

Microbiology in Basic and Clinical Research: Past, Present and Future Perspective

by: Seyed Davar Siadat
2024



- Antonie van Leeuwenhoek – a Dutch merchant with no fortune or university degree - sent a **letter to the Royal Society of London in 1683**, with the first description of a single-celled organism. The date was September 17, the *day that since 2017 was chosen to celebrate the International Microorganism Day*.
- In this famous letter, an exquisite description was made of the first observation of **living bacteria present on the dental plaque**, which was accompanied by drawings of the microorganisms observed and their movements. Finally reaching microscopic life, the foundations of Microbiology were laid.

- Of all the bacteria we encounter in our lives, **only a small minority are dedicated pathogens.**
- While only about **5% of bacterial** species are pathogenic, bacteria have historically been the cause of a disproportionate amount of human disease and death.
- Specifically, about one in a billion microbial species is a human pathogen. Indeed, **approximately 1400 human pathogens** have been described, whereas it has been **estimated that there are one trillion microbial species on Earth**, the vast majority of which remain uncharacterized



Difference Between Biotic and Abiotic Components

The term biotic is made up of two terms: “bio” means living organism and “ic” means like, thus combined they are known as living organisms. Therefore it can also be defined as all living organisms present on earth are known as biotic components.

Example: Plants, animals, human beings, decomposers, yeast, insects, etc. All these biotic components interact to develop new generations i.e to reproduce new organisms to maintain stability in the food chain.



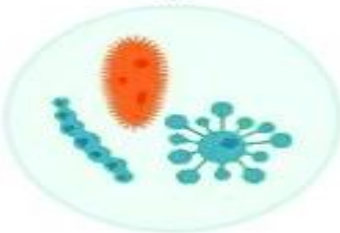
Difference Between Biotic and Abiotic Components:

Biotic Components	Abiotic Components
Living organisms present in the ecosystem are known as biotic components.	Chemical and physical factors present in the ecosystem are known as abiotic components.
They are living in nature.	They are non-living in nature.
For their existence, they need both biotic and abiotic components.	For their existence, they don't need biotic components.
They originated from the biosphere only.	They originated from the lithosphere, hydrosphere, and atmosphere.
Examples: autotrophs, heterotrophs, decomposers, etc.	Examples: light, water, temperature, humidity, etc.



Biotic

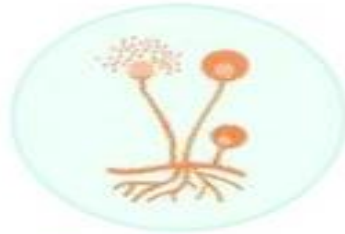
Living things



Bacteria



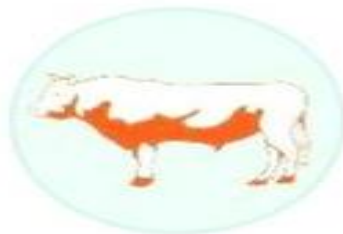
Protists



Fungus



Plants



Animals

Abiotic

Non living things



Water



Air



Minerals



Soil



Light

We're Only About 43% Human

Weight of Organs & their Size

Brain (M)	1400gm (1/50 th BW)
(F)	1250 gm
Heart (M)	300-350 gm
(F)	250-300gm
Kidney	130-150 gm
Liver (M)	1500 gm
(F)	1300 gm
Lungs (Rt)	450gm
(Lt)	400gm
Ovaries	6 gm each
Pancreas	80 gm
Placenta	400-600gm at term
Prostate	20-30 gm
Spleen	200 gm 12x7x2.5
Thyroid	25 gm
Uterus	30-50 gm 1x2x3 inch.
Testes	10-15 gm 5x3x2 cm
Thymus	15 gm
Adrenal	5 gm
Spinal cord	30 gm
Eye	7 gm, 2.5 cm
Pupil Size	3-5mm

- A 'reference man' (one who is 70 kg, 20–30 years old and 1.7 m tall) contains on average about **30 trillion human cells** and **39 trillion bacteria**. Those numbers are approximate but far from the ~~10:1 ratio~~. The researchers produce a ratio for microbial to human cells for the average man of **1.3:1**,
- We have around **20-25,000 genes** in each of our cells, but the human microbiome potentially holds **450** times more

<u>Body region</u>	<u>Numbers</u>
Mouth (total)	10^{10}
Lungs (est.)	$\sim 10^9/\text{ml}$
Breastmilk (est.)	$\sim 10^9/\text{L}$
Skin (total)	10^{12}
GI tract (total)	10^{14}
Vagina	$10^9/\text{ml}$

Meet your microbiome The bacteria that call you home

NOSE
Mass of microbes **10g**
Typical resident *Streptococcus*

MOUTH
Mass of microbes **20g**
Typical resident
Streptococcus (cheek),
Neisseria (teeth)

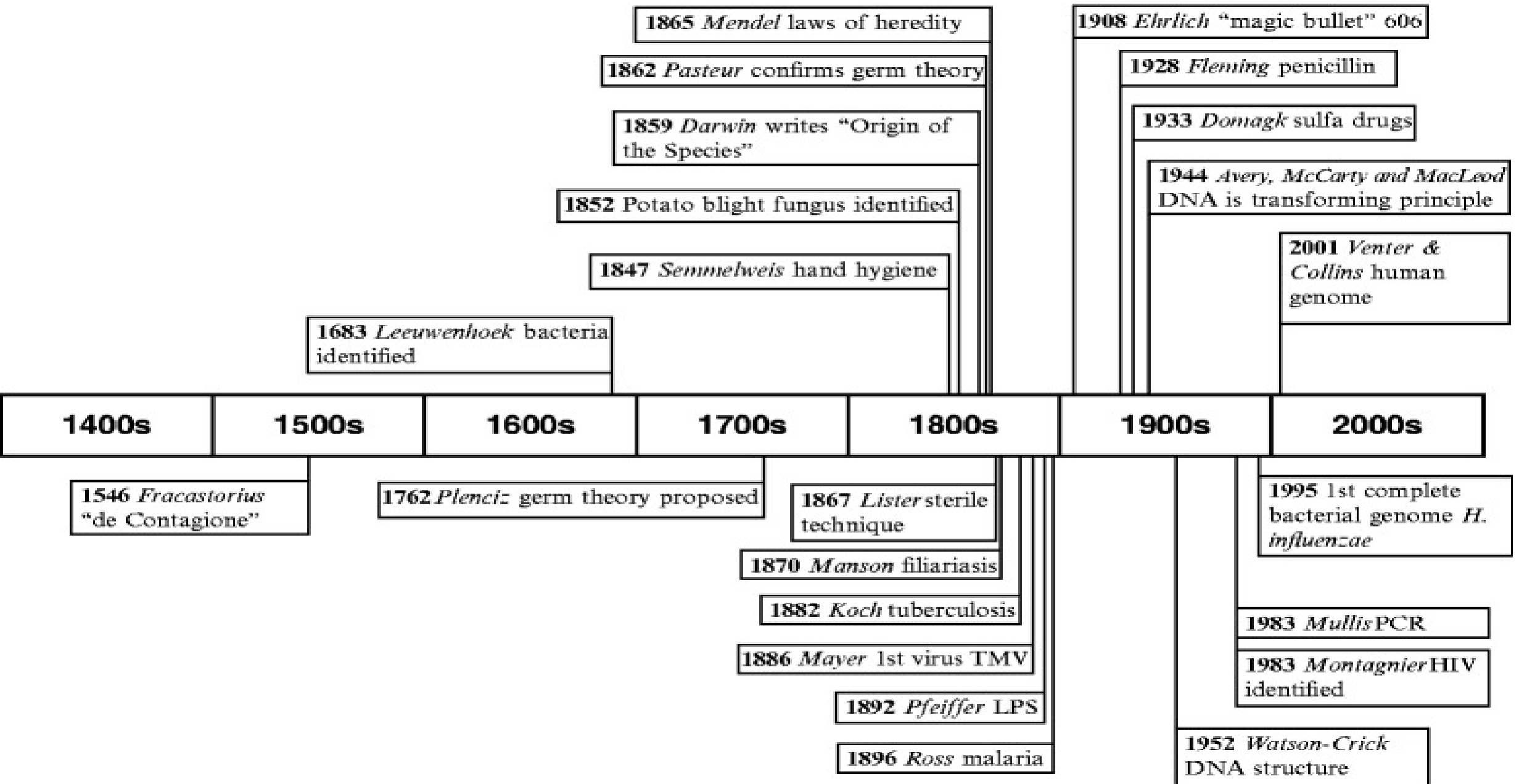
VAGINA
Mass of microbes **20g**
Typical resident *Lactobacillus*

SKIN
Mass of microbes **200g**
Typical resident
Staphylococcus (oily areas),
Corynebacteria (moist areas)

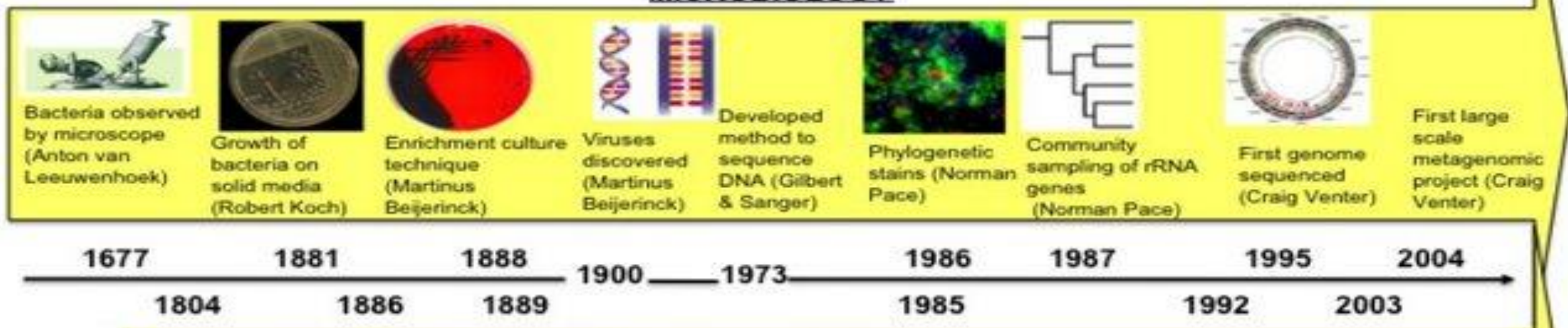
GUT
Mass of microbes **1000g**
Typical resident
Bacteroidetes

MICROBIAL CELLS
OUTNUMBER YOUR
OWN CELLS 10 TO 1
AND HAVE A TOTAL
MASS OF
> 1.2kg

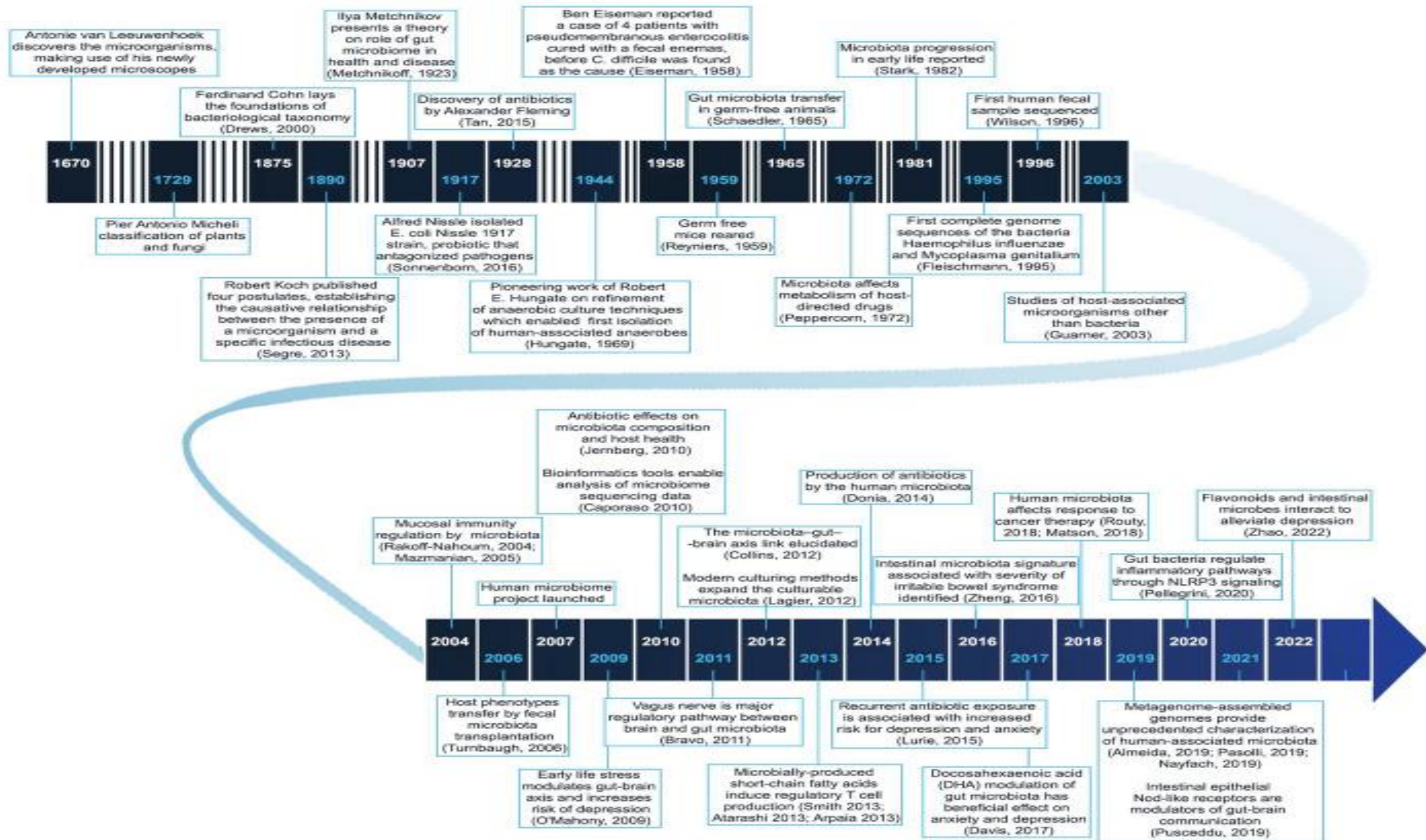
Major Milestones in Microbiology



MICROBIOLOGY



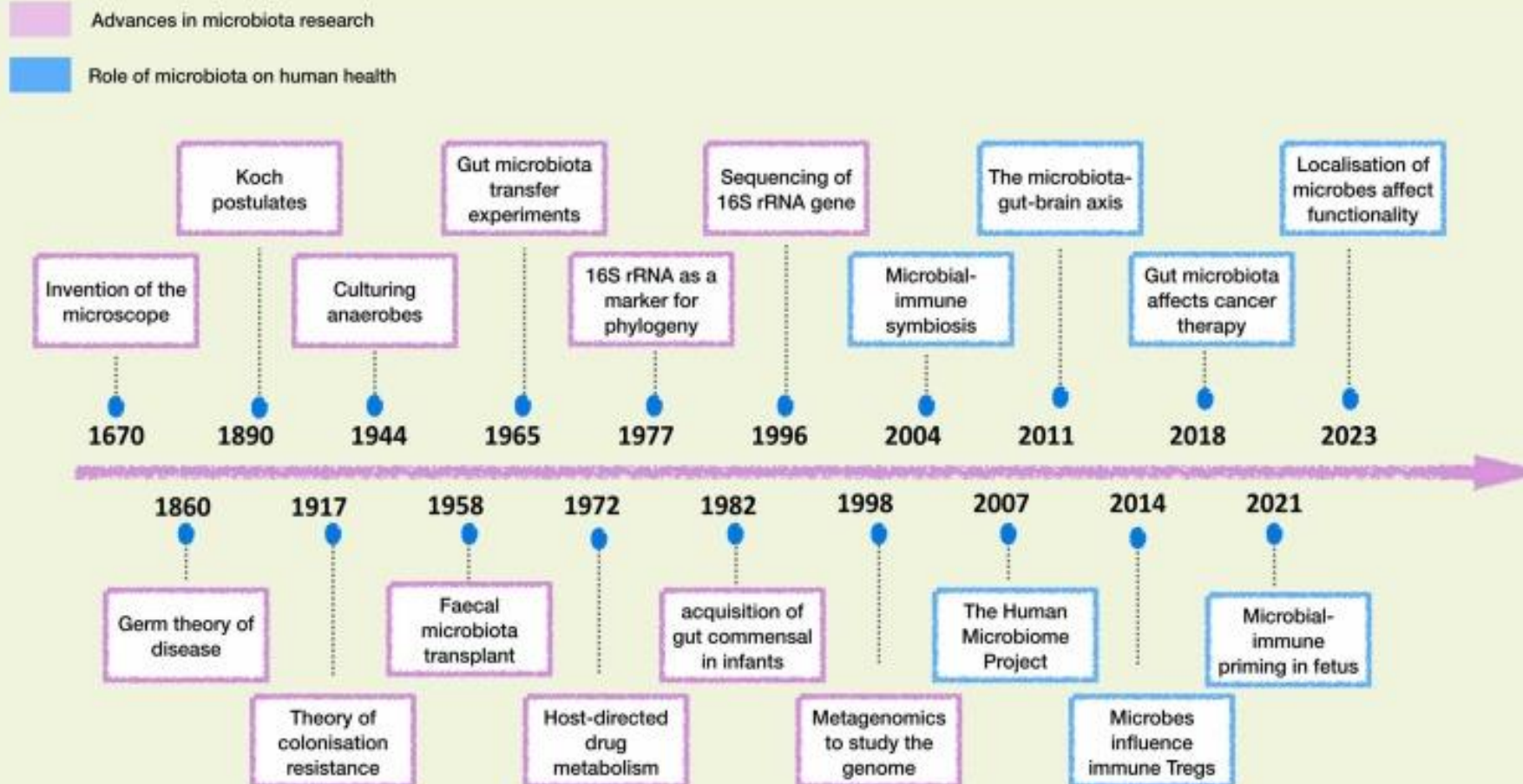
SLOW SAND FILTERS



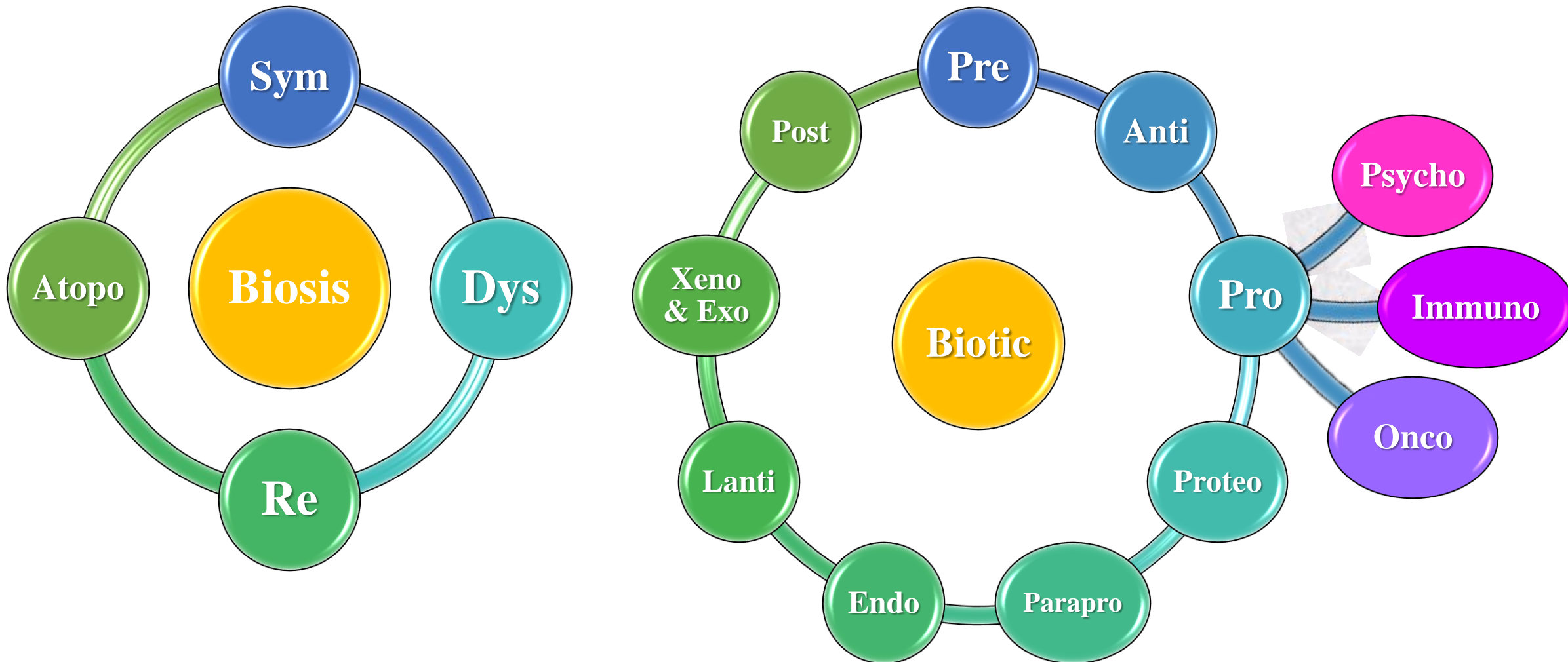
Review

Symbiotic symphony: Understanding host-microbiota dialogues in a spatial context

Soumi Chatterjee^{a, b}, Steven T. Leach^c, Kei Lui^d, Archita Mishra^{a, b}



The word “probiotic” originates from the Latin, meaning “for life”, although there are also links to the Greek language, with bios meaning 'lively' or 'fit for life'



- “The promise of microbiome research results largely on the future of probiotics.... Eventually, it may become possible to restore the health of a depleted microbiome simply by swallowing a capsule crammed with billions of bacterial cells, or by eating yogurt”



[Journal Information](#)
[Journal TOC](#)

[Search APA PsycNet](#)

APA PsycArticles: Journal Article

Review of *The prolongation of life. Optimistic studies.*

[© Request Permissions](#)

Minot, C. S. (1908). Review of *The prolongation of life. Optimistic studies* [Review of the book *The prolongation of life. Optimistic studies*, by E. Metchnikoff]. *The Journal of Abnormal Psychology*, 3(4), 301–302. <https://doi.org/10.1037/h0066131>

Reviews the book, *The prolongation of life. Optimistic studies* by Elie Metchnikoff (1908). The volume, although entitled "The Prolongation of Life," is really a collection of essays, more or less detached in substance from one another, and only in part dealing with the problem which gives its title to the work. In his treatment of old age, Metchnikoff appears as a pleasantly optimistic naturalist, and it is this attitude of optimism which imparts to the volume such unity as one may find in it. His method of dealing with old age is characteristic. He treats it as a special, isolated condition. Metchnikoff's book is certainly well worth reading by those interested in the subjects he discusses, but the reader should not overlook the fact that he deals only with secondary and relatively unimportant details, and never in any part of the book shows ability to measure the full breadth of the biological problems upon which he touches, and never even discusses the essential fundamental phenomena of old age. As his view is narrow, so are his conclusions; and yet the book is enriched with a great number of curious and interesting facts concerning animals and plants in relation to age, longevity, and death, all of which are presented with charming skill. Finally, a word should be said in acknowledgement of the very admirable quality of the English translation of Mr. Mitchell. One could not ask for anything better. (PsycInfo Database Record (c) 2021 APA, all rights reserved)

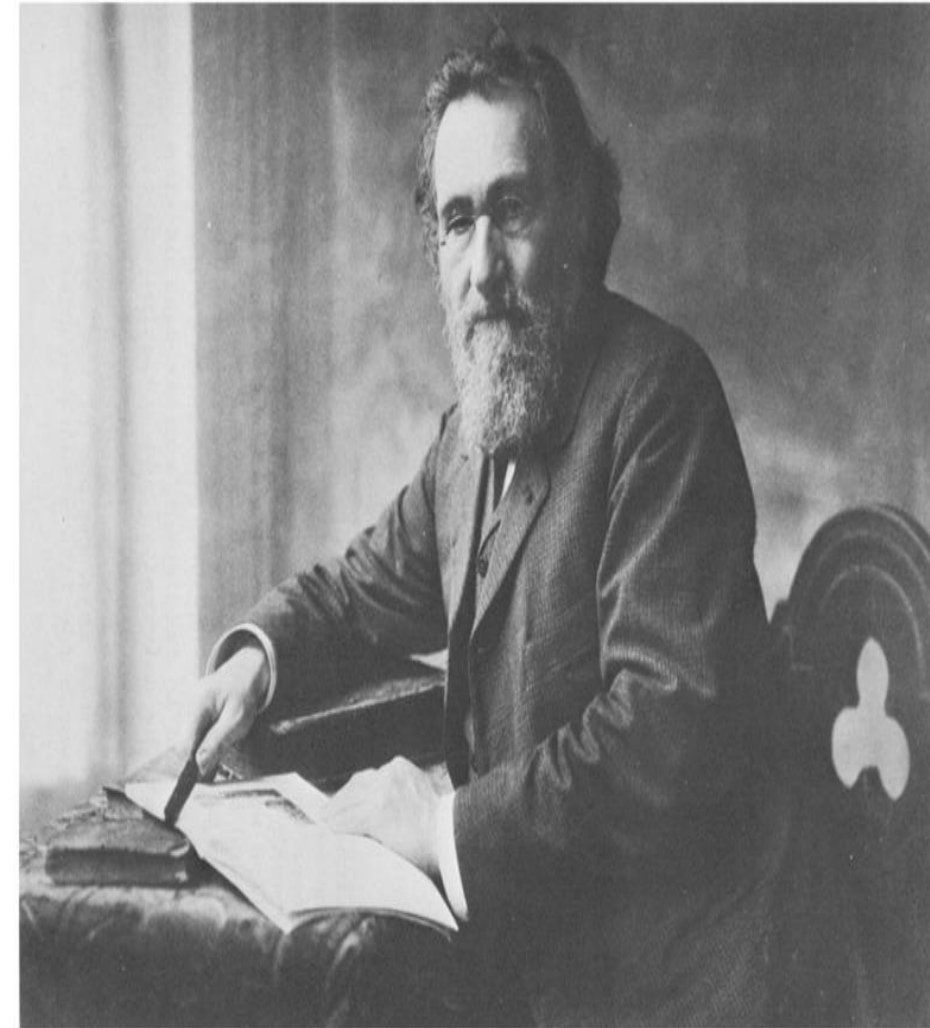
[Get Access](#)

[Accepted Manuscript](#)

The History of Probiotics

Elie Metchnikoff (1845–1916)

- **Probiotics**, as we know them, began their journey over a century ago when they were **discovered by Russian scientist and Nobel Prize winner, Elie Metchnikoff of the Pasteur Institute in Paris.**
- In 1907, whilst working in Bulgaria, Metchnikoff was intrigued as to why certain inhabitants of the Bulgarian population lived much longer than others. He particularly focused his study on centenarians, people who've lived past the age of 100. He researched possible links between their extraordinary age and their lifestyle
- What Metchnikoff discovered was that **the villagers living in the Caucasus Mountains were drinking a fermented yoghurt drink on a daily basis.** His studies into the drink found that it contained a **probiotic called *Lactobacillus bulgaricus* which seemingly improved their health and increased their lifespan.**



born on May 3, 1845 near Kharkow, Russia
(now part of Ukraine).

MICROBIOME

Microbiome studies in the medical sciences and the need for closer multidisciplinary interplay

Nicasio Mancini^{1*}, Francesco Peri^{2*}, Maria Rescigno^{3,4*}, Ivan Zanoni^{5*}

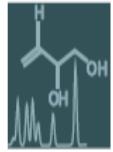
Next-generation sequencing techniques have enabled identification of the microorganisms colonizing mucosal tissues. The International Congress “MicrobiotaMi 2020” (Milan, February 2020) will focus on the mechanisms of microbiota-related functions in health and disease and their clinical application.

Copyright © 2020
The Authors, some
rights reserved;
exclusive licensee
American Association
for the Advancement
of Science. No claim
to original U.S.
Government Works

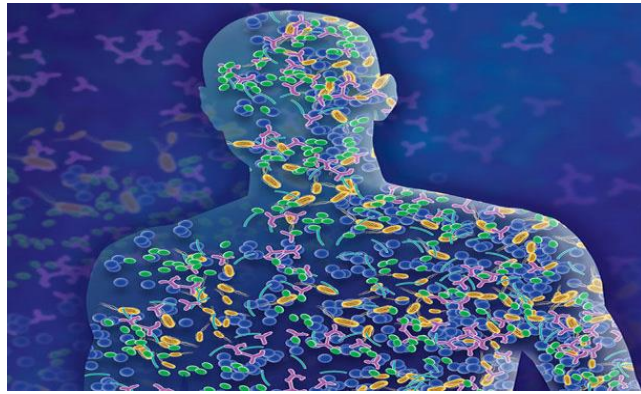
The past 15 years have witnessed a genomic revolution in microbiology and the medical sciences. Next-generation sequencing techniques have fostered the identification of the microorganisms that colonize our mucosal tissues—including the gut, the lung, and the skin—and have enabled the rapid expansion of the field. More than 20,000 scientific

papers have been published on the microbiome, and more than 100,000 articles have been published on the microbiome, some- times with no clear association to their real clinical importance. On the other hand, clinical studies are often correlative and have identified microbes of interest, which are not consistent among studies. In the end, a lack of communication among different research-

ers has led to a fragmented view of the microbiome. GI tract with the microbiota derived from two monozygous twins, highly discordant for their fat mass, led to different weight gain in mice with the same caloric intake (4). Attention moved quickly from the bench to the clinics, and back, also because of the “epidemic” effect of obesity in Western countries. Since then, thousands of data have been gathered



metabolites



Review

An Integrated Multi-Disciplinary Perspective for Addressing Challenges of the Human Gut Microbiome

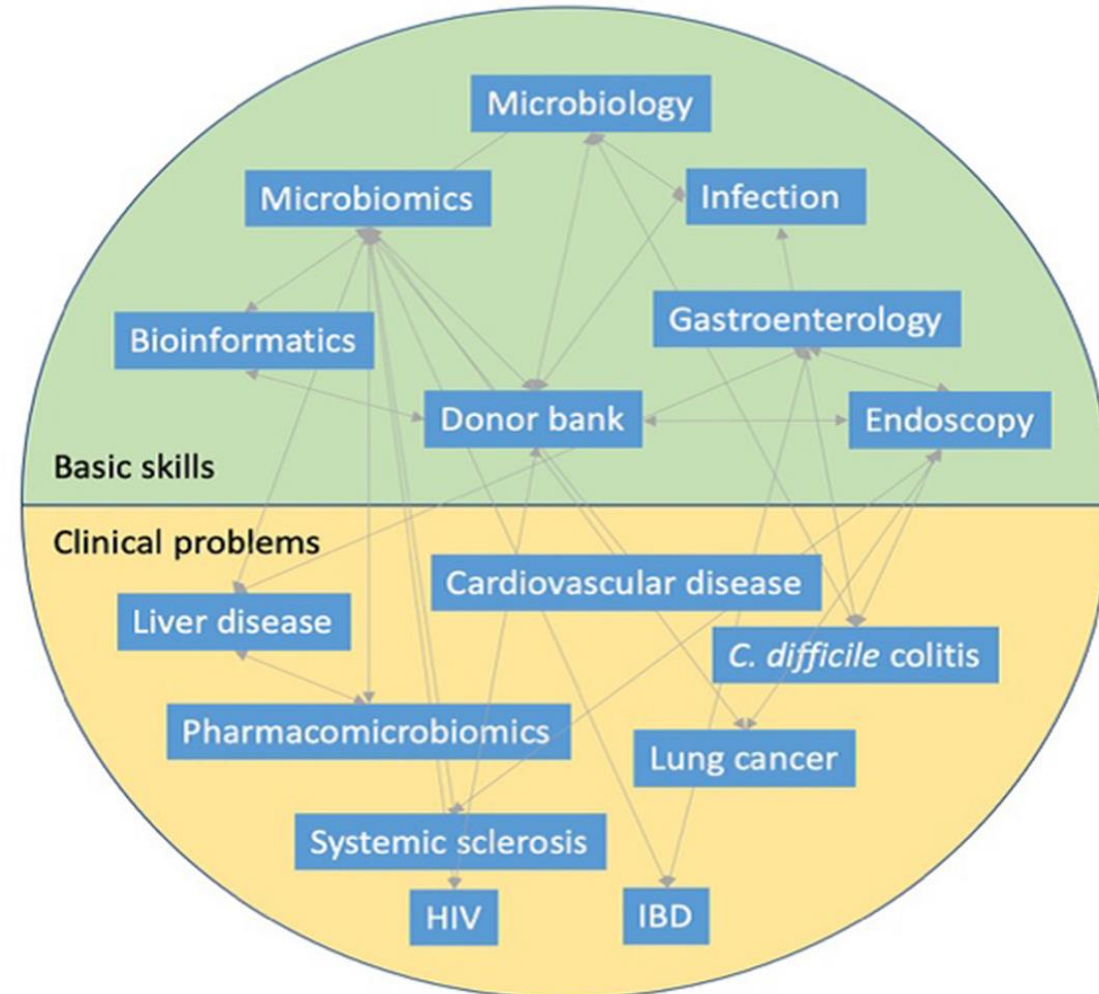
Rohan M. Shah ^{1,2} , Elizabeth J. McKenzie ³ , Magda T. Rosin ³, Snehal R. Jadhav ⁴,
Shakuntla V. Gondalia ⁵, Douglas Rosendale ⁶ and David J. Beale ^{2,*}

¹ Department of Chemistry and Biotechnology, Faculty of Science, Engineering and Technology, Swinburne University of Technology, Hawthorn, VIC 3122, Australia; rshah@swin.edu.au


² Land and Water, Commonwealth Scientific and Industrial Research Organization (CSIRO), Dutton Park, QLD 4102, Australia


³ Liggins Institute, The University of Auckland, Grafton, Auckland 1142, New Zealand; liz.mckenzie@auckland.ac.nz (E.J.M.); m.rosin@auckland.ac.nz (M.T.R.)

⁴ Centre for Advanced Sensory Science, School of Exercise and Nutrition Sciences, Deakin University, Burwood VIC 3125, Australia; snehal.jadhav@deakin.edu.au



Nature Milestones in Human

	A field is born (FOREWORD)
1944	Culturing anaerobes (MILESTONE 1)
1958	Faecal microbiota transplantation for <i>Clostridioides difficile</i> infection (MILESTONE 2)
1965	Gut microbiota transfer experiments in germ-free animals (MILESTONE 3)
1972	The microbiota influences metabolism of host-directed drugs (MILESTONE 4)
1981	Microbiota succession in early life (MILESTONE 5)
1996	Sequence-based identification of human associated microbiota (MILESTONE 6)
1998	Stability and individuality of adult microbiota (MILESTONE 7)
2003	Beyond bacteria: studies of other host-associated microorganisms (MILESTONE 8)
2004	Regulation of mucosal immunity by the microbiota (MILESTONE 9)
2005	The importance of adequately feeding your microbiota (MILESTONE 10)
2006	Transfer of host phenotypes through microbiota transplantation (MILESTONE 11)
2006	Impact of diet-microbiota interactions on human metabolism (MILESTONE 12)
2007	Mechanisms of colonization resistance (MILESTONE 13)
2007	Functional human microbiota analyses in vivo using 'omics technologies (MILESTONE 14)



Nature Milestones in Human Microbiota Research

2010	Antibiotic effects on microbiota composition and host health (MILESTONE 15)
2010	Bioinformatics tools enable the analysis of microbiome sequencing data (MILESTONE 16)
2010	Microbiome analyses in large human populations (MILESTONE 17)
2011	The microbiota–gut–brain axis (MILESTONE 18)
2012	Modern culturing efforts expand the culturable microbiota (MILESTONE 19)
2012	Global human microbiome (MILESTONE 20)
2013	Microbially-produced short-chain fatty acids induce regulatory T cell production (MILESTONE 21)
2014	Production of antibiotics by the human microbiota (MILESTONE 22)
2015	Host-targeted drugs affect microbiota populations (MILESTONE 23)
2018	Human microbiota affects response to cancer therapy (MILESTONE 24)
2019	Metagenome-assembled genomes provide unprecedented characterization of human-associated microbiota (MILESTONE 25)



The goals of the HMP are:

(1) To take advantage of new, high-throughput technologies to characterize the human microbiome more fully by studying samples from multiple body sites from each of at least 250 “normal” volunteers

(2) To determine whether there are associations between changes in the microbiome and health/disease by studying several different medical conditions

(3) To provide both a standardized data resource and new technological approaches to enable such studies to be undertaken broadly in the scientific community

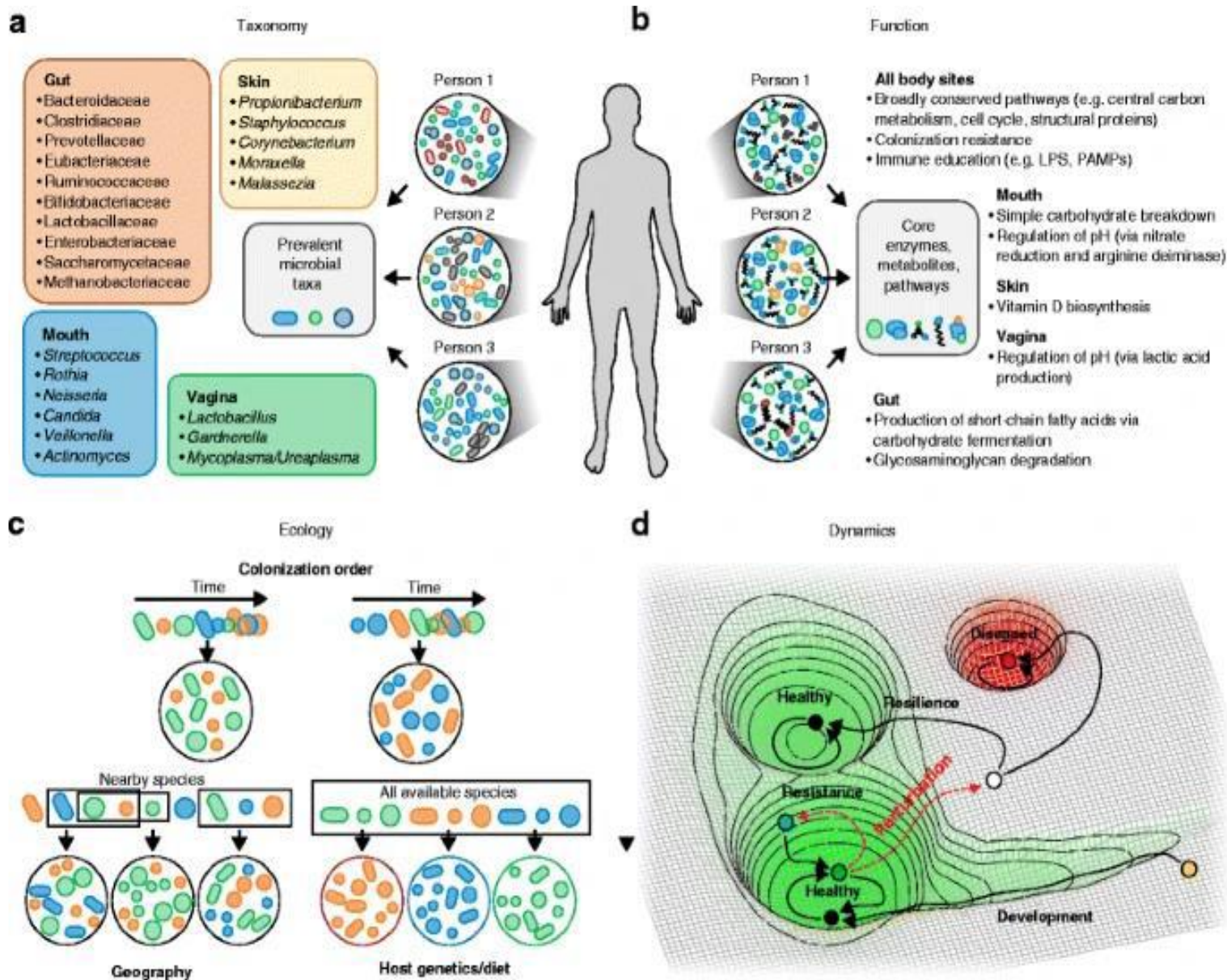
(4) The ultimate objective of the HMP is to demonstrate that there are opportunities to improve human health through monitoring or manipulation of the human microbiome

Achievements of the Human Microbiome Project

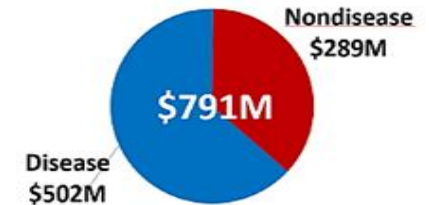
Some of the areas currently being questioned by HMP researchers include the following:

- How a certain microbiome is established in a person and whether or not it changes over time
- How the microbiota and host interact
- How certain microbial combinations influence disease
- How the microbiome is affected by antibiotics
- How microbes affect a person's response to medications
- Whether changing the microbiome can enhance human health

The healthy human microbiome



- HMP Phase One (2007-2012)
Metagenomic analysis of microbial community composition
- HMP Phase Two (2013-2016)
Phase Two (\$25M): Integrative HMP “iHMP”



100+ classes of disease over FY12-16

Type of dysbiosis

A change in microbial community structure

Outgrowth of pathobionts

Loss of commensals

Loss of diversity

Total abundance of bacteria according to the different body sites. Bounds for bacteria number in different organs, derived from bacterial concentrations and volume

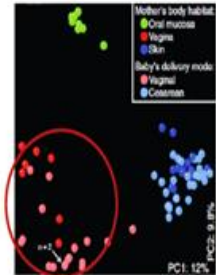
The Human Microbiome

- Thousands of microbial species*, possessing millions of genes, live with humans.
- Known as the microbiome, most are not culturable.

Body region	Numbers
Mouth (total)	10^{10}
Lungs (est.)	$\sim 10^9/\text{ml}$
Breastmilk (est.)	$\sim 10^9/\text{L}$
Skin (total)	10^{12}
GI tract (total)	10^{14}
Vagina	$10^9/\text{ml}$

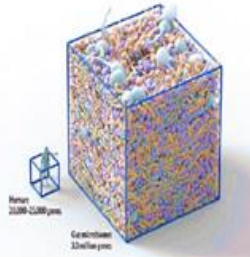


*bacteria, fungi, viruses, phage, archaea, protozoa, (helminths)



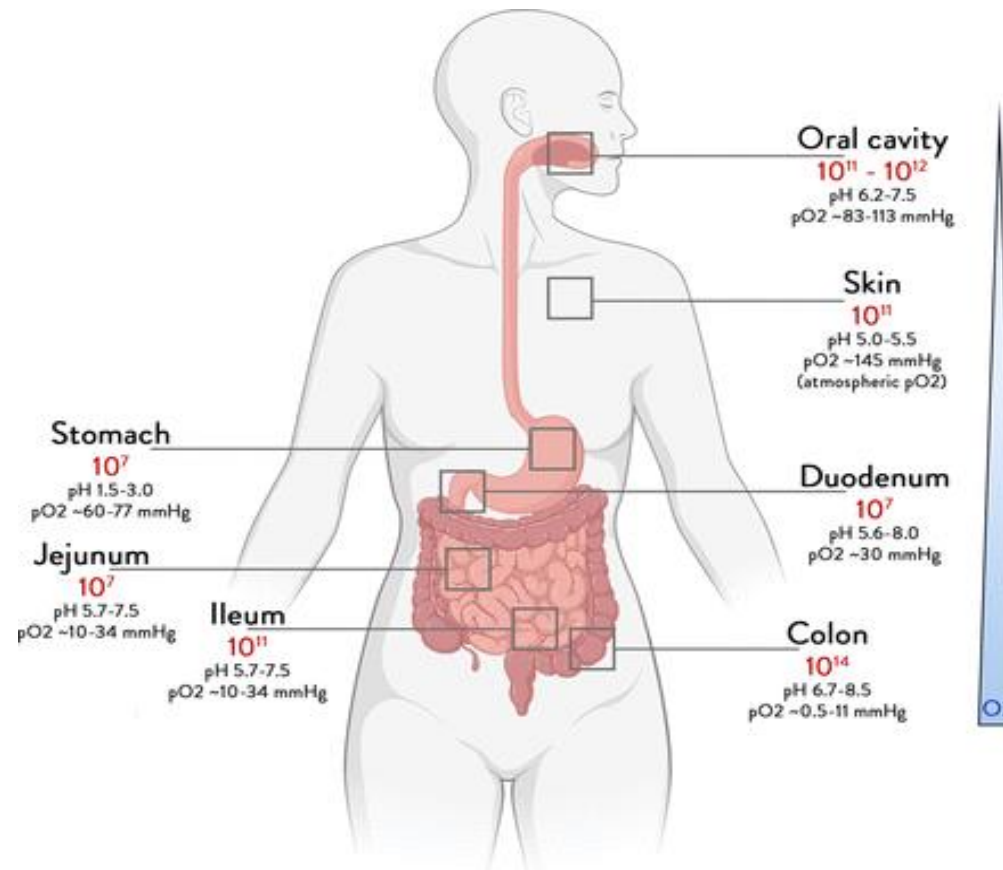
Dominguez-Bello et al. (2010)

- These microbes are acquired each generation.

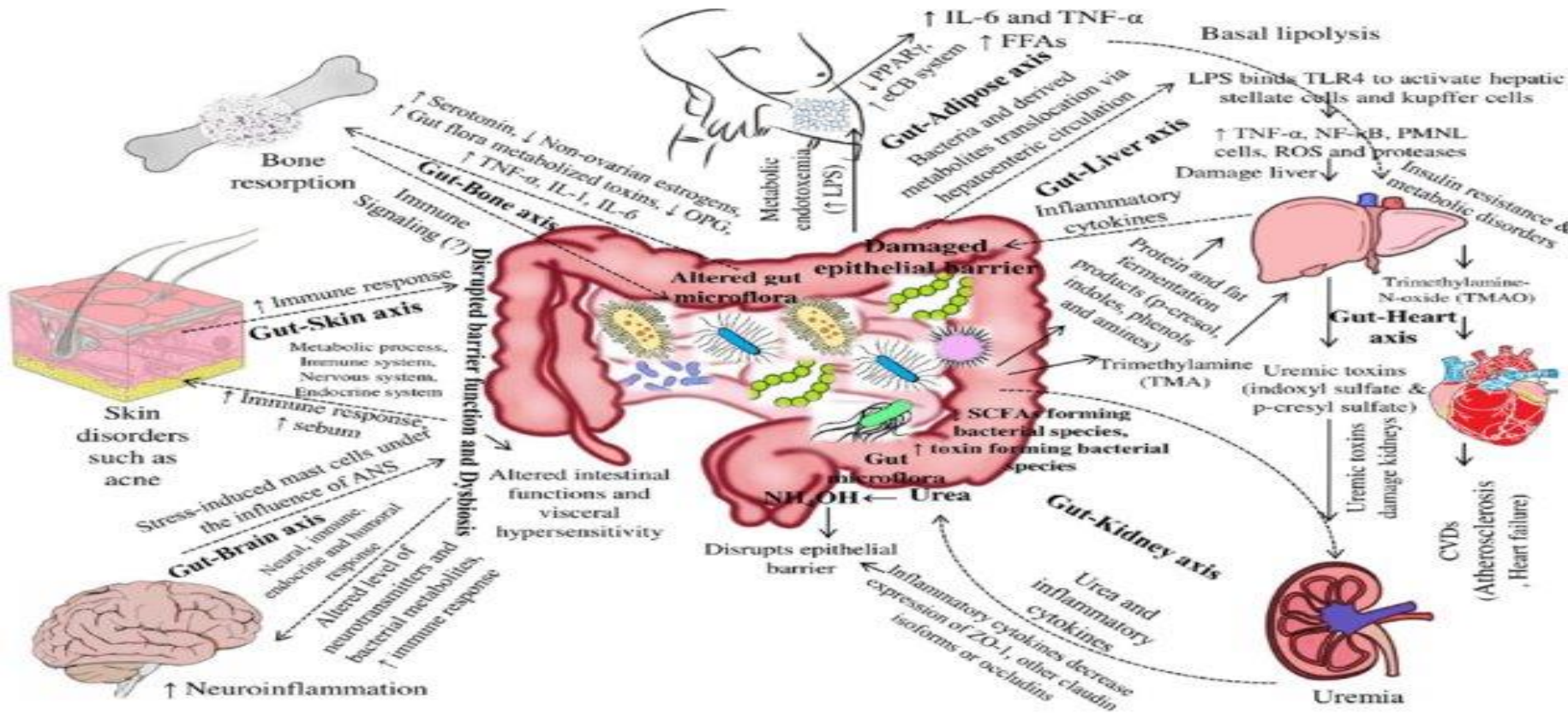


Scientific American (2013)

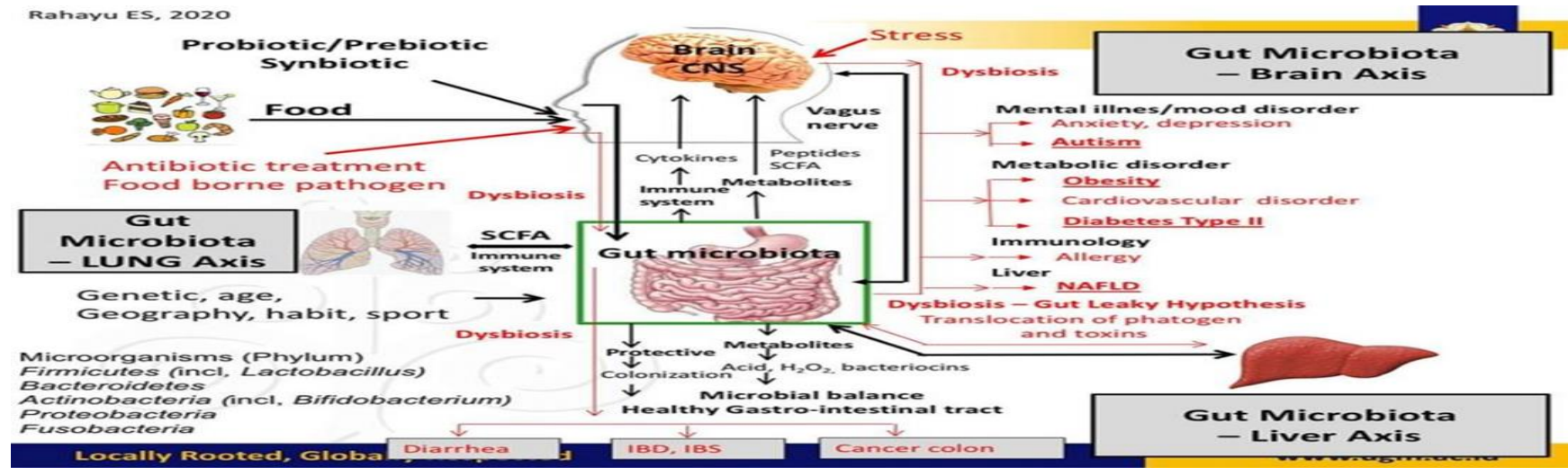
- Microbiome maturation continues to age 2 or 3, along with immune system development.
- These microbial genes encode myriad metabolic capabilities.
- The human microbiome augments/extends capabilities encoded in the human genome.



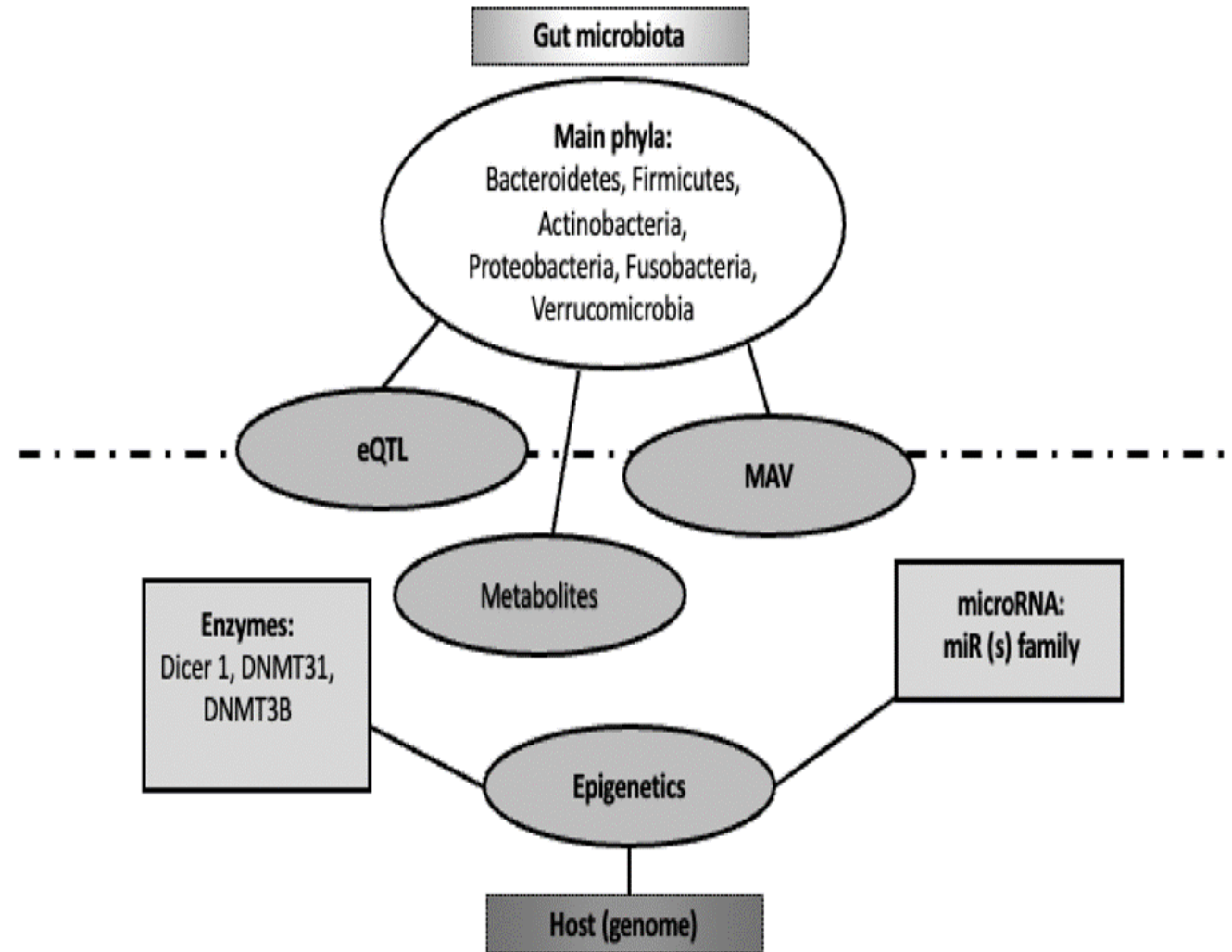
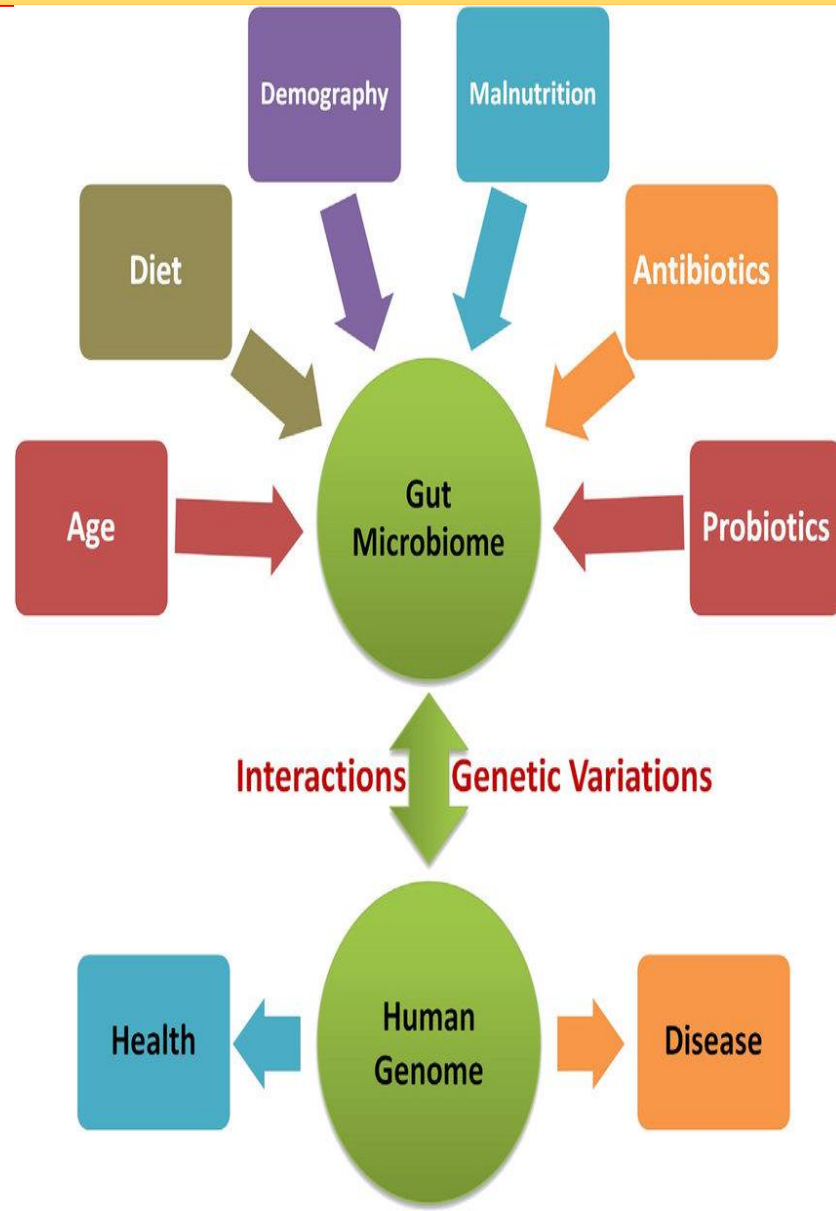
Representation of a bi-or multidirectional communication link or 'axis' between gut, associated microbiota & various organs



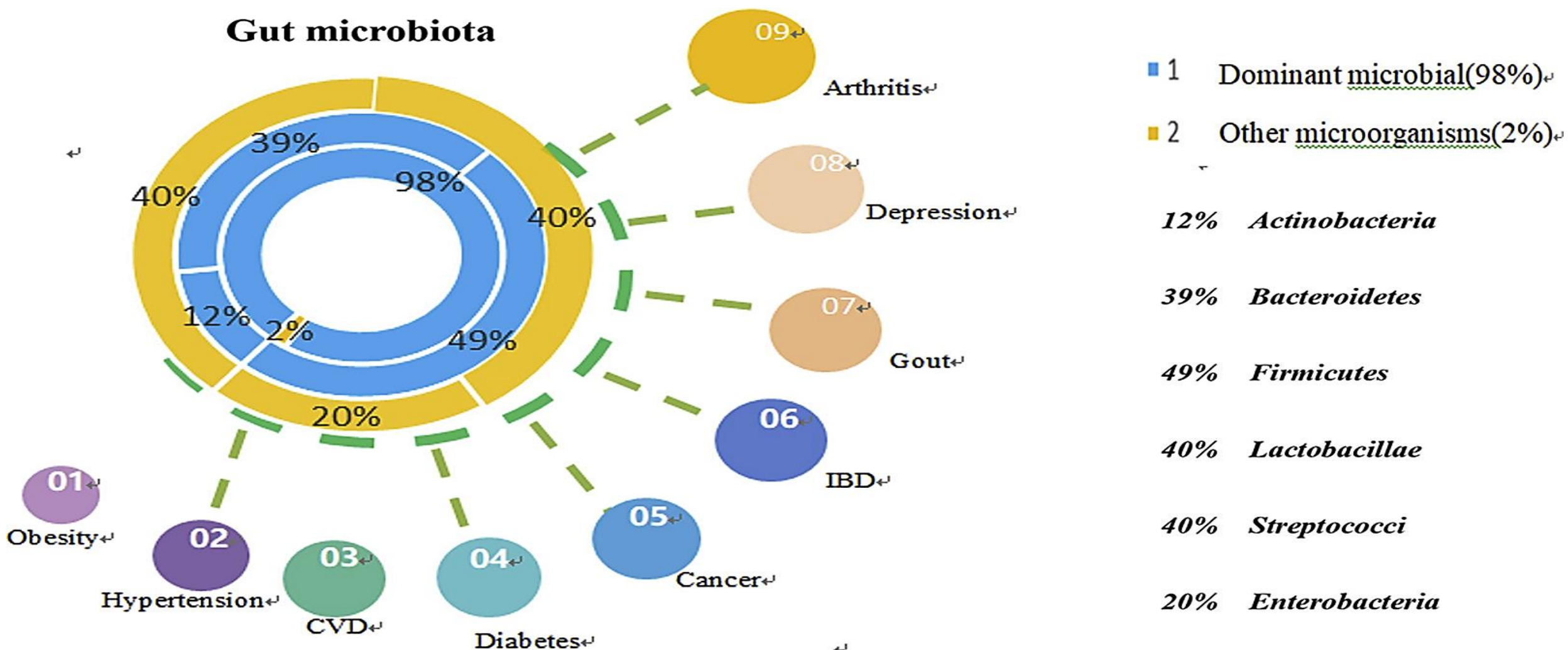
Rahayu ES, 2020



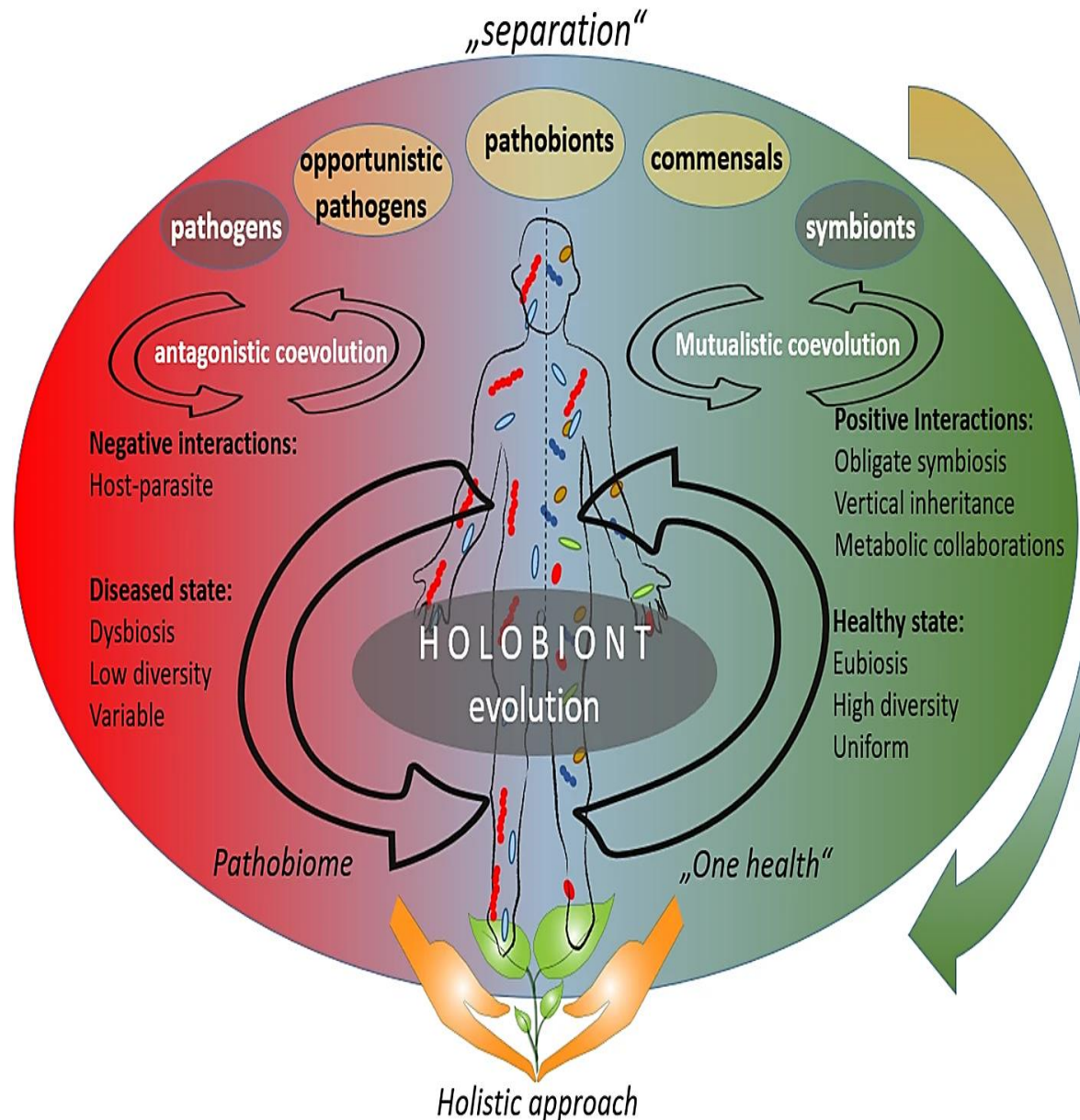
Complex interplay of the human gut microbiome and human genome in human health



Revisit gut microbiota and its impact on human health and disease

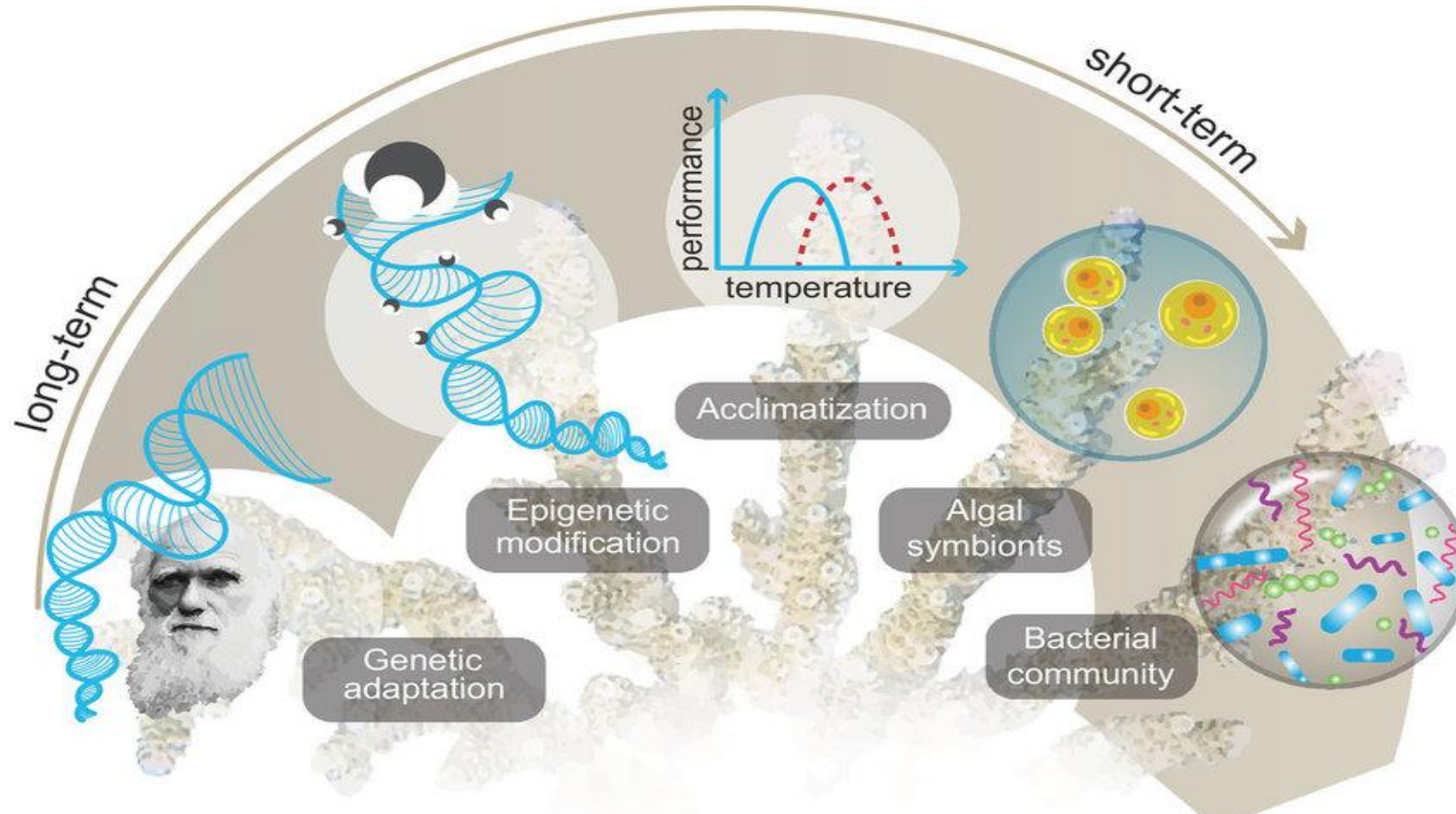


A shift in the understanding of the microbial-host coevolution from the “**separation**” theories to the holistic approach

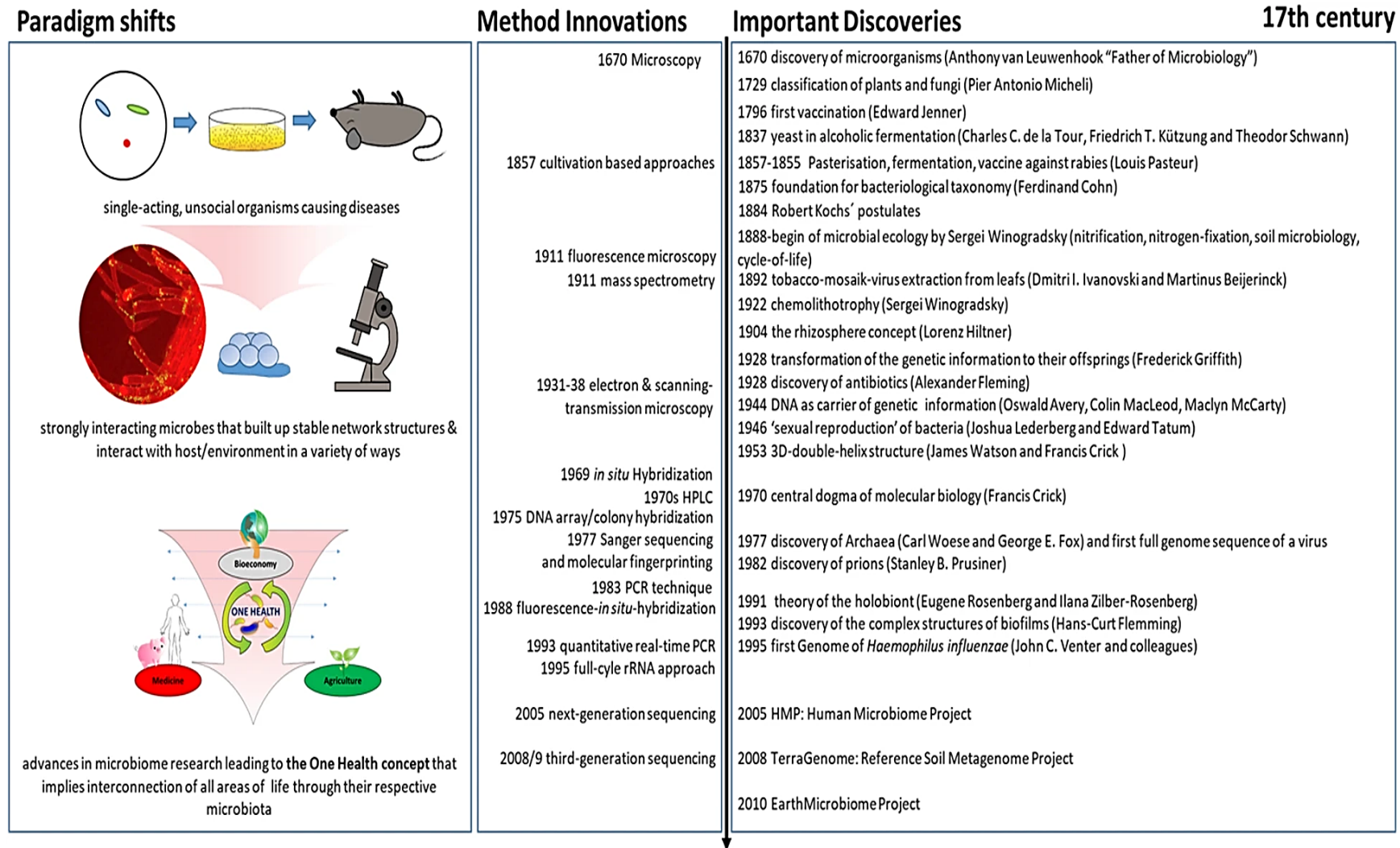


Microbiome flexibility:
The potential for dynamic restructuring of the host microbiome in the face of environmental change.

Overview of (coral) **metaorganism** (ecological) adaptation mechanisms



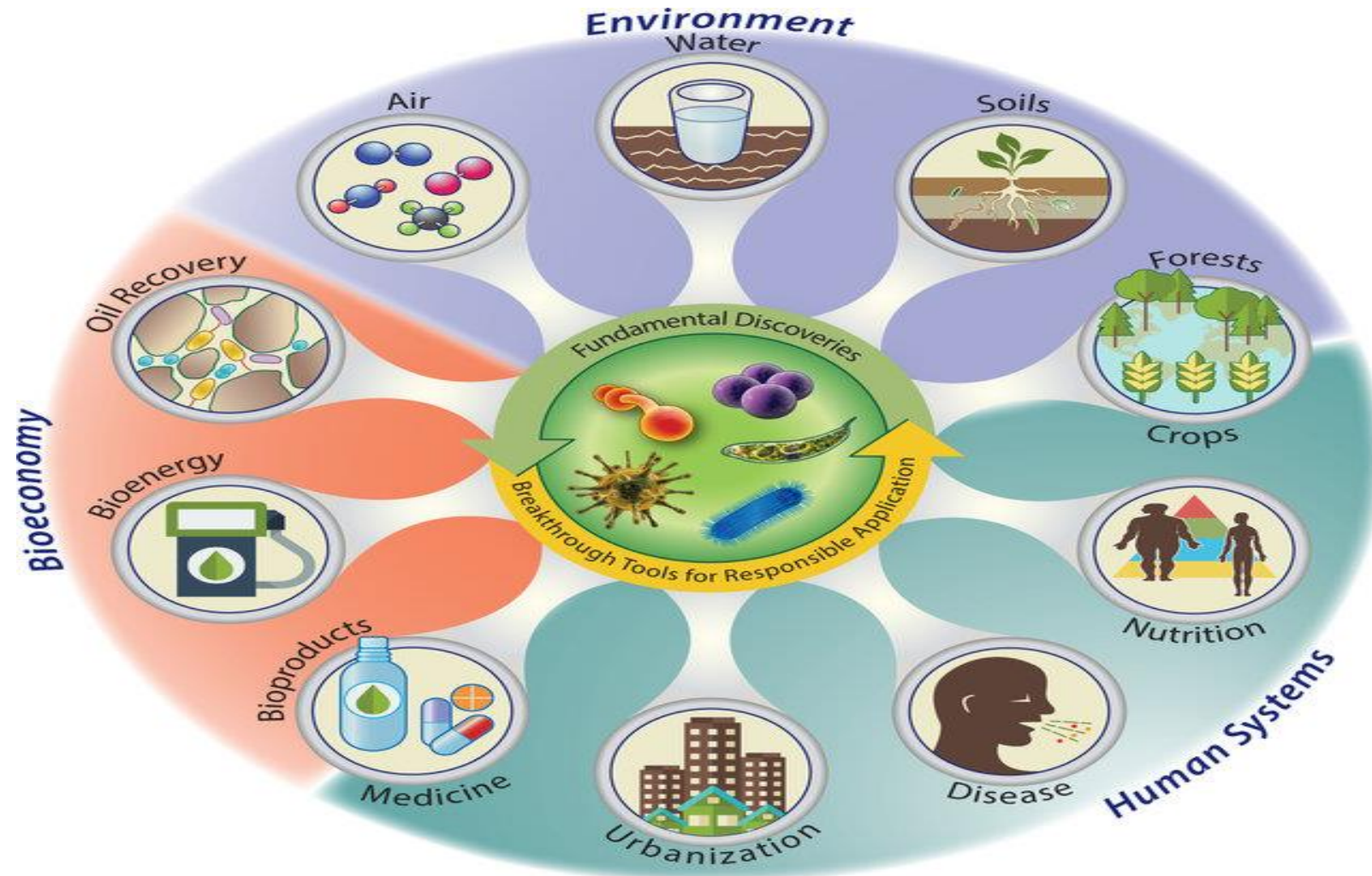
Putative mechanisms are ordered by time scales on which they may occur (from left to right): from **long-term processes** such as (host) genetic adaptation on the left that manifest over the course of generations, to epigenetic modifications that presumably happen over the course of one generation to the next, to physiological acclimation that happens within the lifetime of an individual, to microbial community changes that may happen within the course of months, weeks, or hours. Given the latter, flexible microbial association may constitute a fast-response mechanism to rapid environmental change.



21th century

The history of microbiome research from 17th century until our days, highlighting the shift of the paradigm from microbes as unsocial organisms causing diseases to the **holistic view of microorganisms** being the center of the One Health Concept: **positively interconnecting all areas of our lives.**


Toward a Predictive Understanding of Earth's Microbiomes to Address 21st Century Challenges



MEETING REPORT

Open Access

Microbiome for Mars: surveying microbiome connections to healthcare with implications for long-duration human spaceflight, virtual workshop, July 13, 2020

Michael LaPelusa^{1*}, Dorit Donoviel², Sergio E. Branzini³, Paul E. Carlson Jr⁴, Stephanie Culler⁵, Amrita K. Cheema⁶, Rima Kaddurah-Daouk⁷, Denise Kelly⁸, Isabelle de Cremoux⁸, Rob Knight⁹, Rosa Krajmalnik-Brown^{10,11}, Stephen L. Mayo¹², Sarkis K. Mazmanian¹², Emeran A. Mayer^{13,14,15}, Joseph F. Petrosino¹⁶ and Keith Garrison^{17*} 



frontiers | Frontiers in Soil Science

REVIEW
published: 11 April 2021
doi: 10.3389/fmicb.2021.671584

comment



Microbiome innovations for a sustainable future

The United Nations Sustainable Development Goals (SDGs) are being integrated into bioeconomy strategies around the world, including the European Green Deal. We highlight how microbiome-based innovations can contribute to policies that interface with the SDGs and argue that international cooperation in microbiome science is crucial for success.

Unlocking the Microbiome

Opportunities and challenges of microbiome research for health, agriculture, environment and biotechnology

Microbiome as a Key Player in Sustainable Agriculture and Human Health

Jarupula Suman^{1*}, Amitava Rakshit^{1*}, Siva Devika Ogiroddy¹, Sonam Singh¹, Chinmay Gupta¹ and J. Chandrakala²

¹ Department of Soil Science and Agricultural Chemistry, Biju Patnaik University, Bhubaneswar, India, ² Department of Plant Pathology, Professor Jayashankar Telangana State Agricultural University, Hyderabad, India



Home / Articles / The Role of Microbiology in Sustainable Development

The Role of Microbiology in Sustainable Development

DOI: 10.3389/fmicb.2021.671584

SHARE THIS

Can microbes help save the world? Microbes know no borders, and are adept at adapting, surviving and thriving in extreme and constantly changing environments. While a fraction of microbes is pathogenic, the majority are beneficial or neutral and essential for life. ASM leadership hosted a virtual panel during the United Nations General Assembly (UNGA) Science Summit discussing the role and contribution of science to the attainment of the United Nations Sustainable Development Goals (SDGs). The SDGs include 17 interconnected global objectives identified by the UN as a "blueprint to achieve a better and more sustainable future for all" by 2030.

Microbiome-based innovations can support the achievement of the United Nations Sustainable Development Goals

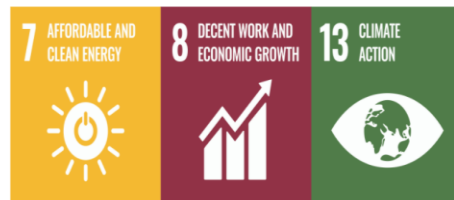
HOW MICROBIOME TECHNOLOGIES COULD CONTRIBUTE TO SDGS

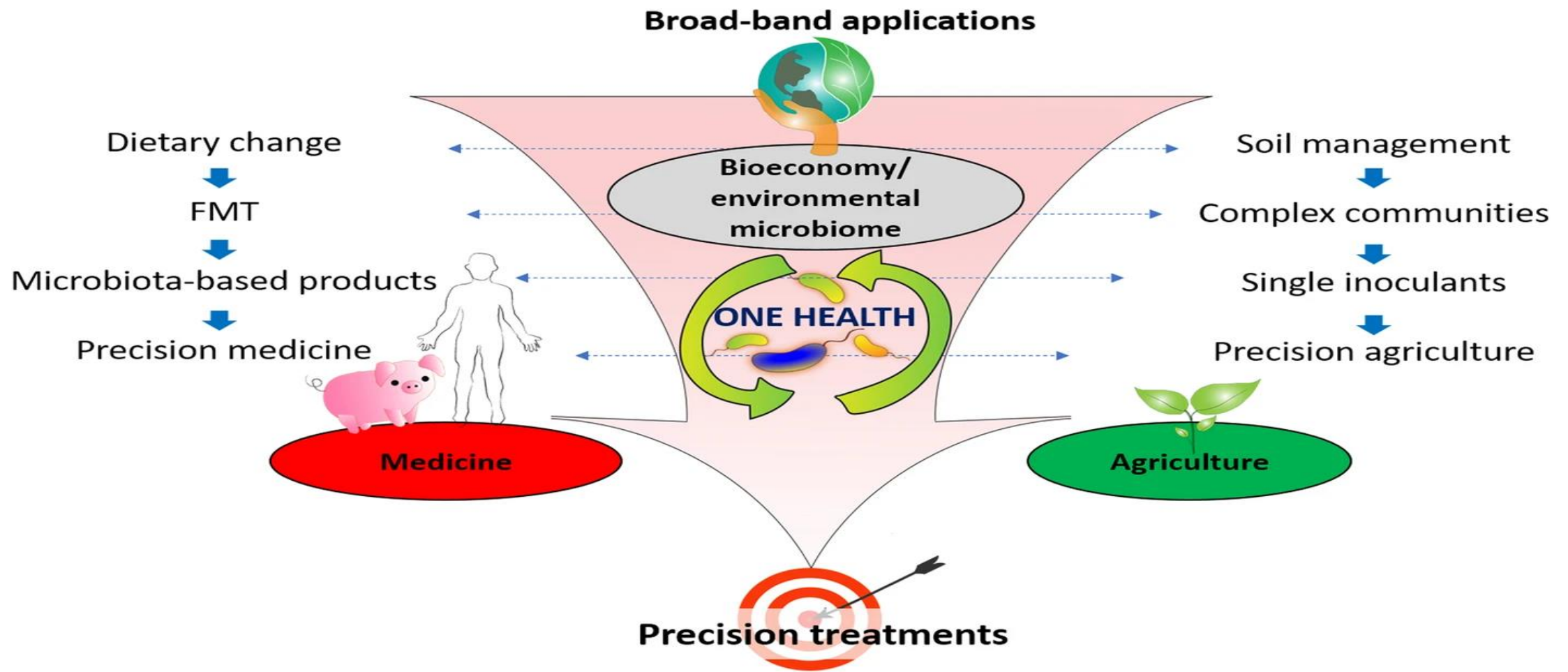
FOOD SUPPLY IN
INDUSTRIALISED
AND URBANISED
SOCIETIES

CLEAN
ENVIRONMENT

CLIMATE CHANGE
MITIGATION

HEALTHY LIVES





The schematic showing the cross-field microbiome-application trend that goes from broad-band applications direction microbiome-based precision treatment in all areas of microbiome research, such as agriculture, human and animal medicine, and bioeconomy, while the interconnection between these areas by the means of the cycling of subsets of microbial communities is an underlying concept behind the One Health approach. The synergies between the microbiome applications in the areas of medicine (left) and agriculture (right) are shown with the horizontal arrows following the flow (vertical arrows) from the broadband applications (upper part) to the precision treatments (lower part)

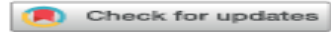
Scientists identified two bacteria from gut microbiota linked to mental health

- That is precisely what researchers of the [Catholic University of Leuven](#), in Belgium, have just done. They have found **most human gut bacteria do produce neurotransmitters**, which are chemicals like dopamine and serotonin that enable communication among neurons, which are the nervous cells in the brain, but also in the enteric nervous system of the gut.
- These **neurotransmitters** are known to influence intestinal functions, but also our **mood** and **behavior**.
- Moreover, scientists, led by [microbiologist Jeroen Raes](#), coauthor of the study that has been [published in Nature Microbiology](#), have discovered **people suffering from depression** lack two bacteria in their gut microbiota, called **Coprococcus** and **Dialister**.

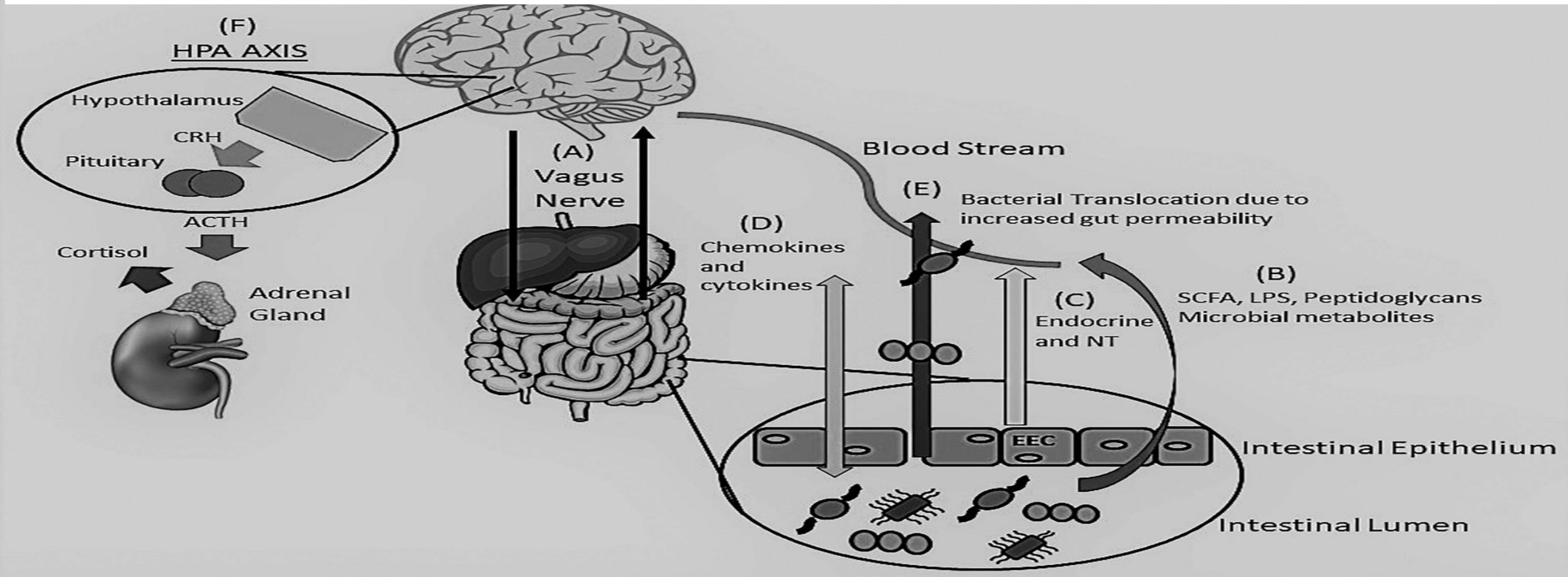


[The neuroactive potential of the human gut microbiota in quality of life and depression](#). Nature Microbiology, 2019. doi: 10.1038/s41564-018-0337-x
Antidepressants affect gut microbiota and *Ruminococcus flavefaciens* is able to abolish their effects on depressive-like behavior
Translational Psychiatry :volume 9, : 133 (2019)

REVIEW ARTICLE

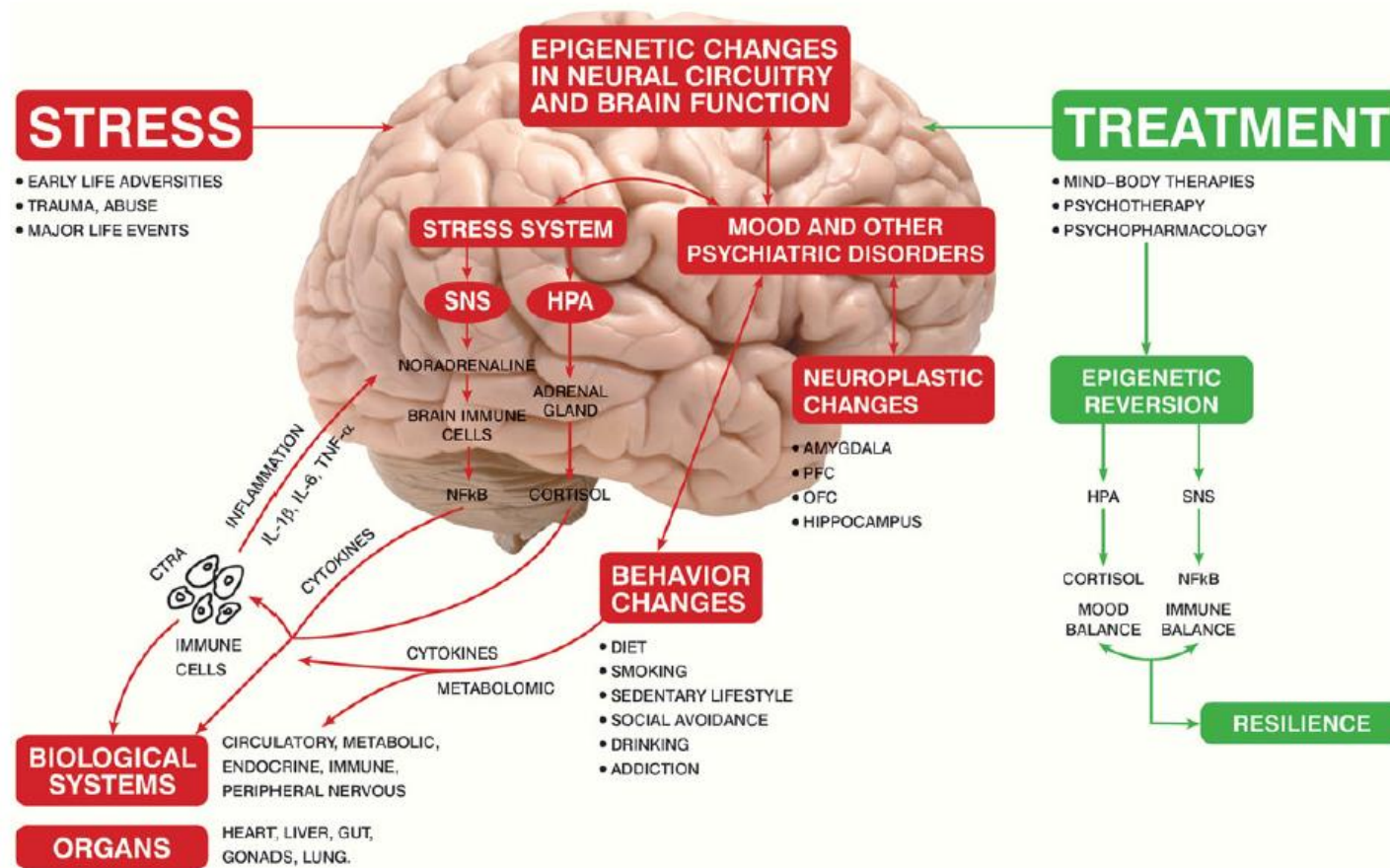


Gut microbes in neurocognitive and mental health disorders



Depiction of the bidirectional (two-way) communication between the brain and gut through the vagus nerve (A) and the immune system. Communication is achieved through various mechanisms including microbial by-products, such as SCFA, LPS and peptidoglycans (B), release of neurotransmitters (GABA, Norepinephrine, Serotonin, Acetylcholine, and others) and endocrine messengers *via* the enteroendocrine cells (C) as well as chemokine and cytokine release that can lead to neuroinflammation (D). Stress can influence the microbiota causing dysbiosis leading to an alteration of the immune system, SCFA and tryptophan levels, increasing gut permeability (“Leaky gut”) (E) and activation of the HPA axis (F).

Stress and the psyche-brain-immune network in psychiatric diseases based on psychoneuroendocrineimmunology

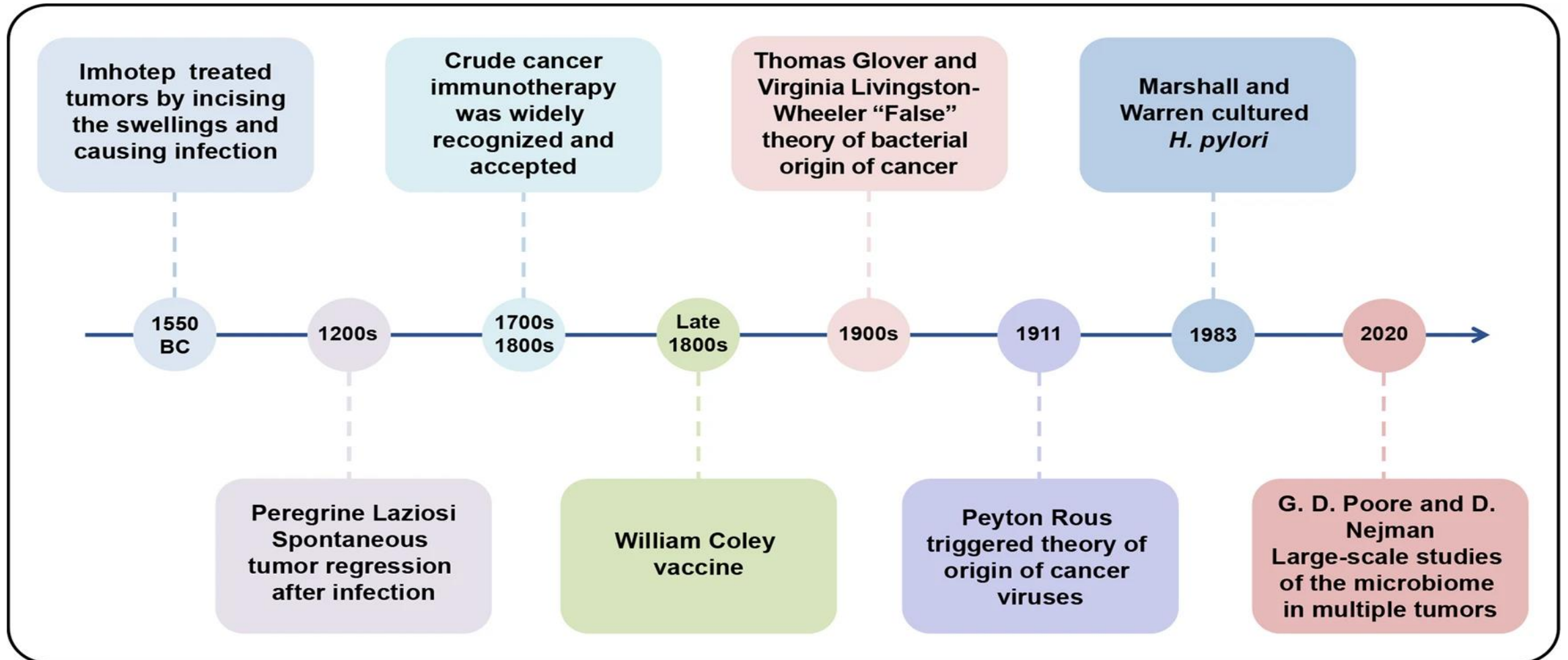


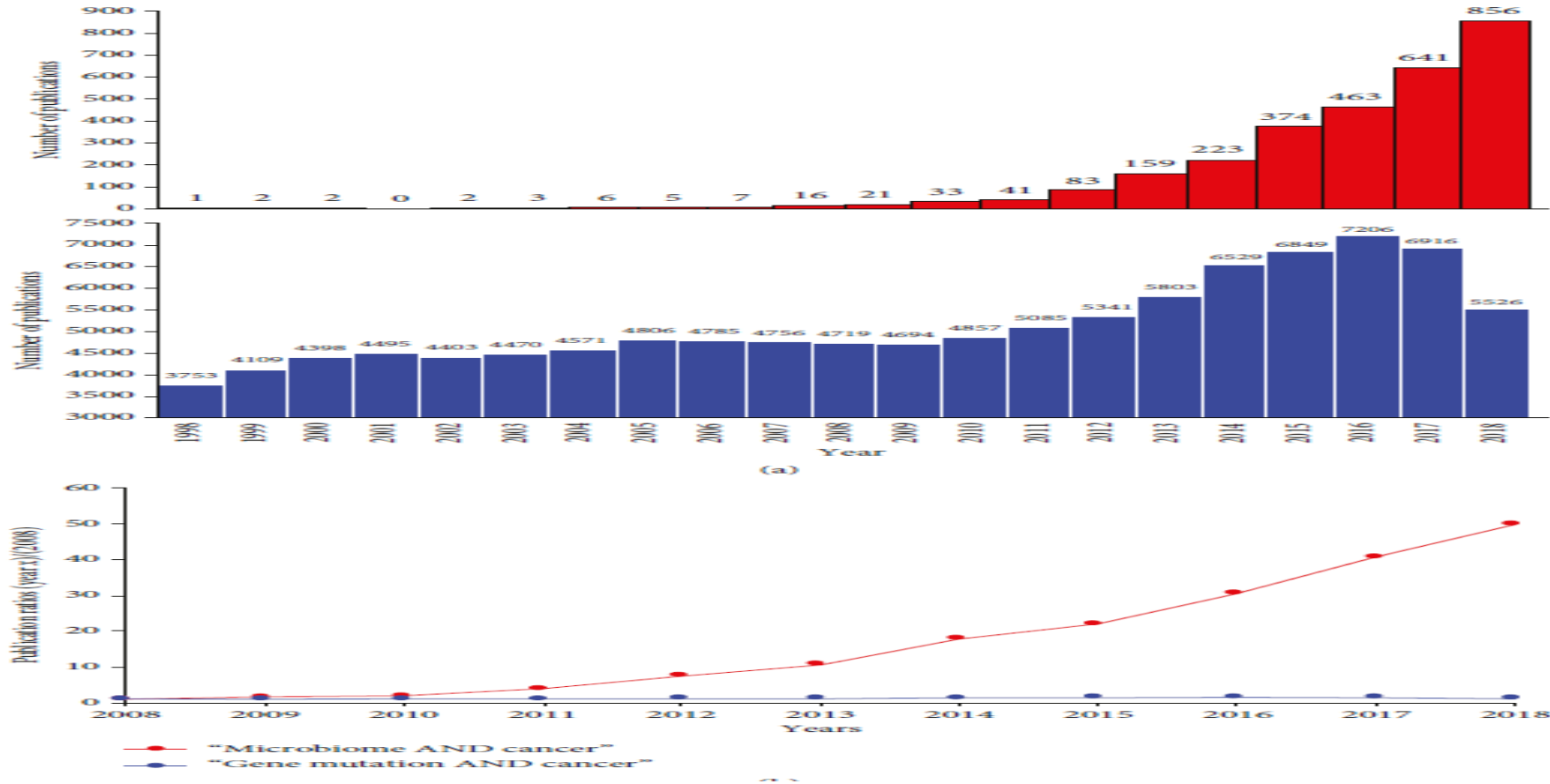
Sr. no.	Neurotransmitter	Gut microbiota families/genera	Examples of Bacterial Strains
1	Acetylcholine	<i>Lactobacillus</i>	<i>Lactobacillus plantarum</i>
2	Dopamine	<i>Bacillus</i> , <i>Escherichia</i>	<i>Escherichia coli</i> , <i>Bacillus subtilis</i>
3	GABA	<i>Bifidobacterium</i> , <i>Lactobacillus</i> , <i>Bacteroides</i> , <i>Parabacteroides</i> , <i>Alistipes</i>	<i>Bifidobacterium adolescentis</i> , <i>Lactobacillus plantarum</i> (ATCC14917), <i>Alistipes putredinis</i>
4	Noradrenaline	<i>Bacillus</i> , <i>Escherichia</i>	<i>Escherichia coli</i> (K-12), <i>Bacillus mycoides</i>
5	Serotonin	<i>Lactobacillus</i> , <i>Streptococcus</i> , <i>Escherichia</i>	<i>Lactobacillus plantarum</i> (F18595), <i>Streptococcus thermophilus</i> (NCFB2392)
6	Histamine	<i>Lactobacillus</i> , <i>Enterobacter</i>	<i>Lactobacillus plantarum</i> (F18595), <i>Lactococcus lactis</i> subsp. <i>cremoris</i> (MG 1363)

Moody Microbiome

Chronic psychosocial stress, that is, early life adversities, trauma, abuse, and major life events, can induce neuroendocrine stress system activation and epigenetic changes in neural circuitry

Timeline of the history and milestones of intratumoral microbiota. The eight key research milestones of intratumoral microbiota were retrospectively summarized from 1550 BC to present day





Importance of the microbiota in cancer. (a) Bar graphs showing the number of manuscripts published by interrogation of the PubMed bibliographic database using the keywords “microbiome AND cancer” (red, top) and “gene mutation AND cancer” (blue, bottom). (b) Graph showing the growth rate of the “microbiome AND cancer” topic (red) vs the “gene mutation AND cancer” topic calculated in the last 10 years

-omics, -ome, -omes

- **Ome and omics** are convenient ways to describe a holistic way of looking at complex systems. In the mid 1990's bioinformaticists started realizing the convenience of -omics and used terms for many fields; such as, Genome, metabolome, textome, interactome, bacteriome, virome, microbiome, mycobiome, resistome, eukaryome, functome, transcriptome, metabolome, connectome, proteome, neurome and so on.
- An “ome” is a totality. So a genome is all the DNA, including the genes, in a cell or organism. All of our proteins make up our proteome. Omic technologies allow researchers to see a more-complete picture of the ome they’re interested in.
- **Genomics and epigenomics**: The cell’s hardware and software
The study of the GENOME; how many GENES, physical map, sequence of their DNA, structure...
- **Transcriptomics**: Sending a message. FUNCTIONAL GENOMICS: The study of the TRANSCRIPTOME; which, when, where and how much mRNA expressed...
- **Proteomics and Proteogenomics**: Doing the work. The study of the PROTEOME; which PROTEINS, when, where and how much...
- **Metabolomics**: Fuel for living
- **Meta-omics of the microbiome: We are not alone**

The Human Project story



The human connectome: just another 'ome?

After the Human Genome Project there came proteomes, transcriptomes, and epigenomes. There was even a Human Microbiome Project launched last year by the US National Institutes of Health. Are neuroscientists just jumping on the 'ome bandwagon, or is there truly a benefit to deciphering and detailing the human connectome? Ruth Williams reports.

We are still a long way from the 40th century of the effects of ... publish findings on the topic. There...

'Ome,' the Sound of the Scientific Universe Expanding



CONNECTOME
COORDINATION FACILITY

Studies ▾

Software

Human Connectome Project for Early Psychosis

[Study Home](#)

[About This Study ▾](#)

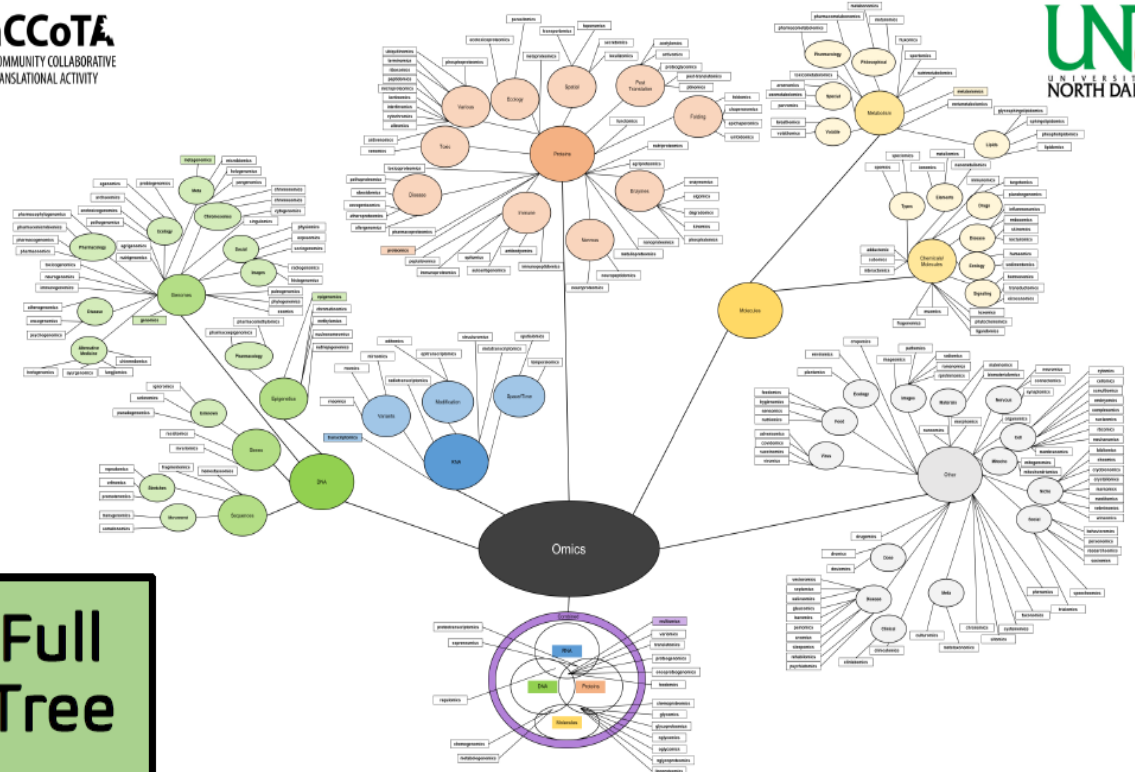
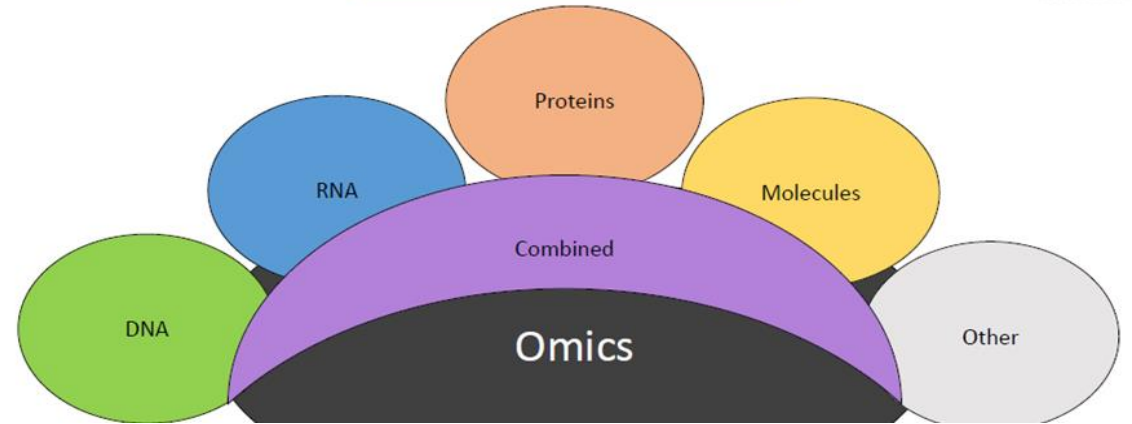
[Data ▾](#)

[Documentation](#)

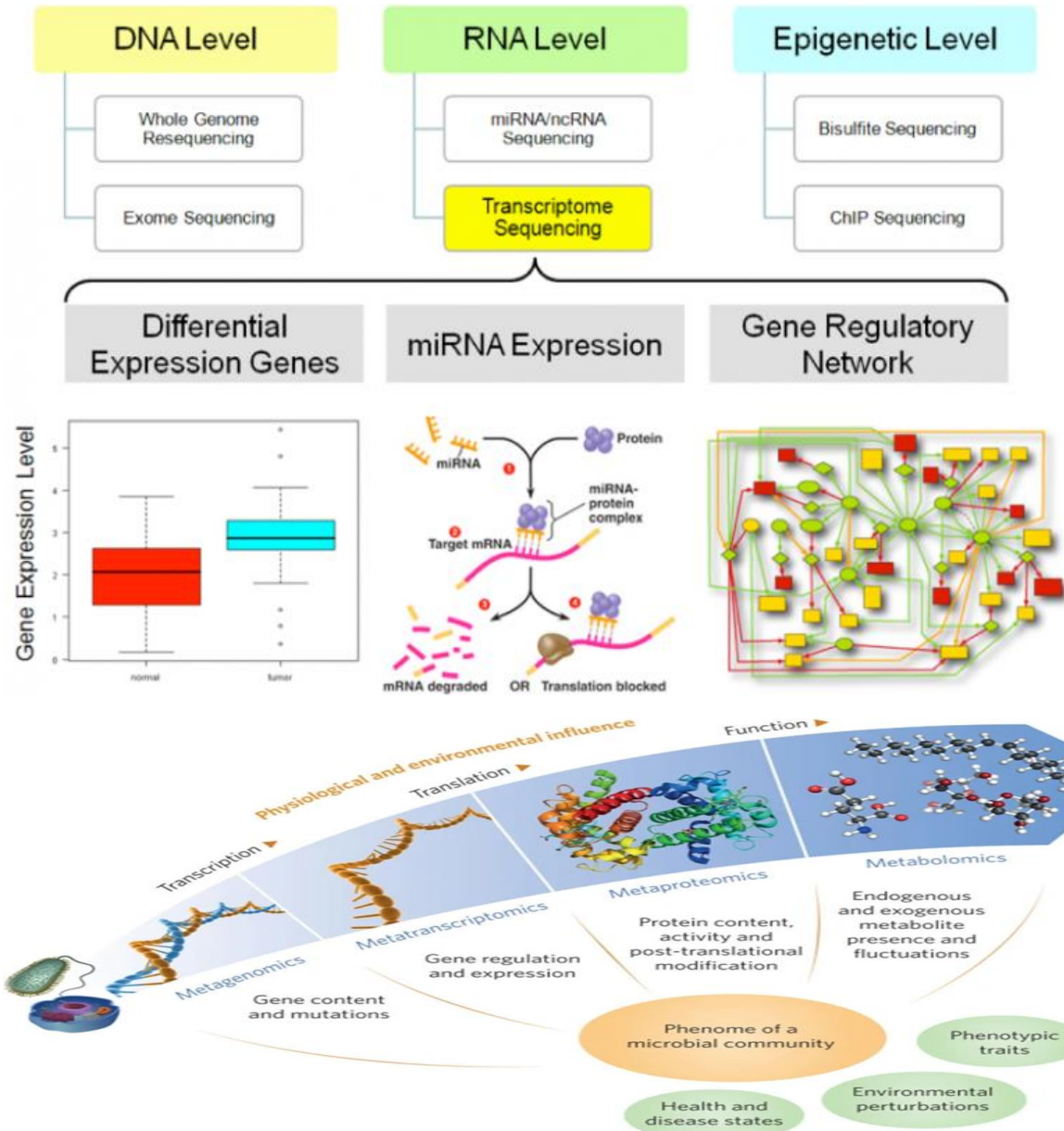
[Contact](#)

>> [DISEASE STUDIES](#) > [HUMAN CONNECTOME PROJECT FOR EARLY PSYCHOSIS](#) > [STUDY CONTACT PAGE](#)

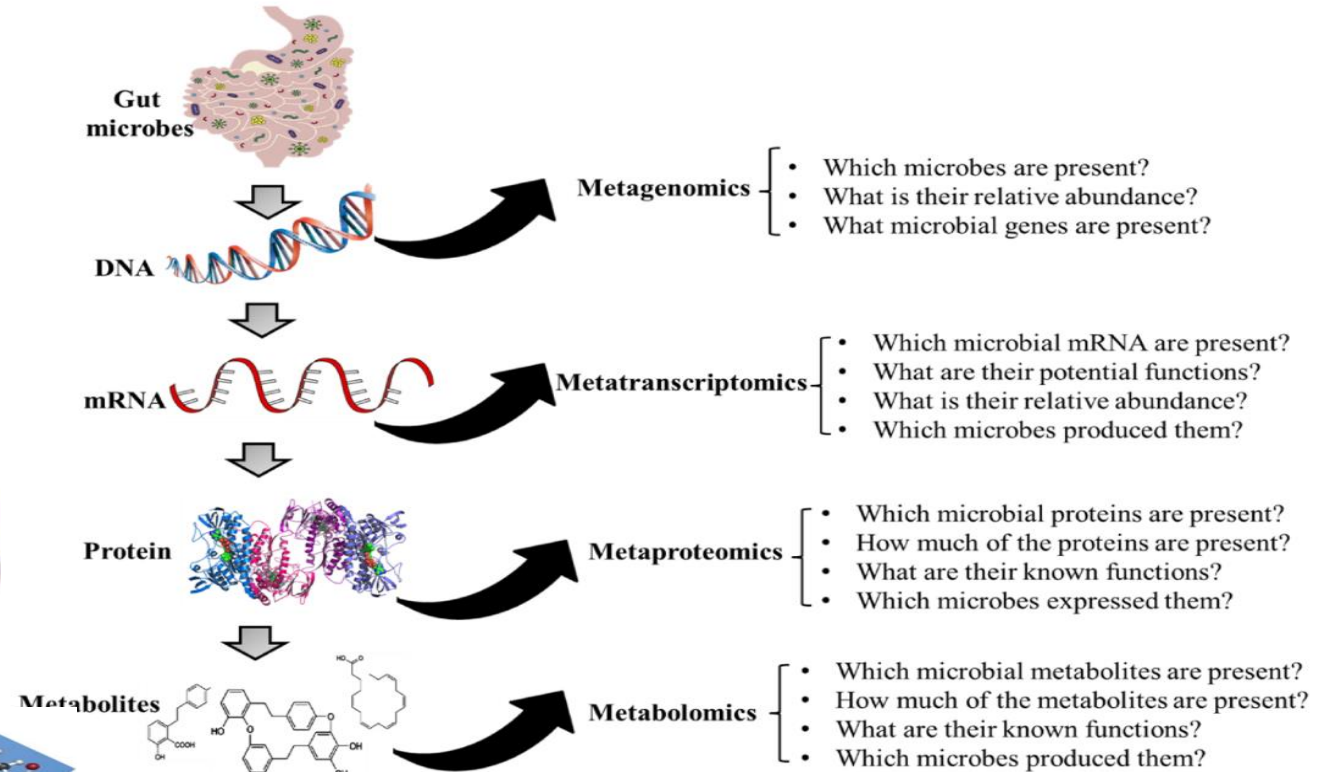
Growth of the “ome-ome”, or the types of “omic” data, over time based on mentions in Medline abstracts. Chao1 analysis indicates that there may be over 3,000 “omes”



Omic technologies and the information they provide in gut-microbiome



Gut microbiome research → Omics technology → Information they provide



Cancer pharmacomicrobiomics:

targeting microbiota to optimise cancer therapy outcomes. The gut microbiota has extremely complex interactions with cancer drugs by means of pharmacokinetics (eg, metabolism, enzymatic degradation) and pharmacodynamics (eg, immunomodulation).



Original article

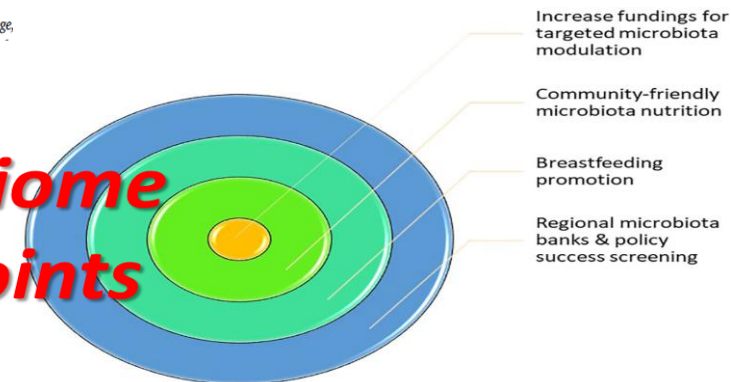
Seeking the Psilocybiome: Psychedelics meet the microbiota-gut-brain axis

John R. Kelly^{a,b,*}, Gerard Clarke^{c,d}, Andrew Harkin^e, Sinead C. Corr^{d,f}, Stephen Galvin^a, Vishnu Pradeep^{a,b}, John F. Cryan^{c,d}, Veronica O'Keane^{a,b,e}, Timothy G. Dinan^{c,d}

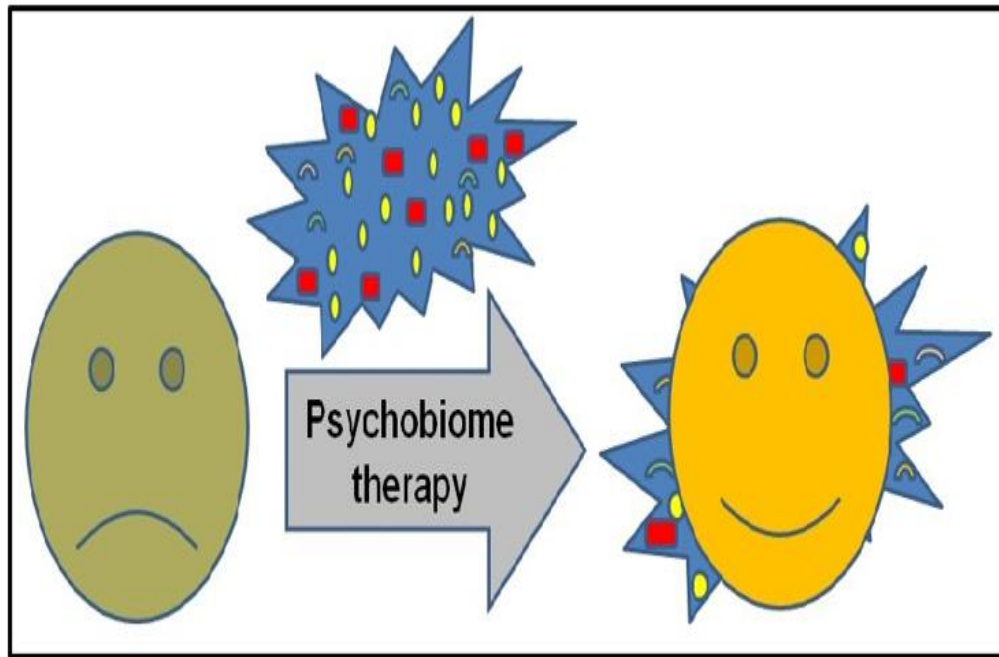
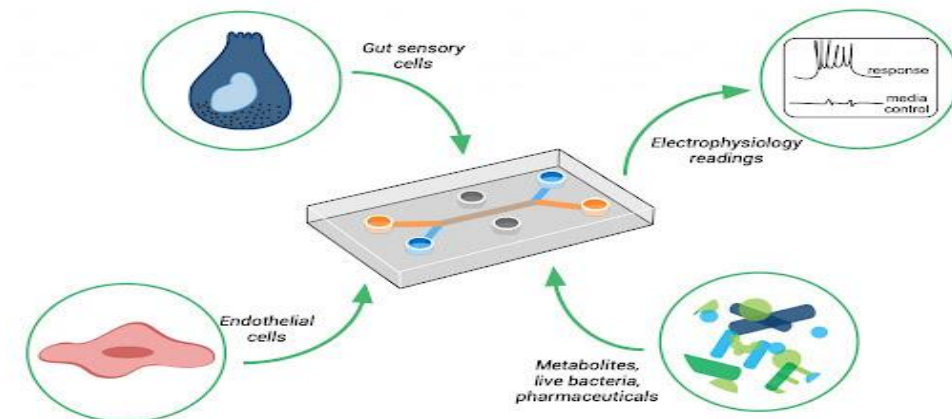
^a Department of Psychiatry, Trinity College,



Sociobiome key points



Neurobiome Start-up



The ultimate goal of psychobiome approach



International Journal of Clinical & Experimental Hypnosis Follow

Literature Review

Article

Full-text available


Hypnobiome: A New, Potential Frontier of Hypnotherapy in the Treatment of Irritable Bowel Syndrome-A Narrative Review of the Literature





The defensome of complex bacterial communities

Received: 13 August 2023

Accepted: 28 February 2024

Published online: 08 March 2024

 Check for updates

Angelina Beavogui¹, Auriane Lacroix¹, Nicolas Wiart², Julie Poulain^{1,3},
Tom O. Delmont^{1,3}, Lucas Paoli ^{4,5}, Patrick Wincker ^{1,3} & Pedro H. Oliveira ¹ 

Bacteria have developed various defense mechanisms to avoid infection and killing in response to the fast evolution and turnover of viruses and other

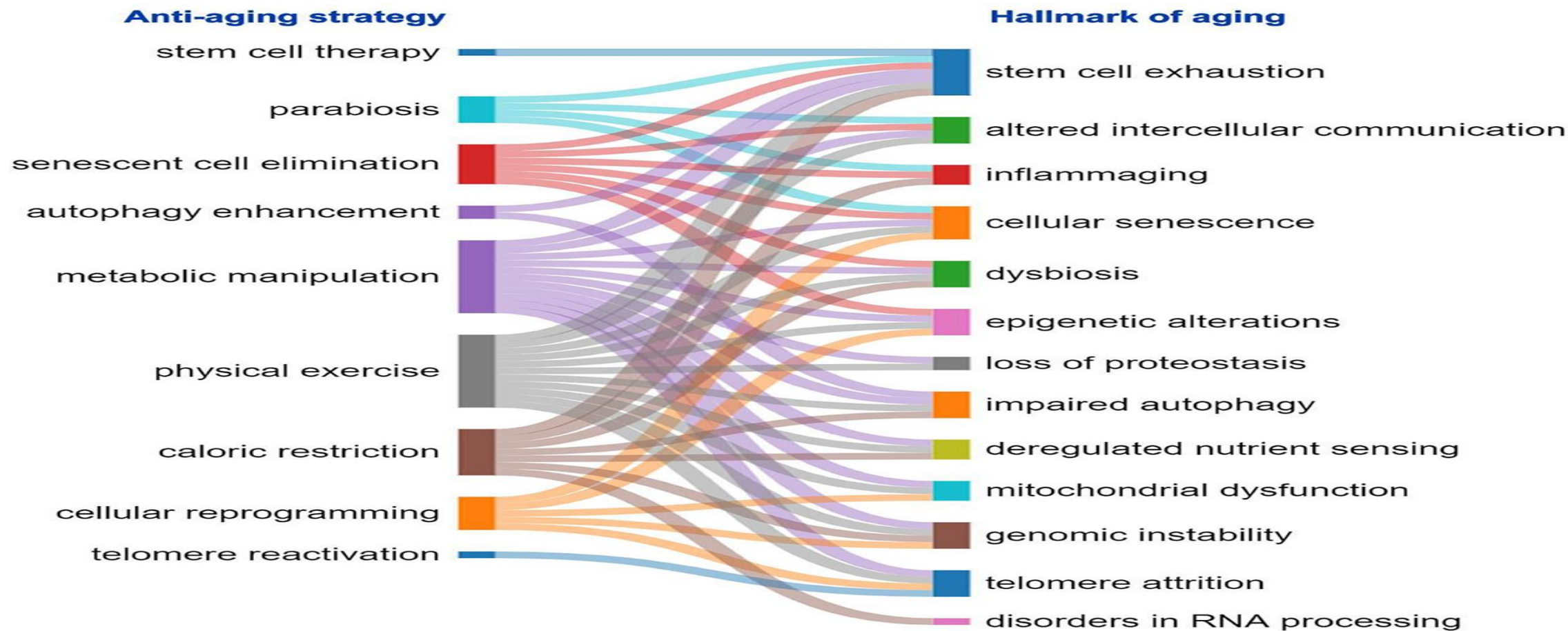
Bacteria have developed various defense mechanisms to avoid infection and killing in response to the fast evolution and turnover of viruses and other genetic parasites. Such pan-immune system (defensome) encompasses a growing number of defense lines that include well-studied innate and adaptive systems such as restriction-modification, CRISPR-Cas and abortive infection, but also newly found ones whose mechanisms are still poorly understood.

the defensomes of 7759 high-quality bacterial population genomes reconstructed from soil, marine, and human gut environments. That observed a wide variation in the frequency and nature of the defensome among large phyla, which correlated with lifestyle, genome size, habitat, and geographic background.

Antiaging Strategies and Remedies: A Landscape of Research Progress and Promise

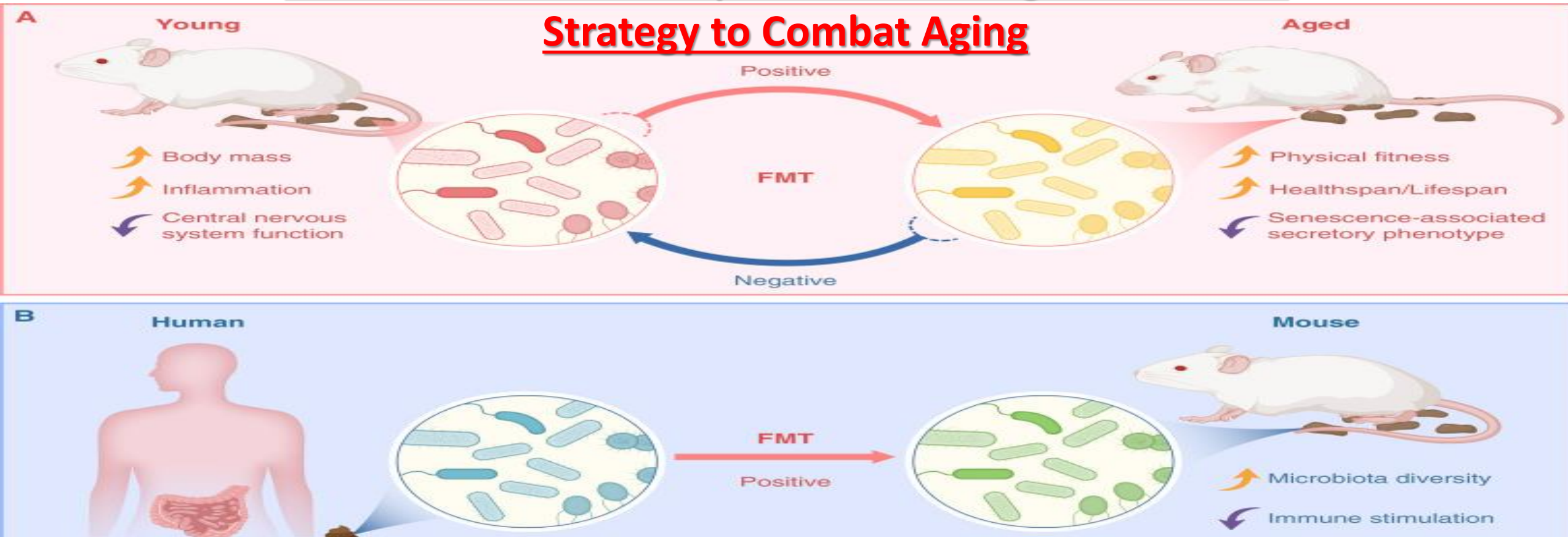
Rumiana Tenchov, Janet M. Sasso, Xinmei Wang, and Qiongqiong Angela Zhou*

Cite This: ACS Chem. Neurosci. 2024, 15, 408–446



Relationship between antiaging strategies and the hallmarks of aging they counteract.

Fecal Microbiota Transplantation Emerges as a Novel Strategy to Combat Aging



potential mechanisms and challenges of FMT, highlighting its potential to enhance aging-related health outcomes.



Aging and Dysbiosis: Age-related changes lead to dysbiosis—an imbalance in gut microbiota.

Restoring Balance: FMT, transferring beneficial microbes from a healthy donor to recipients with disrupted microbiota, shows promise in restoring balance.

Youthful Impact: Studies indicate FMT from young donors yields more significant benefits than from aged donors. Across

Organs: FMT holds potential to ameliorate aging-associated impairments across diverse organs.

A host–microbiota interactome reveals extensive transkingdom connectivity

[Nicole D. Sonnert](#), [Connor E. Rosen](#), [Andrew R. Ghazi](#), [Eric A. Franzosa](#), [Brianna Duncan-Lowey](#), [Jaime A. González-Hernández](#), [John D. Huck](#), [Yi Yang](#), [Yile Dai](#), [Tyler A. Rice](#), [Mytien T. Nguyen](#), [Deguang Song](#), [Yiyun Cao](#), [Anjelica L. Martin](#), [Agata A. Bielecka](#), [Suzanne Fischer](#), [Changhui Guan](#), [Julia Oh](#), [Curtis Huttenhower](#), [Aaron M. Ring](#)  & [Noah W. Palm](#) 

[Nature](#) **628**, 171–179 (2024) | [Cite this article](#)

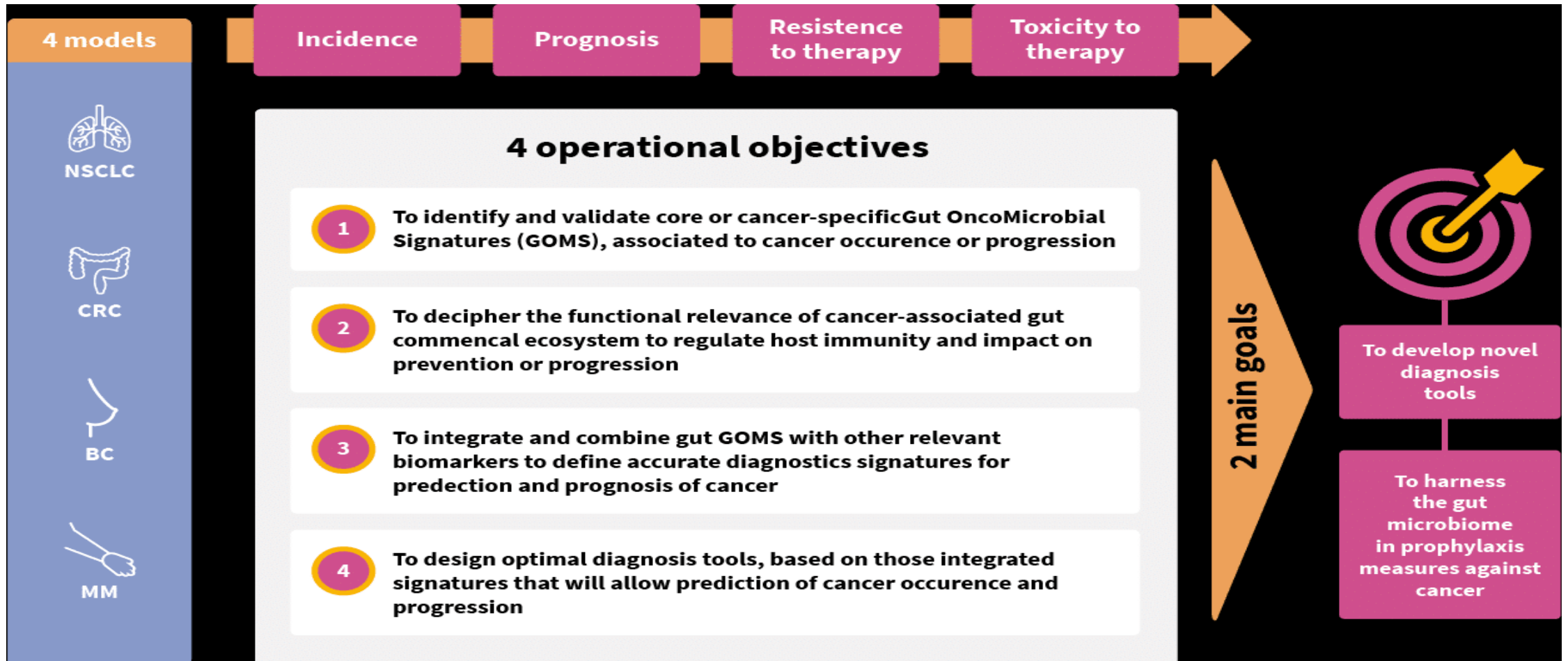
21k Accesses | **1** Citations | **109** Altmetric | [Metrics](#)

- Classical pathogens often invade host tissues and modulate immune responses through interactions with human extracellular and secreted proteins (the ‘exoproteome’). Commensal microorganisms may also facilitate niche colonization and shape host biology by engaging host exoproteins; however, direct exoproteome–microbiota interactions remain largely unexplored.
- Developed and validated a novel technology, BASEHIT, that enables proteome-scale assessment of human exoproteome–microbiome interactions.
- Using BASEHIT, researchers interrogated **more than 1.7 million potential interactions between 519 human-associated bacterial strains from diverse phylogenies and tissues of origin and 3,324 human exoproteins.**
- **The resulting interactome** revealed an extensive network of transkingdom connectivity consisting of thousands of previously undescribed host–microorganism interactions involving 383 strains and 651 host proteins. Specific binding patterns within this network implied underlying biological logic; for example, conspecific strains exhibited shared exoprotein-binding patterns, and individual tissue isolates uniquely bound tissue-specific exoproteins.

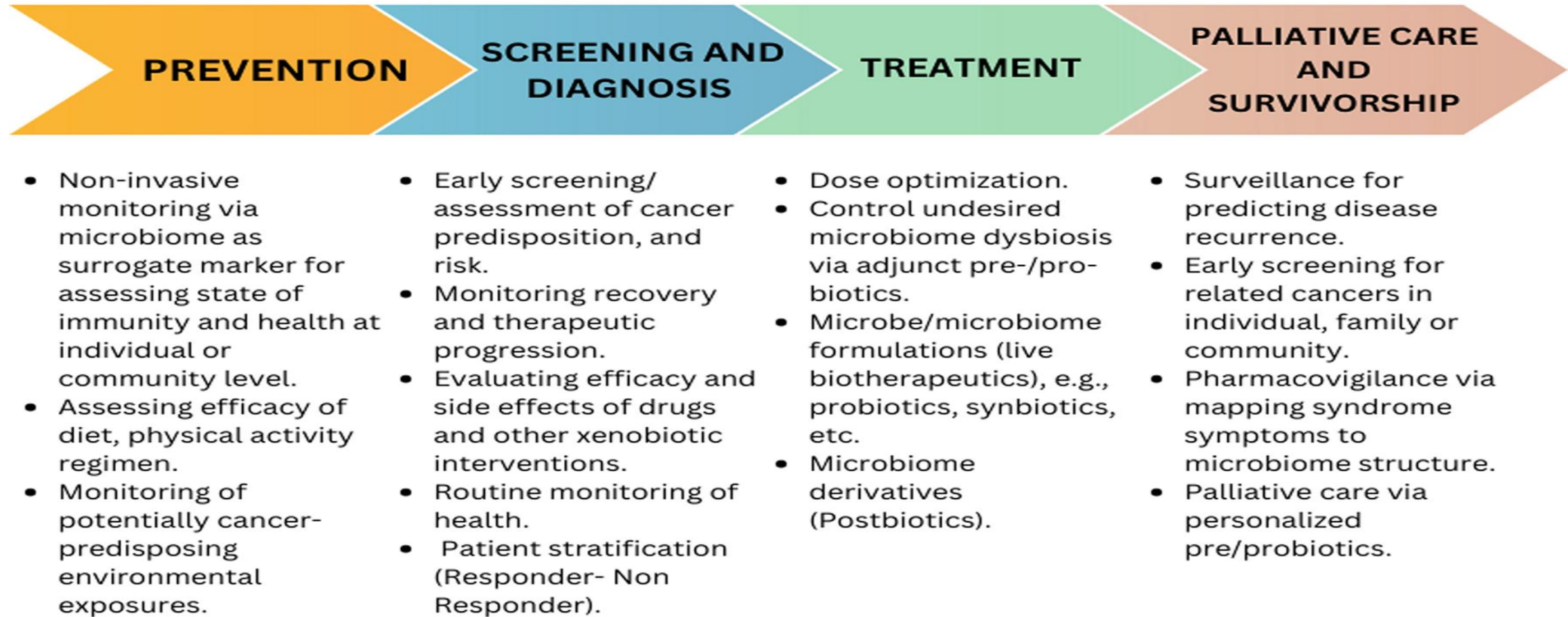
potential roles in niche colonization, tissue remodelling and immunomodulation,

Oncobiome Project presentation

In view of the world-wide epidemic of cancer, which is linked to environmental and life-style factors, there is an unmet medical need in breakthrough concepts to understand the causes of neoplasia.

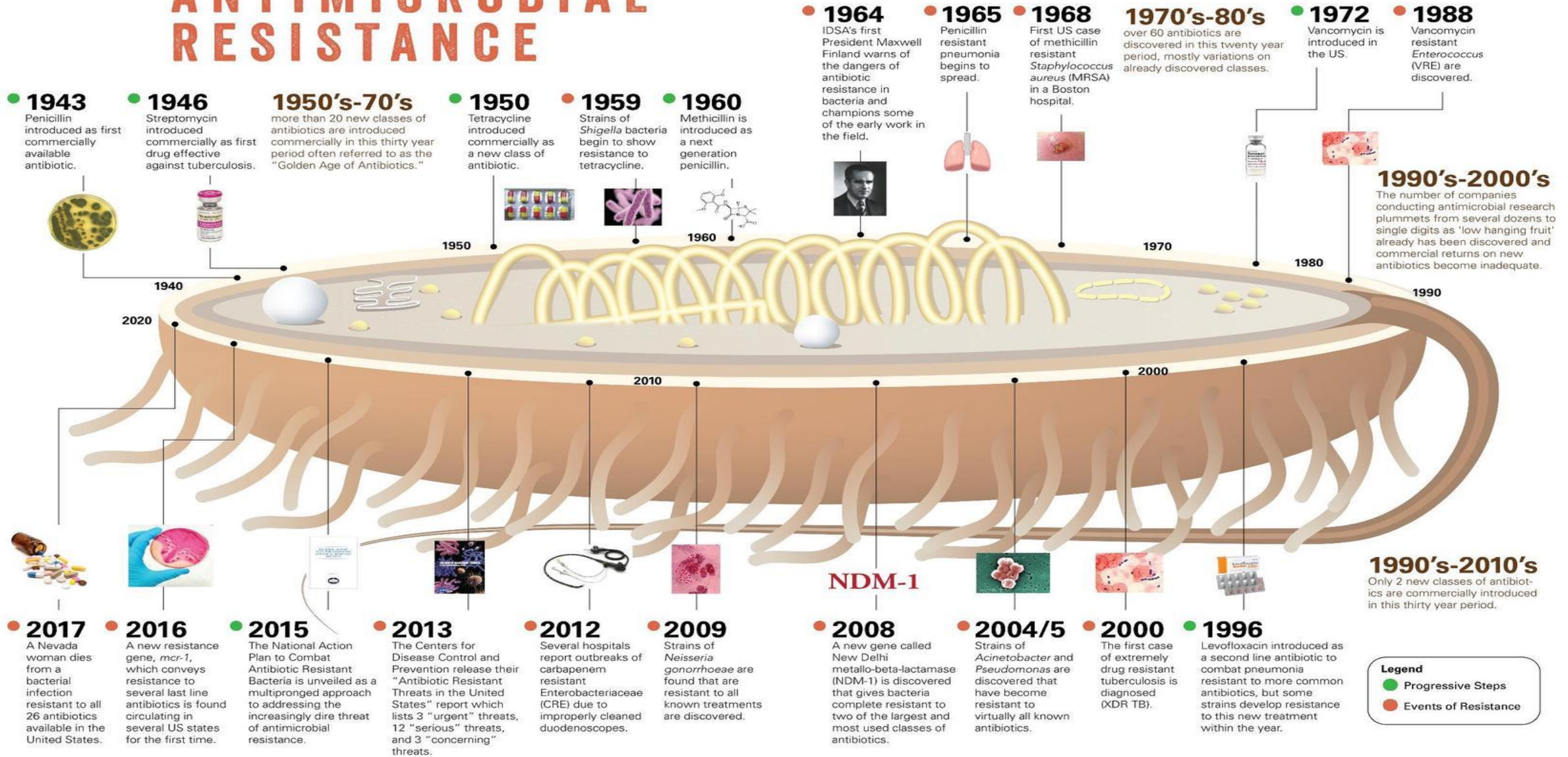


THE HUMAN MICROBIOTA: A Novel Scientific Avenue with Potential for Improving Services Across the Entire Continuum of Cancer Care



The Human Microbiota: A Novel Scientific Avenue with Potential for Improving Services Across the Entire Continuum of Cancer Care. The figure illustrates the potential role of the human microbiota in various stages of cancer care, including prevention, screening, diagnosis, treatment, palliative & supportive care.

The Development of ANTIMICROBIAL RESISTANCE



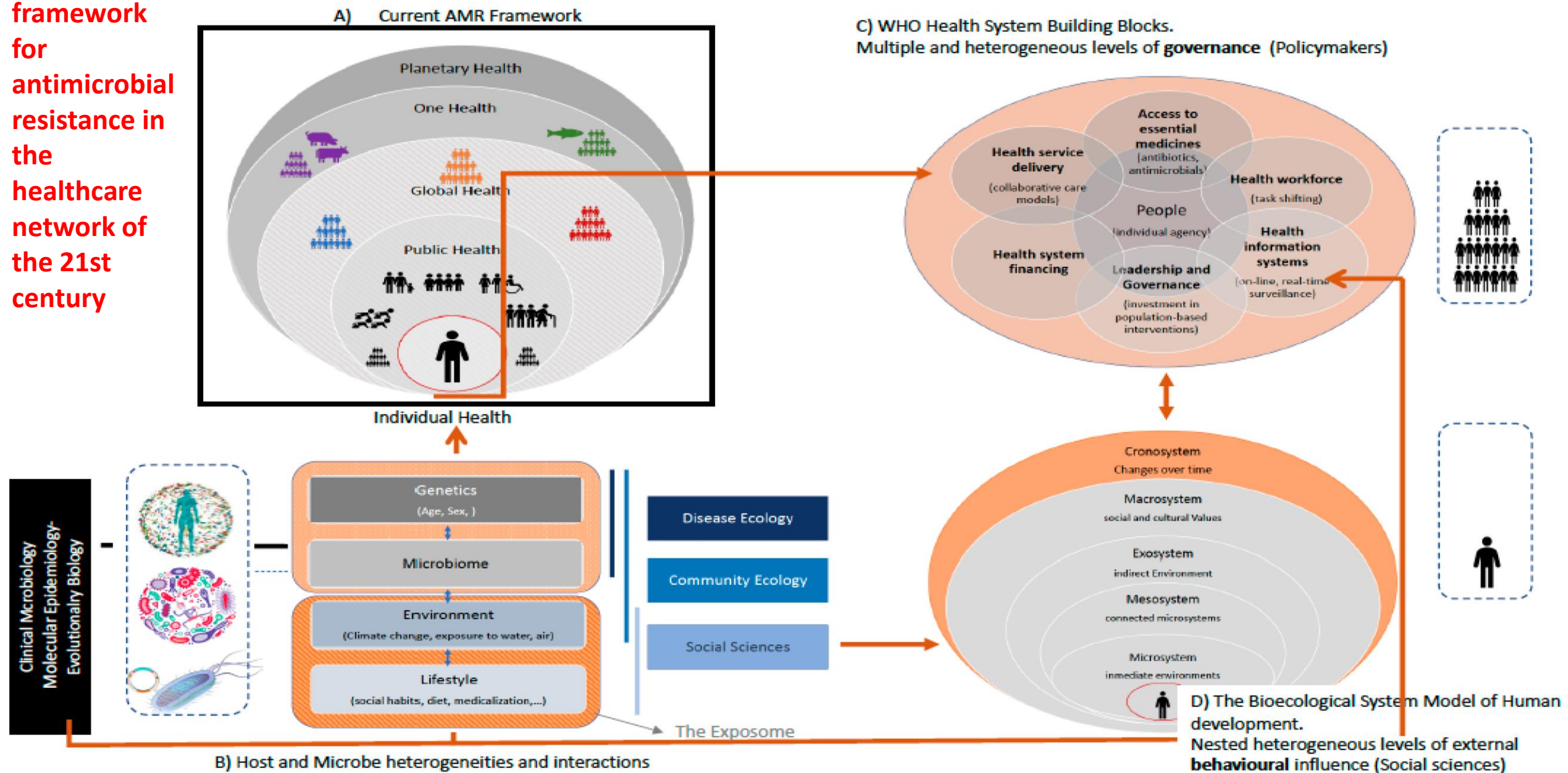
The antibiotic resistome: what's new?

The term “antibiotic resistome” was first coined in 2006 by Gerry Wright’s group. Later, the resistome was defined as “a collection of all the ARGs and their precursors in pathogenic and nonpathogenic bacteria. Its constituents were precisely described as “all ARGs, including those circulating in pathogenic bacteria, antibiotic producers, and benign nonpathogenic bacteria”. Considering the origin of ARGs, the resistome has been suggested to include protoresistance genes as a deep reservoir of ARG precursors, as well as clinical, environmental, and intrinsic

In summary, the antibiotic resistome encompasses all types of ARGs (acquired and intrinsic resistance genes), their precursors, and some potential resistance mechanisms within microbial communities that require evolution or alterations in the expression context to confer resistance

Resistome	<ul style="list-style-type: none">• Group of all existing resistance genes (known or unknown) in the world
Acquired resistance	<ul style="list-style-type: none">• Phenotypically resistant to an antibiotic due to the presence of a resistance gene that is not natively present in other taxonomically related bacteria.• Resistance gene is present on a plasmid or on the chromosome• Resistance can be vertically or horizontally transferred
Intrinsic resistance	<ul style="list-style-type: none">• Phenotypically resistant due to a trait common to all taxonomically related bacteria (e.g. LPS, efflux pumps)• Resistance gene(s) is/are present on the chromosome only• Resistance is vertically transmitted
Silent/cryptic resistance	<ul style="list-style-type: none">• Phenotypically sensitive (no growth in presence of antibiotic)• Resistance genes are functional, but are <i>not expressed</i>• Clinical/environmental prevalence unknown• May become clinically significant if expression is restored by either mutation or mobilization
Proto-resistance	<ul style="list-style-type: none">• Phenotypically sensitive (no growth in presence of antibiotic)• Proto-resistance genes have little/no activity against antibiotics, but could gain activity if mutations occur• Genes are part of the environmental reservoir but are farthest from clinical significance due to need for both activation and mobilization.• Prevalence unknown
Environmental resistance	<ul style="list-style-type: none">• Any of the above types of resistance when noted in a <i>non-pathogenic</i> strain of bacteria
Clinical resistance	<ul style="list-style-type: none">• Any of the above types of resistance when noted in a <i>pathogenic</i> strain of bacteria

framework
for
antimicrobial
resistance in
the
healthcare
network of
the 21st
century



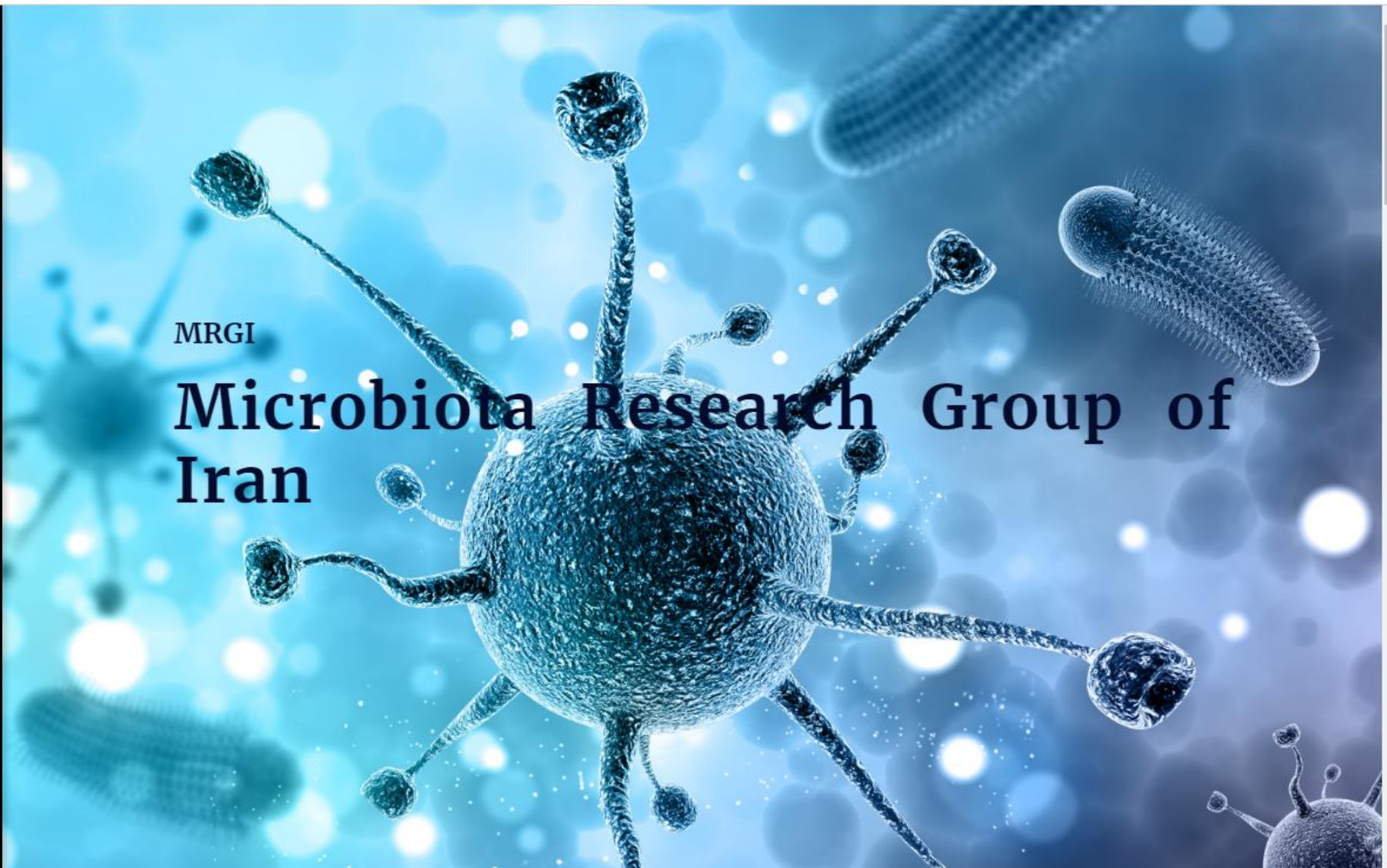
Brown arrows represent connections between the various levels. Dotted boxes reflect the central targeted unit, namely humans, in (A,D); human groups in (C); and microbes and hosts in (B). **Orange-colored areas represent the influence of time in all systems (human, microbial, individual species, and institutions).**



- Home
- Database
- Covid-19
- Scientometrics
- People
- Publications
- Projects
- Videos
- Events
- Contact Us

MRGI

Microbiota Research Group of Iran



11TH
WORLD
CONGRESS

TARGETING MICROBIOTA

International Society
of **m**icrobiota

Towards Clinical Revolution

October 14, 15, 2024 - Corinthia Palace, Malta



***World
Microbiome
Day | 27th June***

Thanks for your attention



INSTITUT
PASTEUR

[THE INSTITUT PASTEUR](#)

[OUR MISSIONS](#)

[SUPPORT US](#)

[MEDICAL CENTER](#)

[THE RESEARCH JOURNAL](#)

[PRESS AREA](#)



[Home](#) > [The research journal](#) > [News](#) > [The gut microbiota: an incredibly rich ecosystem](#)

THE RESEARCH JOURNAL

THE GUT MICROBIOTA: AN INCREDIBLY RICH ECOSYSTEM

