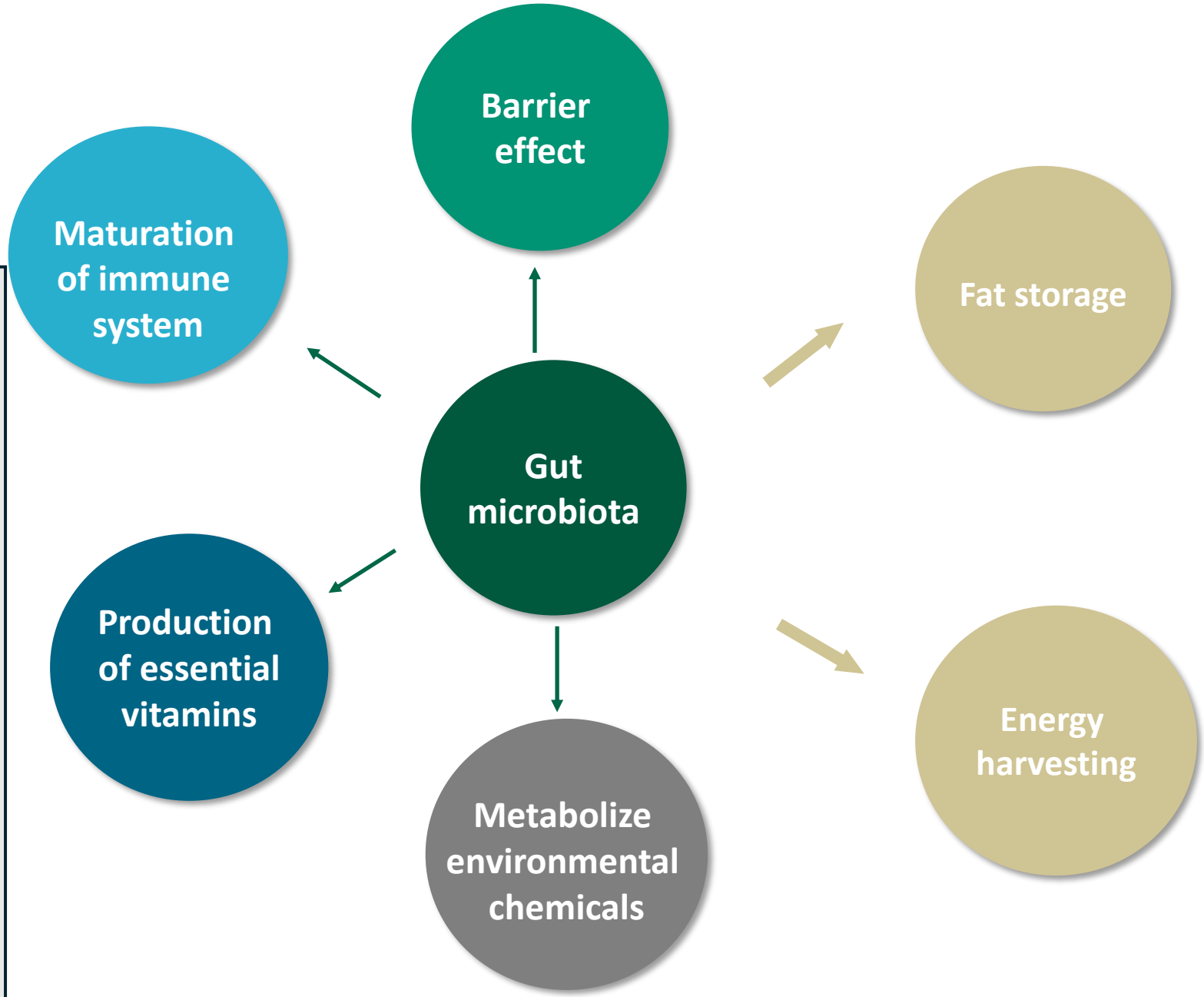
Les microbiomes definissent notre phenotype

Medicaments

- Antibiotiques

-Interactions bilaterales:
Medicament
↕
Microbiome

Ex:
Metformine
Statines
L-DOPA



Le microbiome humain integre les effets de l'environnement sur le vieillissement.

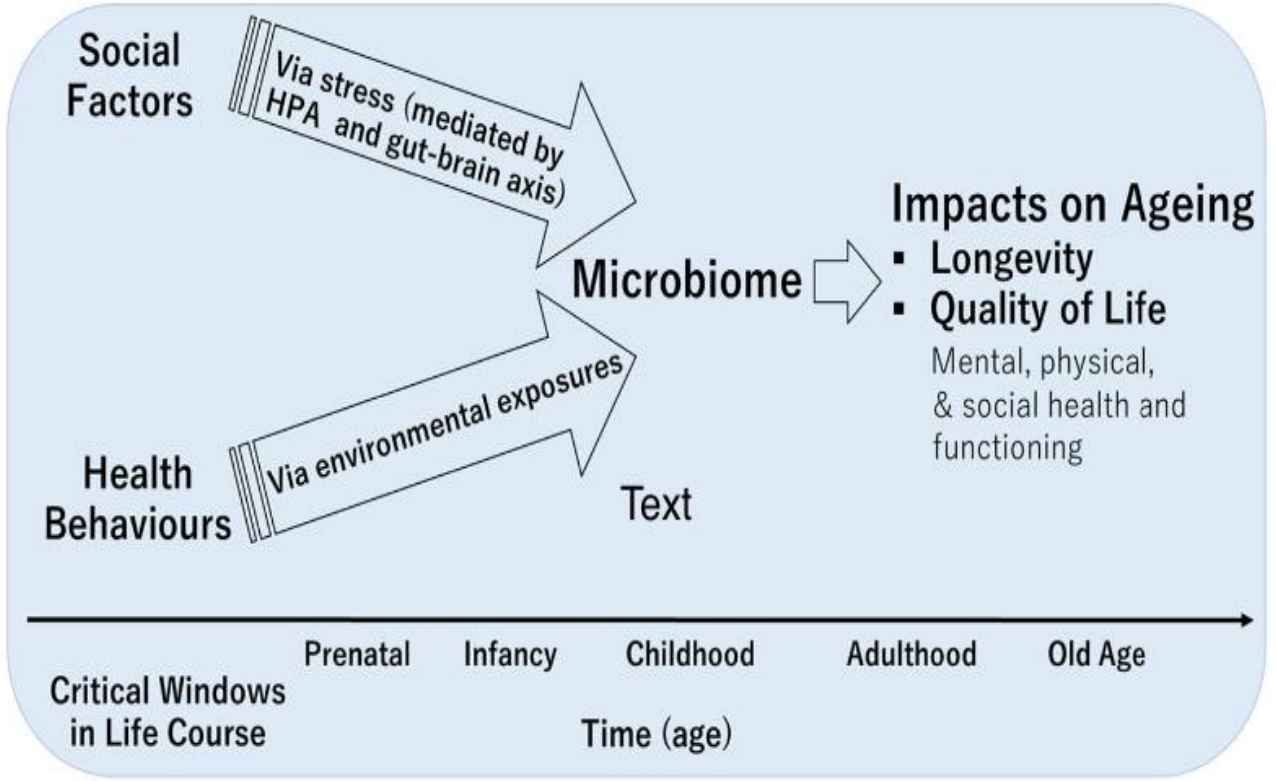
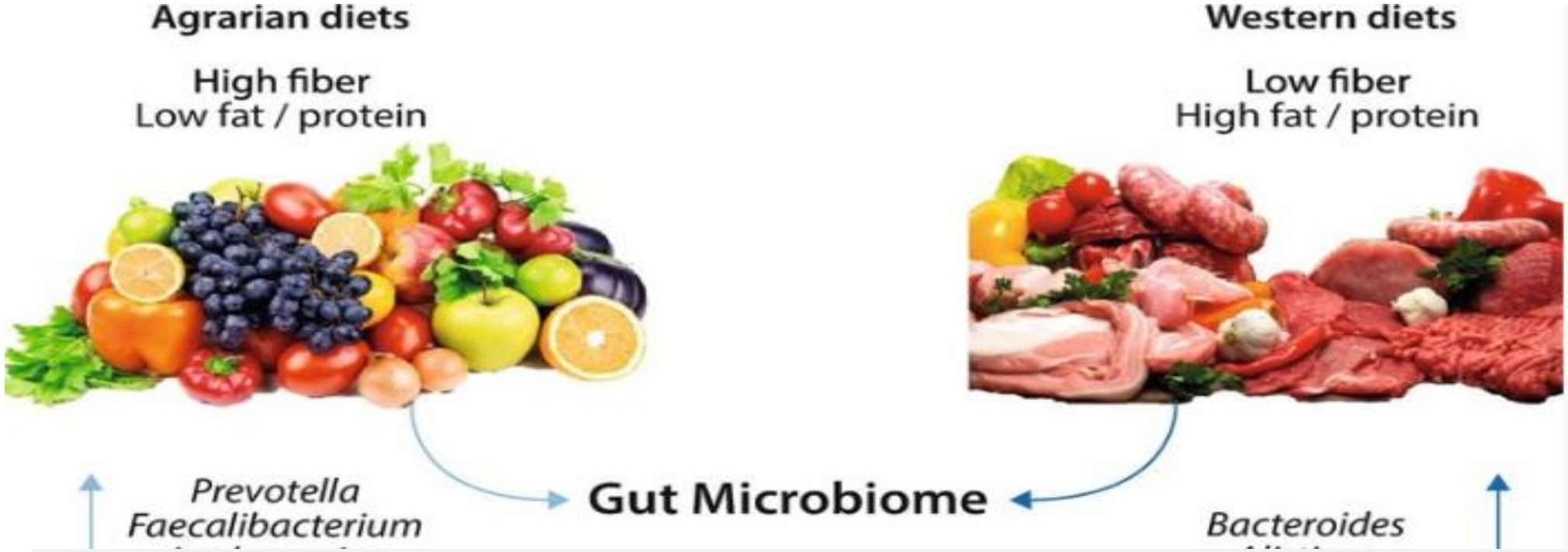


Figure 2. Conceptual model of how social factors (e.g., socioeconomic status, work–life balance, expectations, and beliefs) and health behaviors (e.g., diet, exercise, and sleep) may impact longevity and quality of life via the microbiome. Some effects may be bidirectional, with aging impacting the microbiome and the microbiome impacting the biosocial factors (e.g., eating behavior, sleep, and health status). These effects may differ throughout the life course, at different developmental windows, and may also be moderated by sex hormones.

Finlay et al, 2019

L’alimentation est un element majeur de la composition du microbiome intestinal

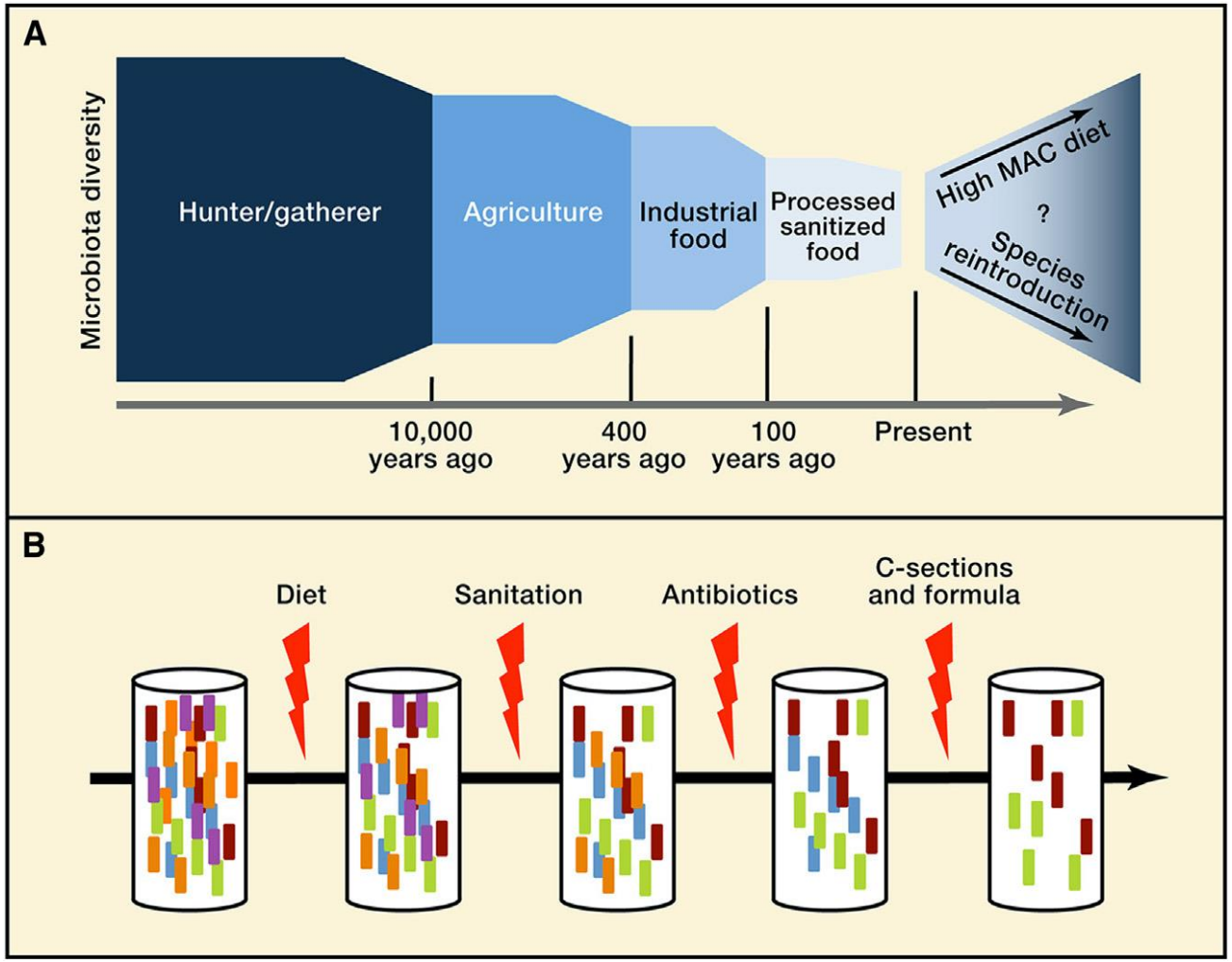


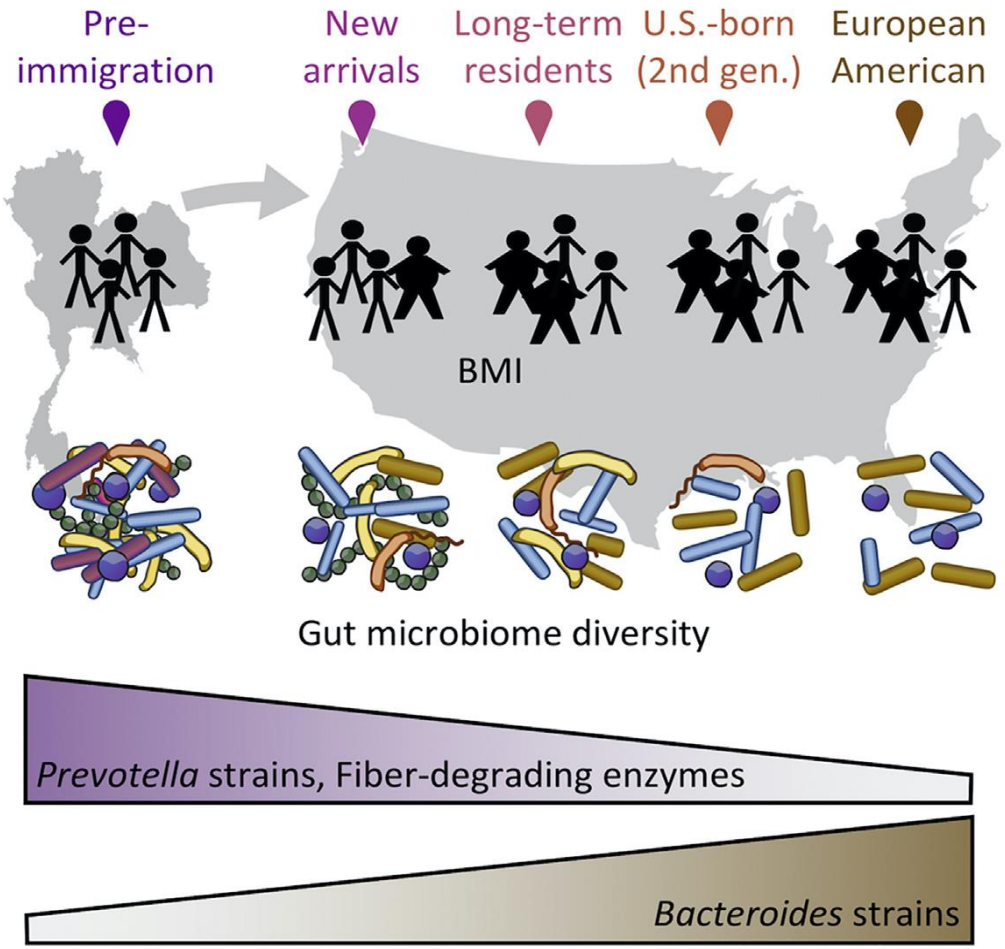
Fermentation

Externe (Yoghourts etc..)

Interne: Microbiome de l’intestin (colon)

Des évolutions majeures du microbiome au cours de l'evolution de Homo Sapiens

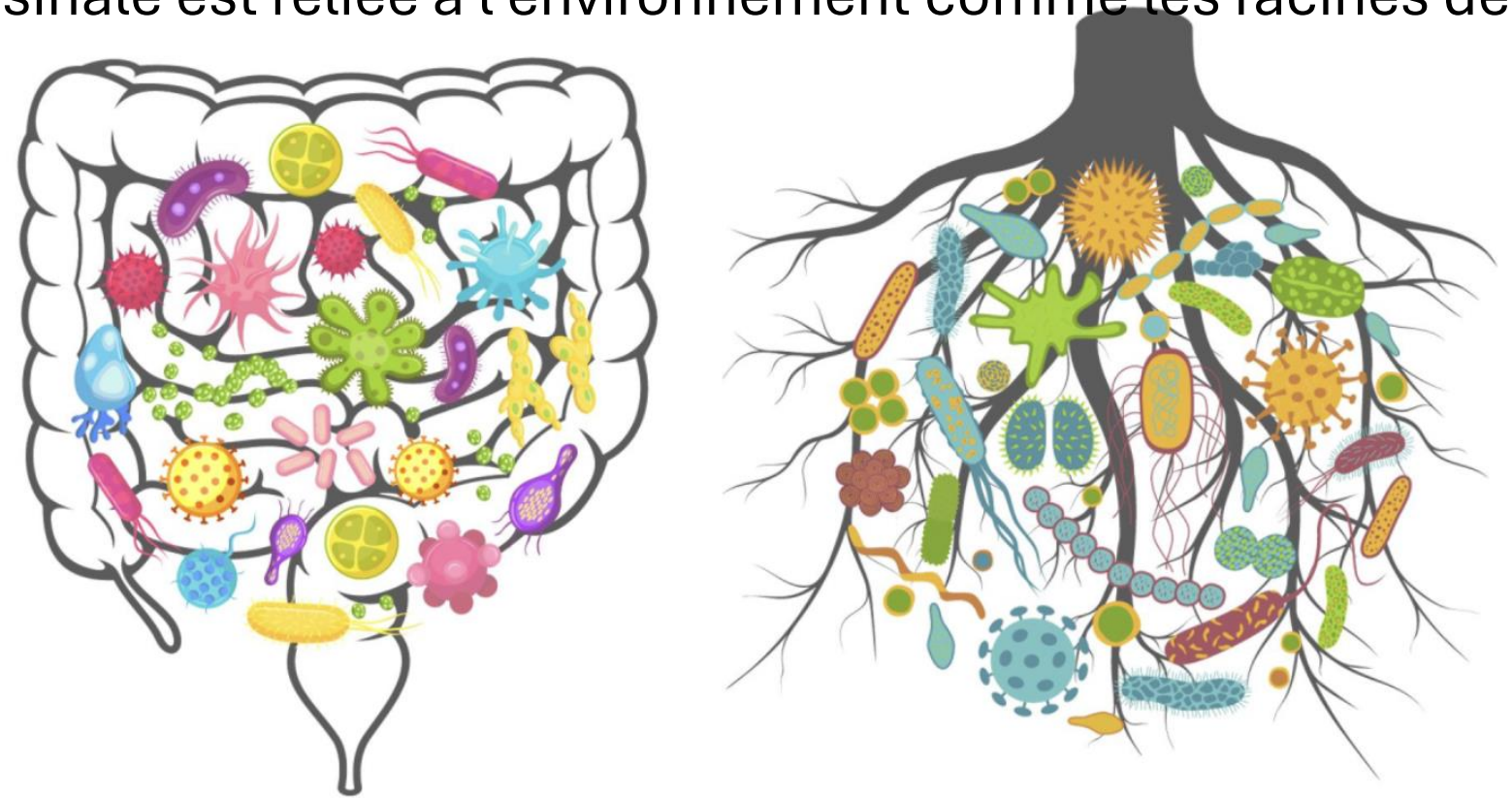




Vangay et al Cell 2016

Microbiome intestinal humain, Microbiomes du sol: ecosystemes differents, meme principes.

La muqueuse intesinale est reliee a l’environnement comme les racines des arbres



Gut Microbiome, Soil Microbiome: Different Ecosystems, Same Principles

Visit ›

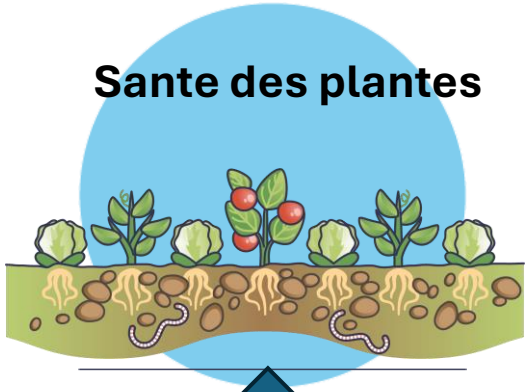
Medium.com Oct 2023

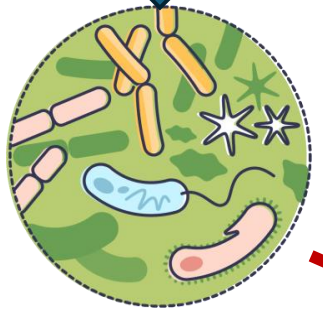
Habitat	Number of Cells per g	Number of Cells per mL	Species Diversity
Soil	10^7–10^9 [22]	10^{10} [23]	4×10^3–5×10^4 species per g soil [22]
Sewage		10^9 [24,25]	25 per mL [24]
Marine water		10^5–10^6 [18]	
Air		1 (=10^6 cells/m^3) [17]	
Human gut	10^{12} [26] 10^{11} [28]		4×10^2 species per g feces [27] 5×10^3 species per g feces [18]
Colon (large intestine)		10^{11} [29] 10^{11}–10^{12} [30]	
Ileum (lower small intestine)		10^8 [29]	
Duodenum and jejunum (upper small intestine)		10^3–10^4 [29]	
Human mouth (saliva)		10^8 [18]	

Sante de l'animal

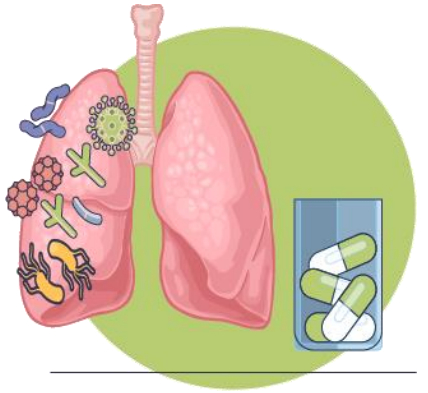
Sante des plantes

Sante humaine





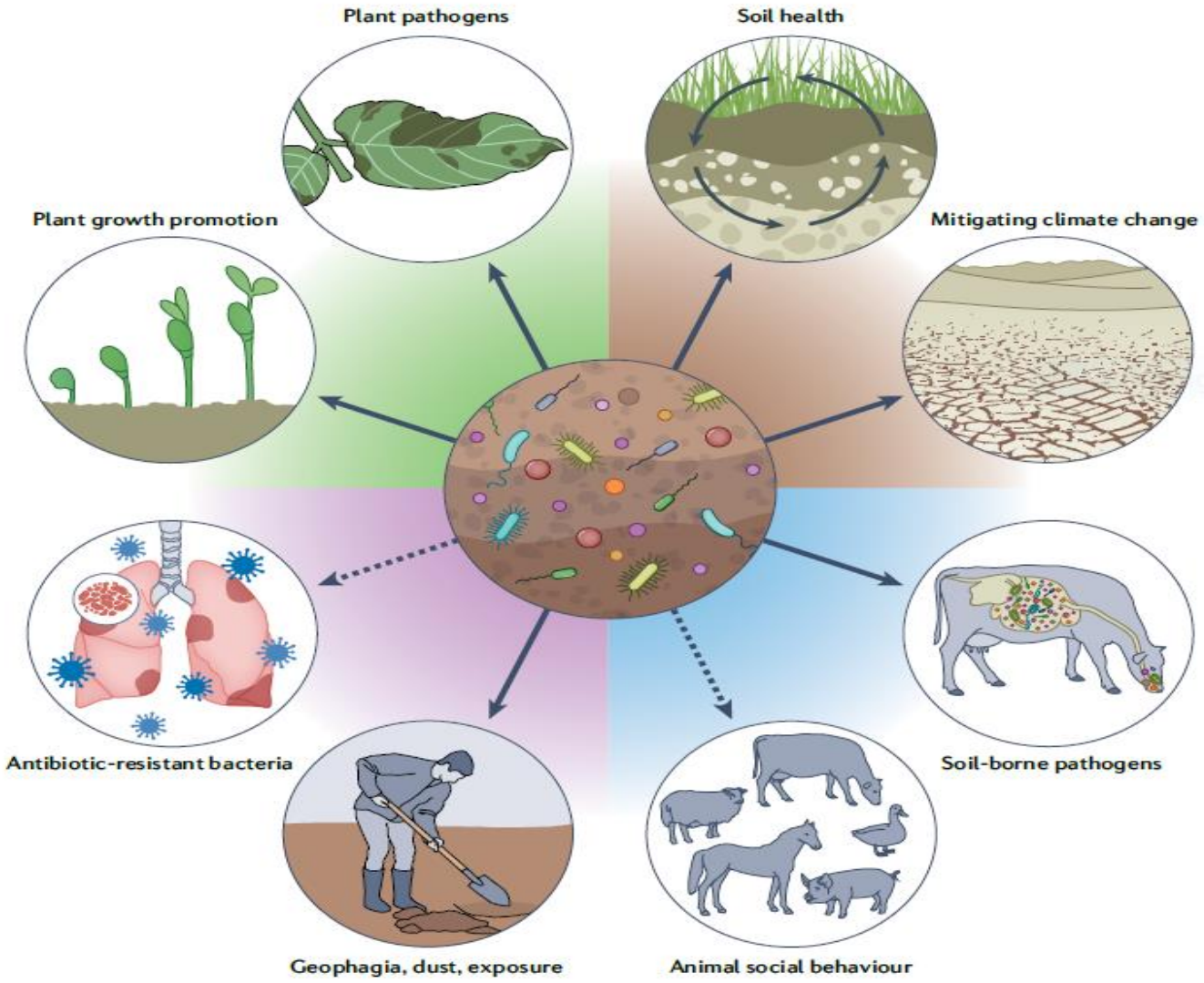
Microbiome du sol



Bacteries pathogenes pour les plantes

Resistance aux antibiotiques

Les microbiomes du sol sont des acteurs majeurs de “Global and One Health”



Soil microbiomes and one health

Samiran Banerjee1 ✉ *and Marcel G. A. van der Heijden* Nature Reviews | **Microbiology 2022**

Analyse des microbiomes

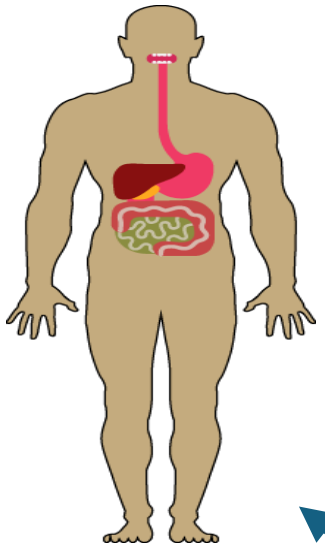
- **Trois parametres:**

Diversite
Quantite de bacteries
Sequences et fonction

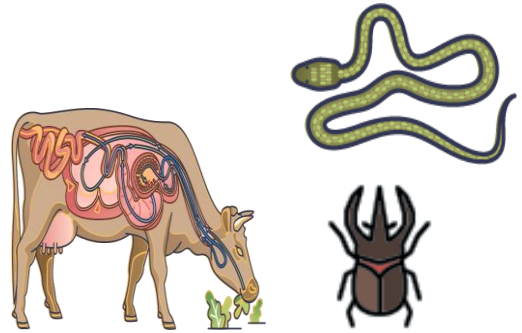
Analyses descriptives
Et fonctionnelles:
ARN 16 S
Metagenomique
Culturomique
Metabolomique

Intervention
Transplantation de microbiote intestinal
Animaux Germe Free
Gnotobiotic mice

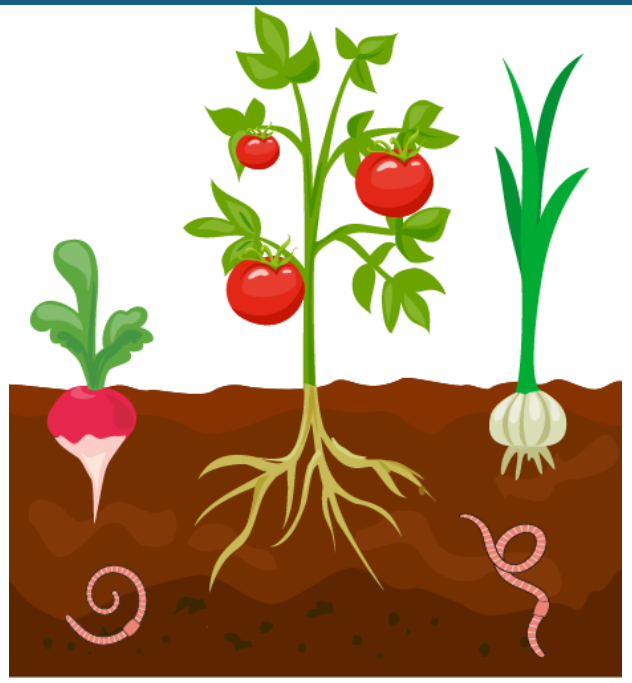
Inoculation de bacteries dans les sols
Ingenierie des microbiomes des sols



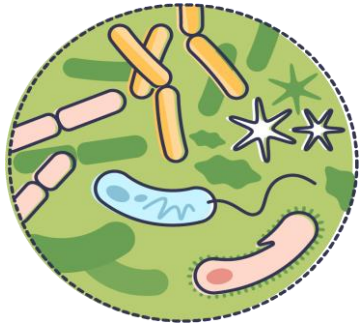
Nourriture



Nourriture

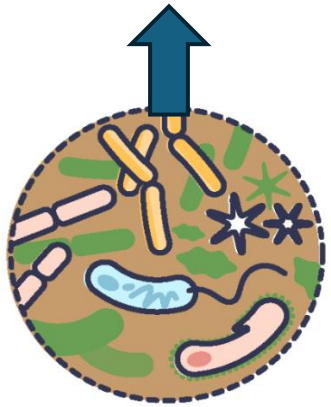


Nourriture



Microbiome humain

Poussieres
Geophagie



Microbiome du sol et des plantes

Poussieres
Geophagie

Microbiome de l’animal

GUT MICROBES
2023, VOL. 15, NO. 2, 2258565
https://doi.org/10.1080/19490976.2023.2258565

Taylor & Francis
Taylor & Francis Group

RESEARCH PAPER

OPEN ACCESS Check for updates

The edible plant microbiome: evidence for the occurrence of fruit and vegetable bacteria in the human gut

Wisnu Adi Wicaksono[a], Tomislav Cernava[a,b], Birgit Wassermann[a], Ahmed Abdelfattah[a,c], Maria J. Soto-Giron[d], Gerardo V. Toledo[d], Suvi M. Virtanen[e,f,g,h], Mikael Knip[i,j], Heikki Hyöty[k], and Gabriele Berg[a,c,l]

[a]Institute of Environmental Biotechnology, Graz University of Technology, Graz, Austria; [b]School of Biological Sciences, Faculty of Environmental and Life Sciences, University of Southampton, Southampton, UK; [c]Leibniz Institute for Agricultural Engineering and Bioeconomy (ATB), Potsdam, Germany; [d]Solarea Bio, Cambridge, MA, USA; [e]Finnish Institute for Health and Welfare, Helsinki, Finland; [f]Center for Child Health Research, Tampere University and Tampere University Hospital, Tampere, Finland; [g]Faculty of Social Sciences, Tampere University, Tampere, Finland; [h]Research, Development and Innovation Center, Tampere University Hospital, Tampere, Finland; [i]Research Program for Clinical and Molecular Metabolism, Faculty of Medicine, University of Helsinki, Helsinki, Finland; [j]Pediatric Research Center, Children's Hospital, University of Helsinki, Helsinki, Finland; [k]Faculty of Medicine and Health Technology, Tampere University, and Fimlab Laboratories, Tampere, Finland; [l]Institute for Biochemistry and Biology, University of Potsdam, Potsdam, Germany

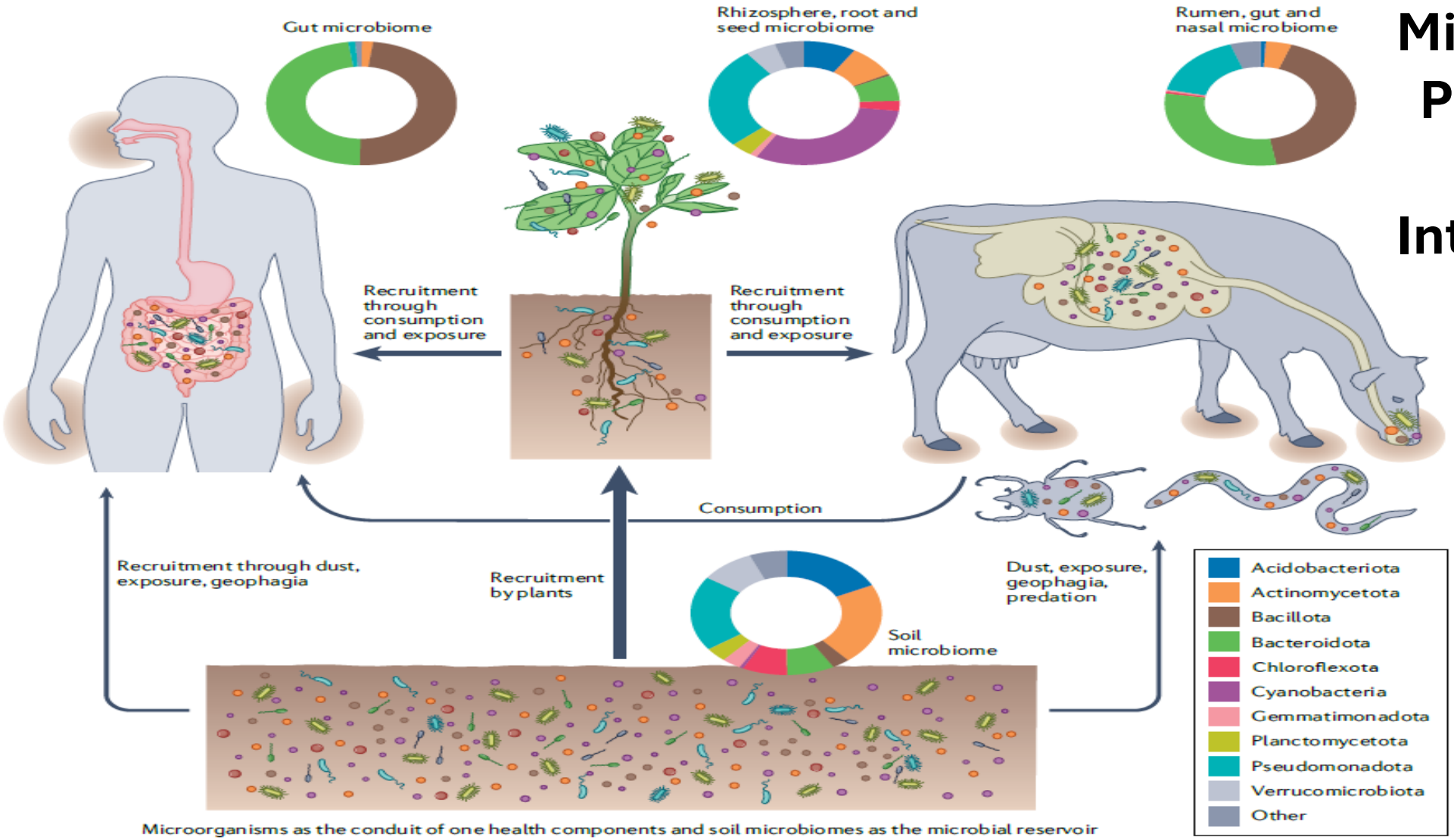
ABSTRACT

Diversity of the gut microbiota is crucial for human health. However, whether fruit and vegetable associated bacteria contribute to overall gut bacterial diversity is still unknown. We reconstructed metagenome-assembled genomes from 156 fruit and vegetable metagenomes to investigate the prevalence of associated bacteria in 2,426 publicly available gut metagenomes. The microbiomes of fresh fruits and vegetables and the human gut are represented by members in common such as *Enterobacterales, Burkholderiales*, and *Lactobacillales*. Exposure to bacteria via fruit and vegetable consumption potentially has a beneficial impact on the functional diversity of gut microbiota particularly due to the presence of putative health-promoting genes for the production of vitamin and short-chain fatty acids. In the human gut, they were consistently present, although at a low abundance, approx. 2.2%. Host age, vegetable consumption frequency, and the diversity of plants consumed were drivers favoring a higher proportion. Overall, these results provide one of the primary links between the human microbiome and the environmental microbiome. This study revealed evidence that fruit and vegetable-derived microbes could be found in the human gut and contribute to gut microbiome diversity.

ARTICLE HISTORY
Received 19 June 2023
Revised 30 August 2023
Accepted 8 September 2023

KEYWORDS
Plant microbiome; fruit; and vegetable; metagenome-assembled genomes; gut microbiome

Les microbiomes du sol, des animaux et des humains sont directement connectes



Microorganisms as the conduit of one health components and soil microbiomes as the microbial reservoir

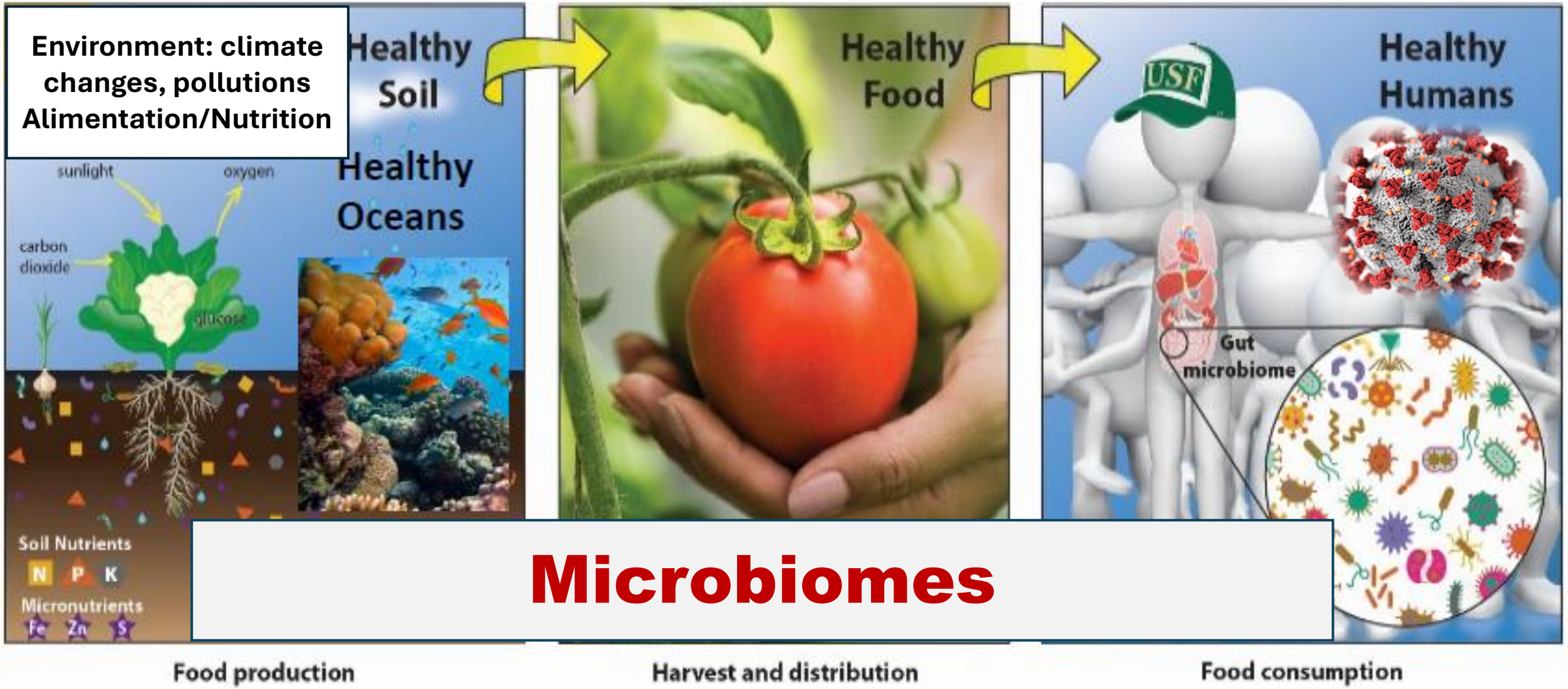
Microbiomes Peau et sol

Intestin et sol

Soil microbiomes and one health

Samiran Banerjee1 ✉ *and Marcel G. A. van der Heijden* Nature Reviews | **Microbiology 2022**

Les microbiomes integrent les effets de l'environnement et de l'alimentation/nutrition



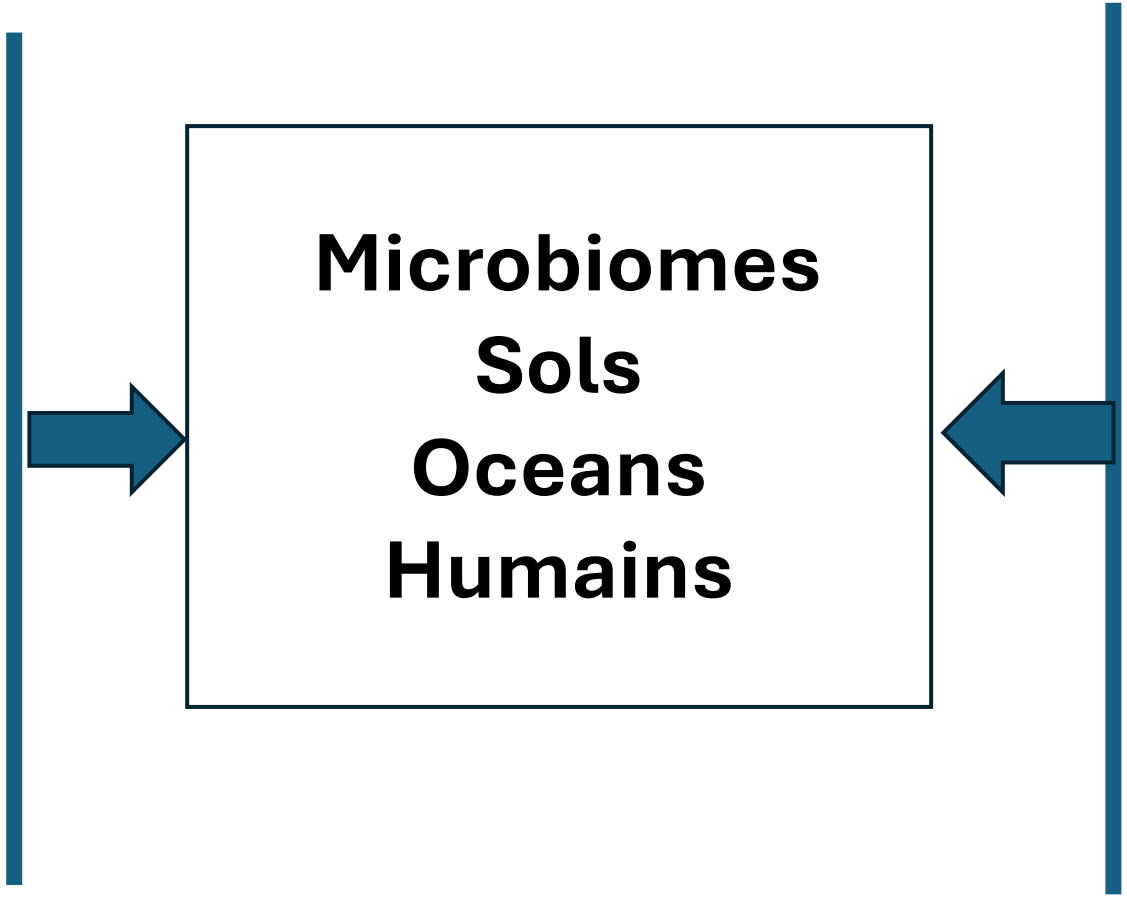
Alterations des microbiomes

Alimentation:
"Western" style
Aliments ultratransformes

Medicaments
Antibiotiques
Metformine
Etc..

Hygiene

Pollution



Agriculture intensive:
Intrants, Engrais, etc.
Labours
Deforestation
Disparition des haies

Antibiotiques

Dechets:
Plastiques, microplastiques

Solutions?

Interventions?

Ingenierie des sols basee sur les microbiomes

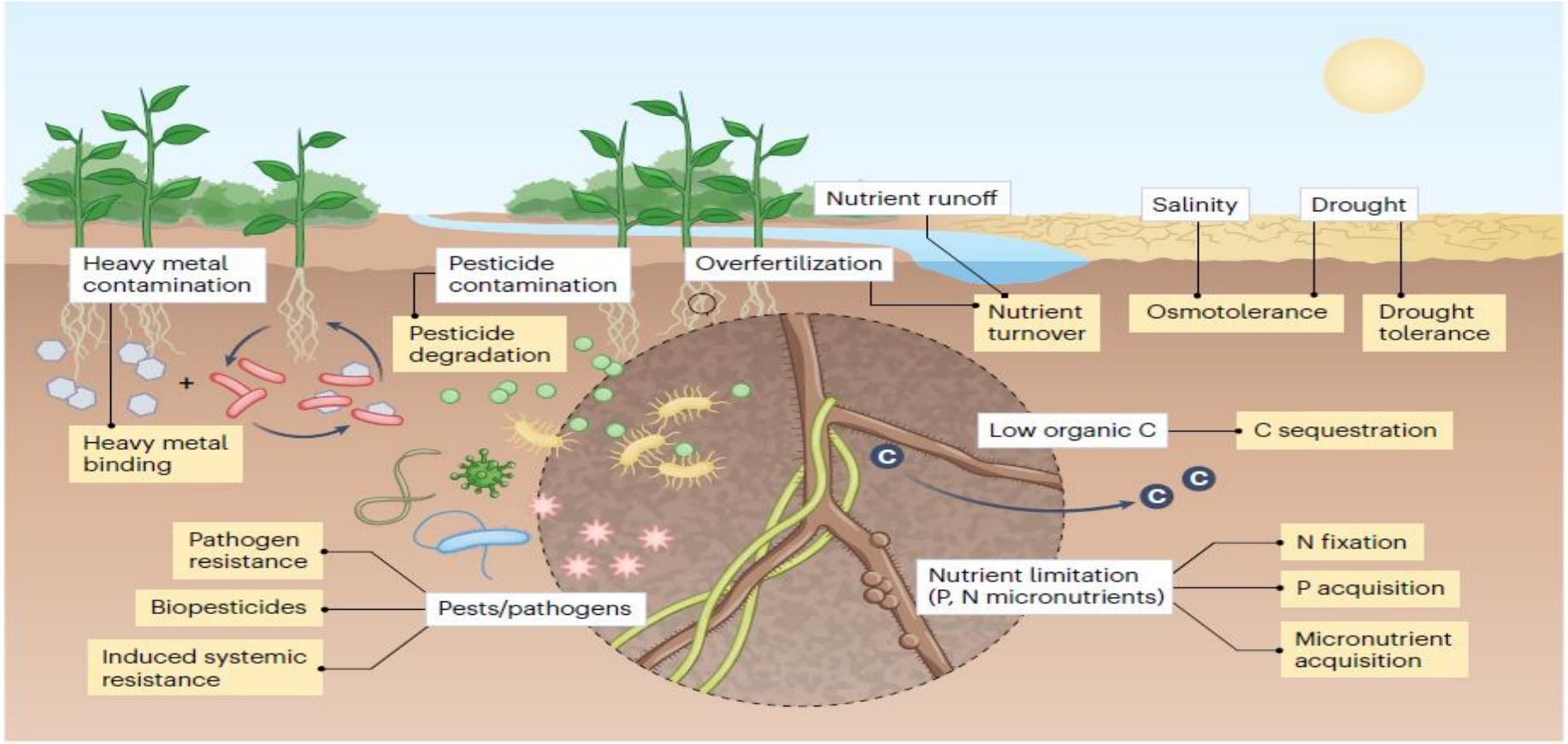


Fig. 1 | Soil microorganisms carry out key ecosystem services and have the potential to help mitigate a variety of deleterious anthropogenic impacts on soil ecosystems. White-boxed text indicates different deleterious anthropogenic impacts. Yellow-boxed text indicates different biological mitigation strategies. The rhizosphere is highlighted in the circle in the center, with associated mycorrhizal fungi (green threads), nitrogen-fixing nodule-forming bacteria (brown nodules on the root) and a variety of root-associated microorganisms that are indicated by the pink and yellow symbols. Top left, heavy metals (gray hexagons) that can be bound by heavy metal-binding bacteria (red rods) and pesticides (light green dots) that can be degraded by rhizosphere microorganisms. Bottom left, potential pests that include viruses (dark green sphere with knobs), bacteria (blue rod) and nematodes (green ribbon). C, carbon; N, nitrogen; P, phosphorus.

Soil microbiome engineering for sustainability in a changing environment. Janet K. Jansson , Ryan McClure & Robert G. Egbert **nature biotechnology October 2023**

Prebiotiques

Probiotiques

Postbiotiques

Medecine des sols

Medecine des hommes

Inoculation de bacteries dans les sols (Rhizospheres)

Ingenierie du sol

Bacteries isolees ou “consortia”?

Bacteries synthetiques?

Devenir des inoculums? Evaluation++
Cooperation avec les autres microorganismes
Impact de la localization geographique
Facteurs predictifs?

L’evolution des probiotiques

- **“Classiques” :**
  Lactobacillus
  Bifidobacterium

- **Nouvelle generation:**
  Akkermansia

  Faecalibacterium prauznitzii

- **Futur?:**

Bacteries synthetiques?
Consortia?
Nouvelles approches pour identifier des candidats?

Nouvelles approaches pour identifier de futurs candidats pre-pro-postbiotiques

Oscillibacter

⬇

Metabolisme du Cholesterol

⬇

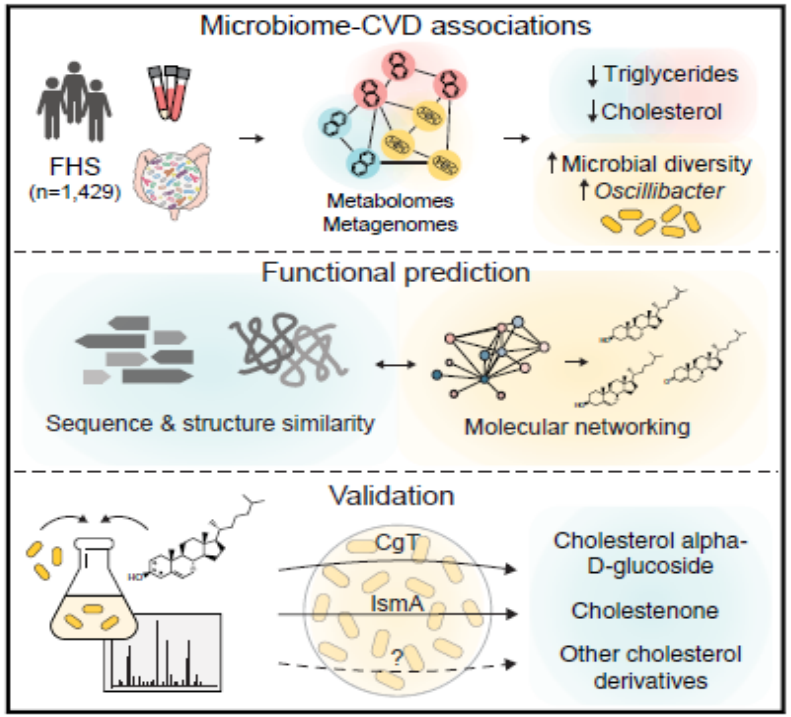
Maladies cardiovasculaires et metaboliques?

Cell

Article

Gut microbiome and metabolome profiling in Framingham heart study reveals cholesterol-metabolizing bacteria

Graphical abstract



Authors

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Correspondence

xavier@molbio.mgh.harvard.edu

In brief

The gut microbiomes and metabolomes of 1,429 participants from the Framingham Heart Study were comprehensively profiled toward the identification of associations between microbes, metabolites, and cardiovascular disease markers.

Transplantation de microbiote intestinal

Clostridium Difficile
Maladies inflammatoires du tube digestif?
Maladies Metaboliques?
Autres?

Medecine des sols

Medecine des hommes

Sols “suppressifs”

Transplantation

Bacteries isolees ou “cocktails”?

Bacteries synthetiques?

Heterogeneite geographique

Analyse des donnees (bioinformatique)

Devenir des inoculums?
Facteurs predictifs?

Etudes interventionnelles

SCIENCE ADVANCES | RESEARCH ARTICLE 2024

ENVIRONMENTAL STUDIES

Biodiversity intervention enhances immune regulation and health-associated commensal microbiota among daycare children

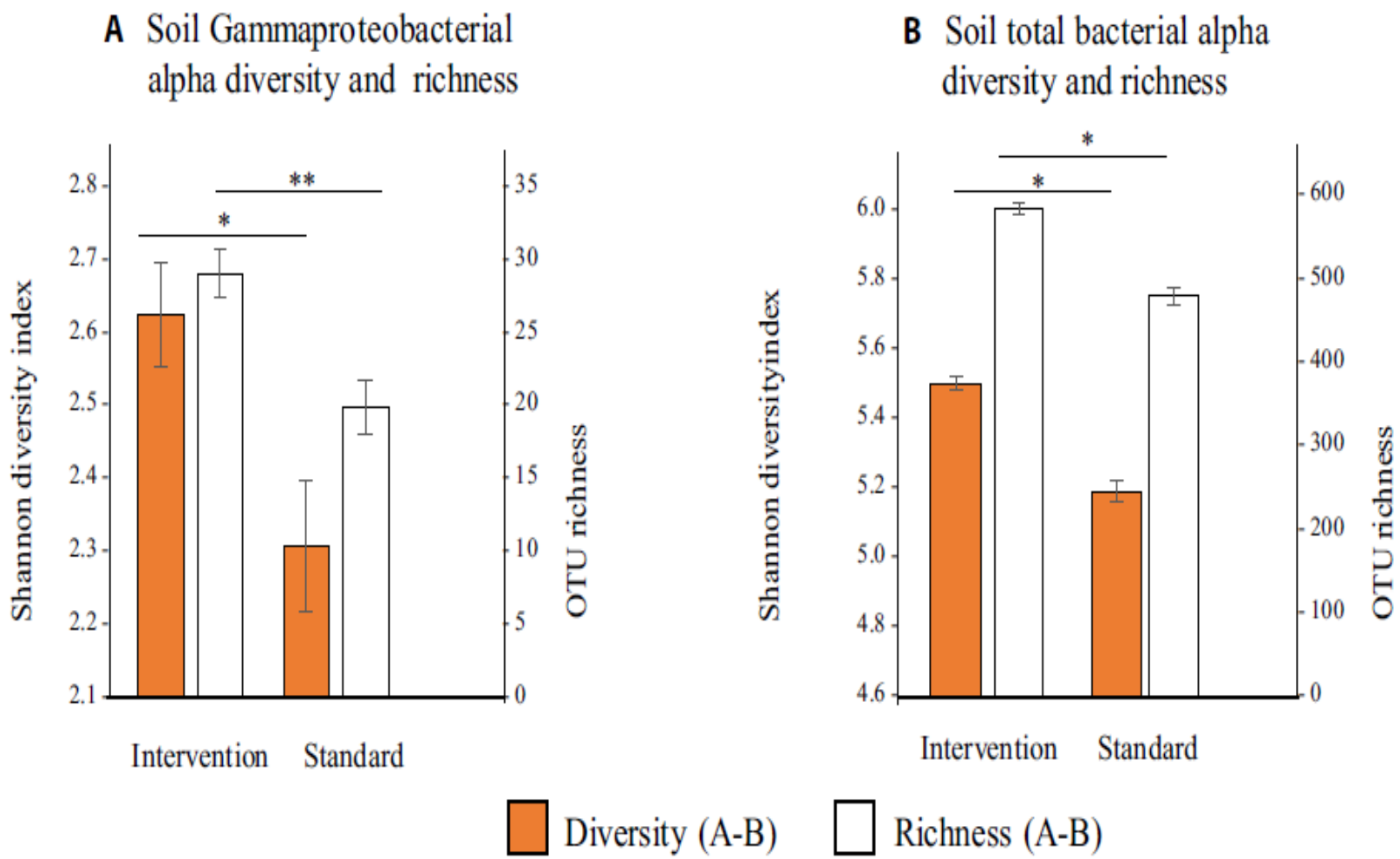
Marja I. Roslund1, Riikka Puhakka1, Mira Grönroos1, Noora Nurminen2, Sami Oikarinen2, Ahmad M. Gazali3*, Ondřej Cinek4, Lenka Kramná4, Nathan Siter5, Heli K. Vari1, Laura Soininen1, Anirudra Parajuli1, Juho Rajaniemi5, Tuure Kinnunen3,6, Olli H. Laitinen2, Heikki Hyöty2, Aki Sinkkonen1,7†, ADELE research group‡

Etudes interventionnelles

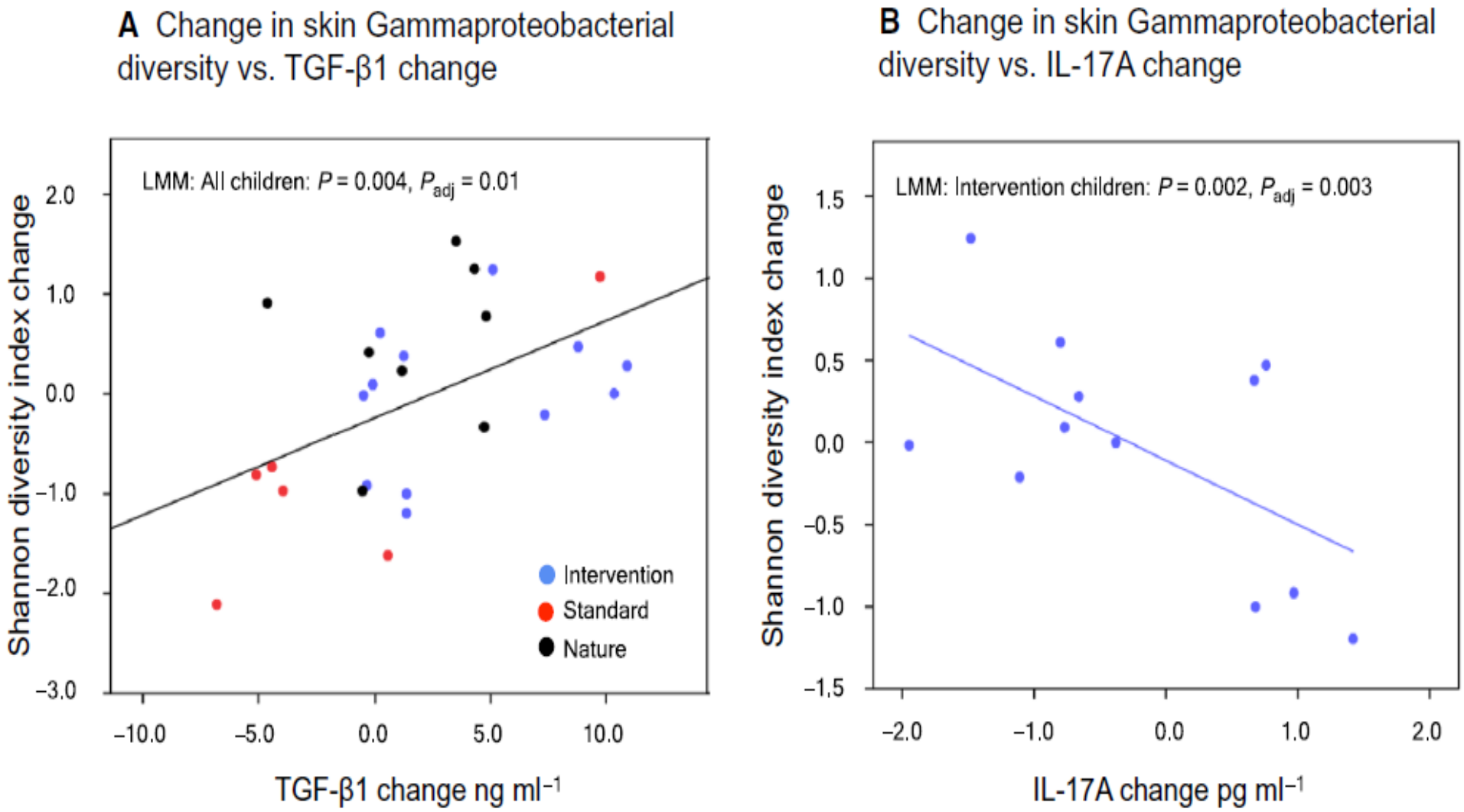
Table 1. Number, age, gender, and reasons for exclusion of study participants in each daycare group and in total. Each child spent daily (Monday to Friday) approximately 1.5 hours outdoors.

	Intervention* 4 centers	Standard† 3 centers	Nature‡ 3 centers	Total children 10 centers
Total children	36	16	23	75
Boys	18	9	10	37
Girls	18	7	13	38
Age§	4.3 ± 0.6	4.9 ± 0.3	4.7 ± 0.5	4.6 ± 0.6
Excluded‖				
Antibiotic users	2	1	0	3
Probiotic users	1	0	1	2
Medication users	3	2	3	8

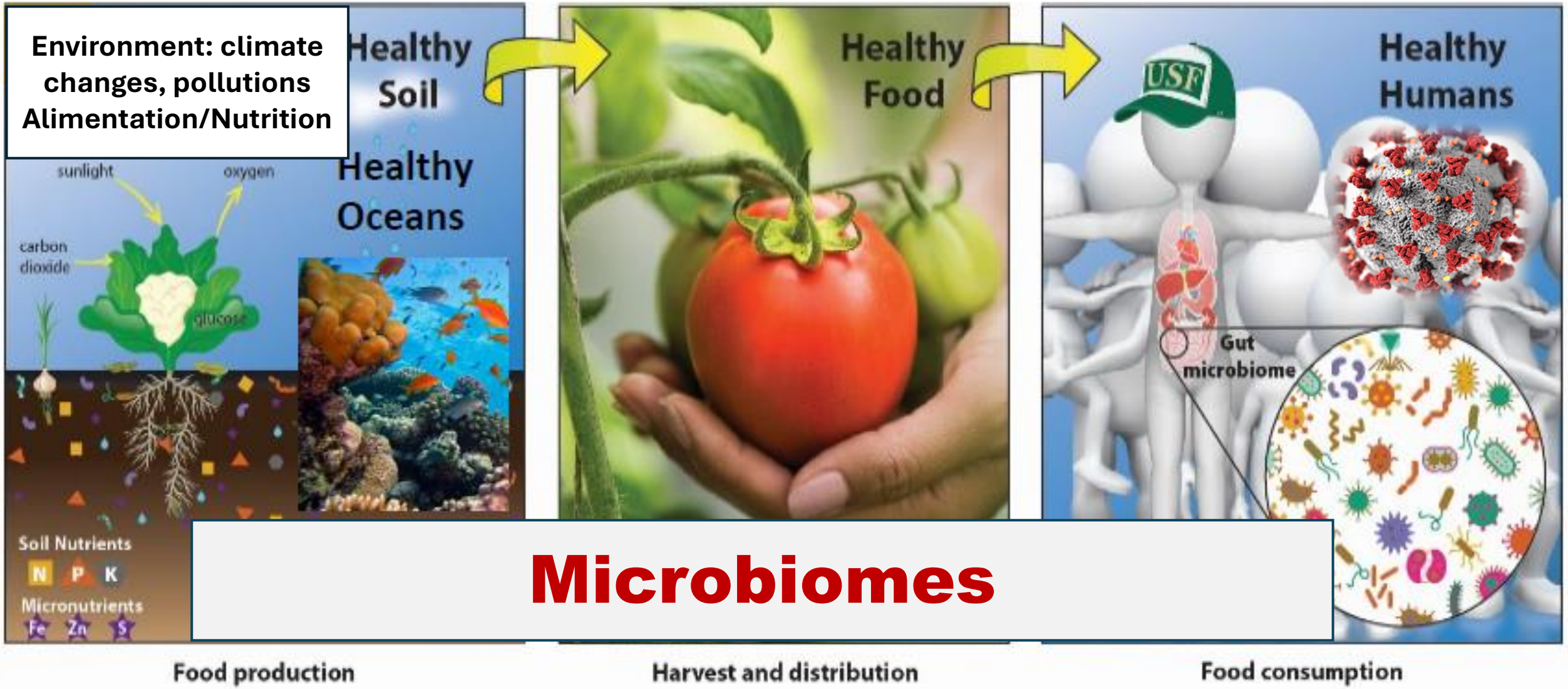
*Children in intervention daycare centers. †Children in standard, nonmodified daycare centers. ‡Children in nature-oriented daycare centers where children visited boreal forests on a daily basis. §Age is presented as means ± SD. ‖Children using probiotics, antibiotics, or medication (paracetamol, desloratadine, pyrvin, cetirizine, and salbutamol) were excluded from the gut microbiome and cytokine analyses. One child with pinworm infection was excluded from all analyses.


A Soil Gammaproteobacterial alpha diversity and richness
Shannon diversity index
OTU richness
2.8
2.7
2.6
2.5
2.4
2.3
2.2
2.1
35
30
25
20
15
10
5
0
**
*
Intervention
Standard
B Soil total bacterial alpha diversity and richness
Shannon diversityindex
OTU richness
6.0
5.8
5.6
5.4
5.2
5.0
4.8
4.6
600
500
400
300
200
100
0
*
*
Intervention
Standard
Diversity (A-B)
Richness (A-B)

Increased IL10; Decreased IL-17A. Increased Treg upon 28 days of intervention



Les microbiomes integrent les effets de l'environnement et de l'alimentation/nutrition



UNIVERSITY of SOUTH FLORIDA
Microbiomes Institute

Flagship Program Metropolitan Food Project

- Biodiversity, Soil, Nutrition, and Human Health

The University of South Florida (USF) **Metropolitan Food Project (MFP)** brings together a diverse team of soil ecology, marine biology, and human health and nutrition experts from colleges across the USF system, centered on the connections between the biodiversity of soil, oceans, and human microbiomes and their direct and indirect effects on the environment and human health.

ENGAGING MICROBIOMES

METROPOLITAN FOOD PROJECT

Biodiversity · Food Security · Nutrition · Health

15th St ECO FARM

Local Food Systems

"Local food systems"

- Onsite programs
- Development of regenerative agriculture in urban , peri arms and food hubs
- Greater healthy food access
- Experiential learning

UNIVERSITY of SOUTH FLORIDA
Microbiomes Institute

International Conference

The international conference on **“Microbiomes, Biodiversity and Their Impact on Global and One He…** held in Annecy, France on October 2023.

October 29-31
USF Tampa

The meeeting brought together more than 30 experts from a wide range of backgrounds: members of **intergovernmental organizations** (**WHO, FAO**) and **international initiatives** (**Lancet Eat**), experts in the microbial ecology of **oceans, soils, plants,** and people, specialists in **nutrition and human health** in relation to microbiomes, promoters, and implementers of **environmentally-friendly agricultural practices**, and **industrial players** developing solutions as part of an eco-responsible agri-food chain.

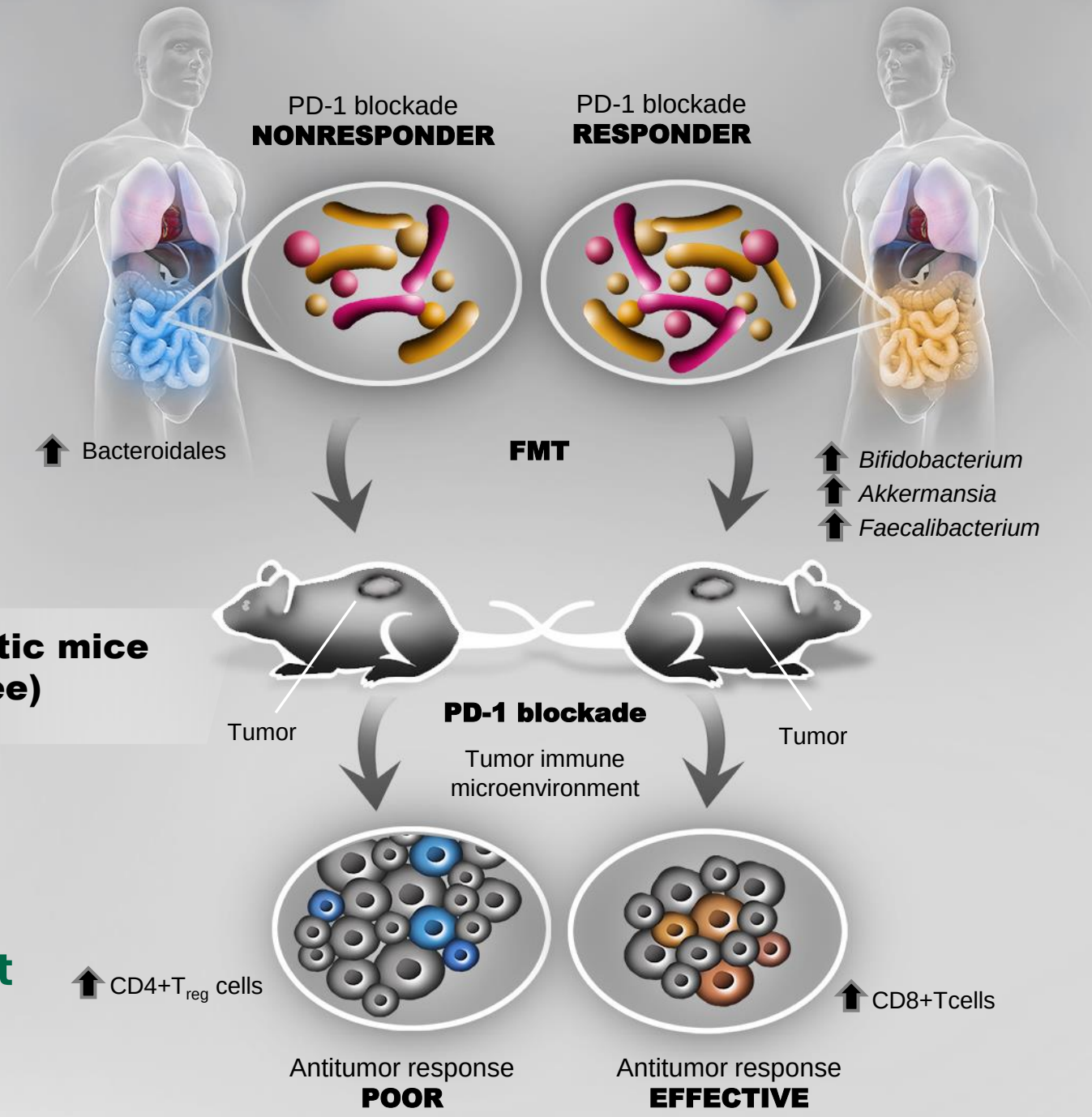
A follow-up meeting will be hosted at USF in October 2024.

Back up

Dysbiosis: causal or consequence?

Fecal Microbiota Transplantation (FMT)

Gnotobiotic mice (Germ-free)



Precision medicine using intestinal microbiota influences cancer patient responses to immunotherapy

Agroecologie
Quelques exemples

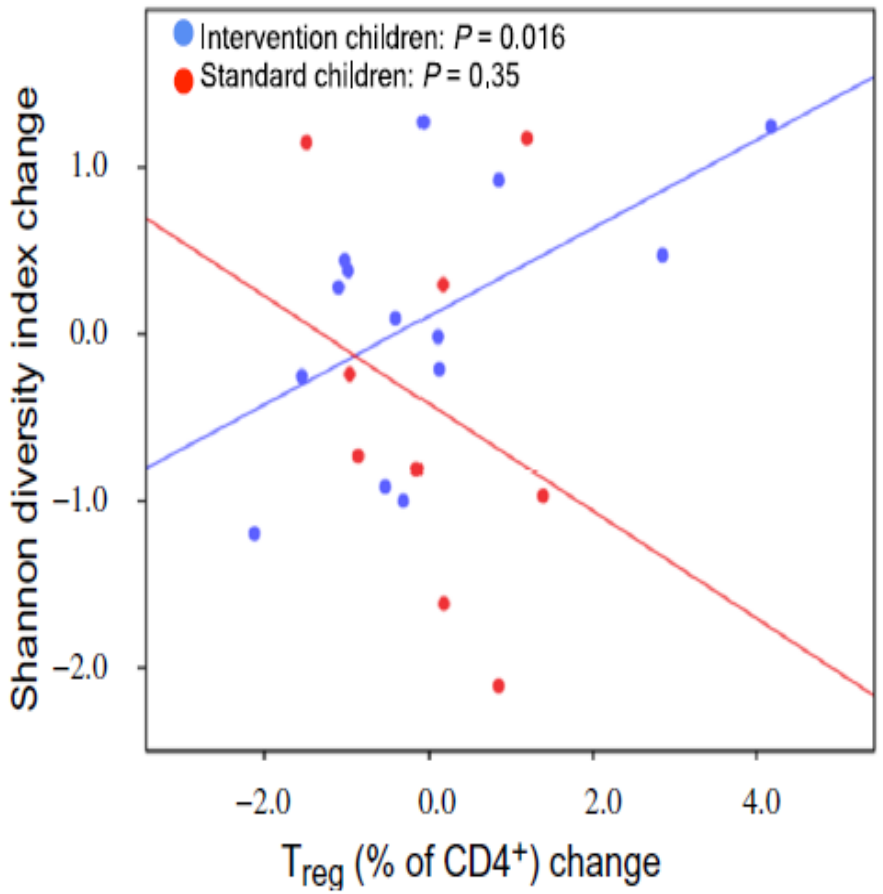
- **Des modeles “vertueux”:**
  exemple: agriculture sud-corenne

- **Biochar**

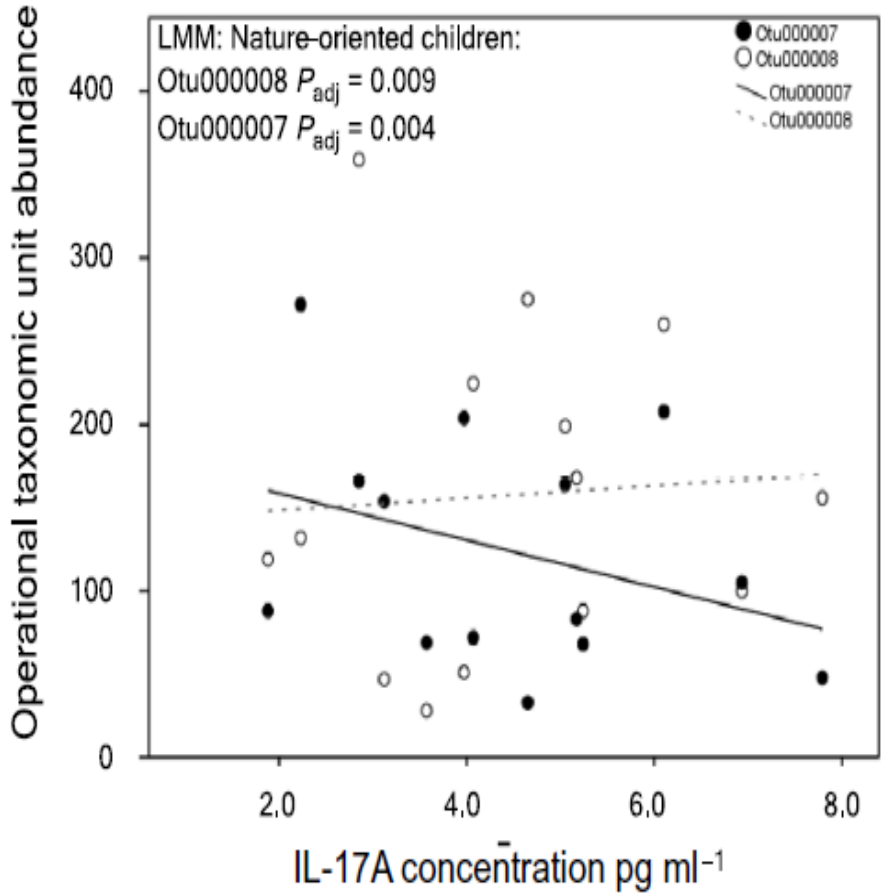
- **Compost**

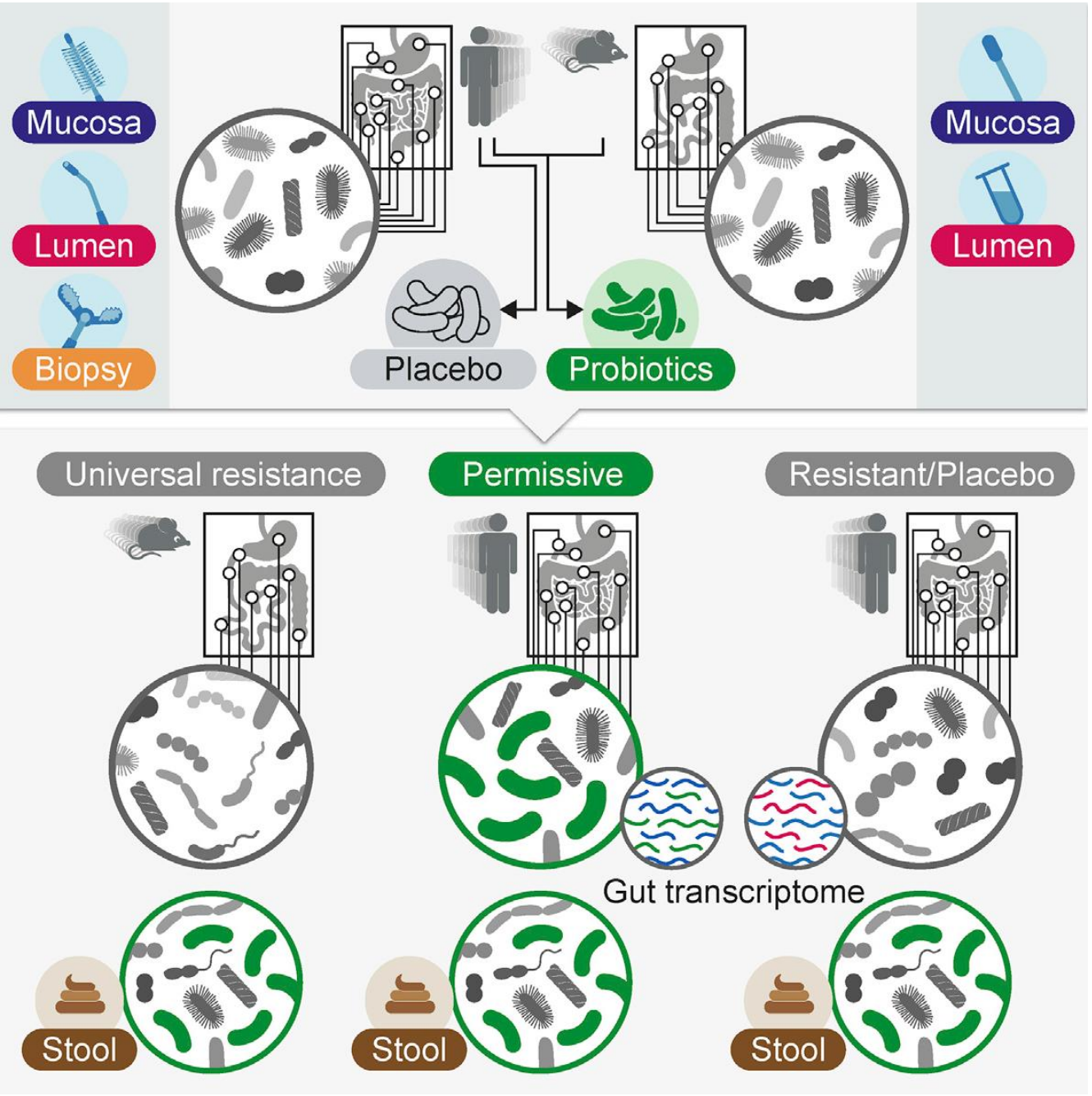
- **Evaluation: Quentin Sannie; Genesis**

C Change in skin Gammaproteobacterial diversity vs. change in T_{reg} frequency



D Relative abundance of *Faecalibacterium* vs. IL-17A expression





The probiotics case

Personalized Gut Mucosal Colonization Resistance to Empiric Probiotics Is Associated with Unique Host and Microbiome Features

Niv Zmora, Gili Zilberman-Schapira, Jotham Suez, ..., Zamir Halpern, Eran Segal, Eran Elinav

Cell 2018, 174, 1388–1405

Production

Quantite  Qualite

Solutions

- Introduire les microbiomes du sol, des oceans et humains dans les reflexions
- Tenir compte des lecons anciennes
- Definir une approche equilibree entre solutions locales et generales:
  local food systems
- Ne pas oublier les pays a faible revenu