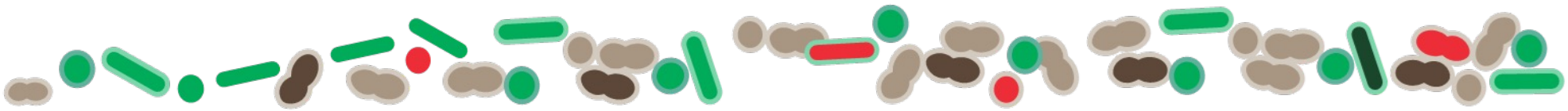
University College Roosevelt

HartVaatHAG
Hart- en Vaatziekten Huisartsen Advies Groep

HVZ en het microbioom



Thomas van Luyn

Buikschaamte en doodsangst

Ik ben weer eens gedoken in mijn buikje. Dat komt, ik moet voor een podcast iets bedenken waar ik me voor schaam. Dat vond ik moeilijk, want schaamte bestrijkt een spectrum met aan het ene eind het gevoel wanneer je een scheet moet laten op de fiets en merkt dat er iemand vlak achter je rijdt, tot aan je echtgenote vermoorden en in je tuin begraven, en dat je met je onwetende kinderen staat te barbecuen en de hond haar ineens opgraaft en je kinderen zien dat mama helemaal niet naar Groenland is verhuisd zoals papa al die tijd beweerde.

Dus ik dacht: laat ik het simpel houden en het hebben over mijn buikje. Hoewel schaamte een veel te groot woord is voor

Als sporten en minder eten niet de manier is, wat dan wel? Ik vond een podcast met een heuse professor in Engeland die het allemaal heeft uitgevogeld. Alles is de schuld van ons bioom. Ons wat? Ons bioom. Dat betekent zoiets als vegetatiezone. Je weet wel: loofbossen, naaldbossen, enzovoorts. Wij hebben nameliik ook een bioom in ons: onze darmflora. En omdat we veel te weinig verschillende dingen eten, hebben we te weinig darmplantjes en daarom zijn we te dik.

Zoiets.

Wat ik daaraan kon doen bleek ingewikkeld. Er bleek namelijk niet één oplossing te zijn, zoals: eet meer fruit. Want ieders bioom reageert anders op verschillende soorten voedsel, dus iedereen moet een eigen dieet hebben. En laat deze professor daar nou toevallig een bedrijf voor hebben. Je moet ze regelmatig poep en bloed

Thomas van Luyn



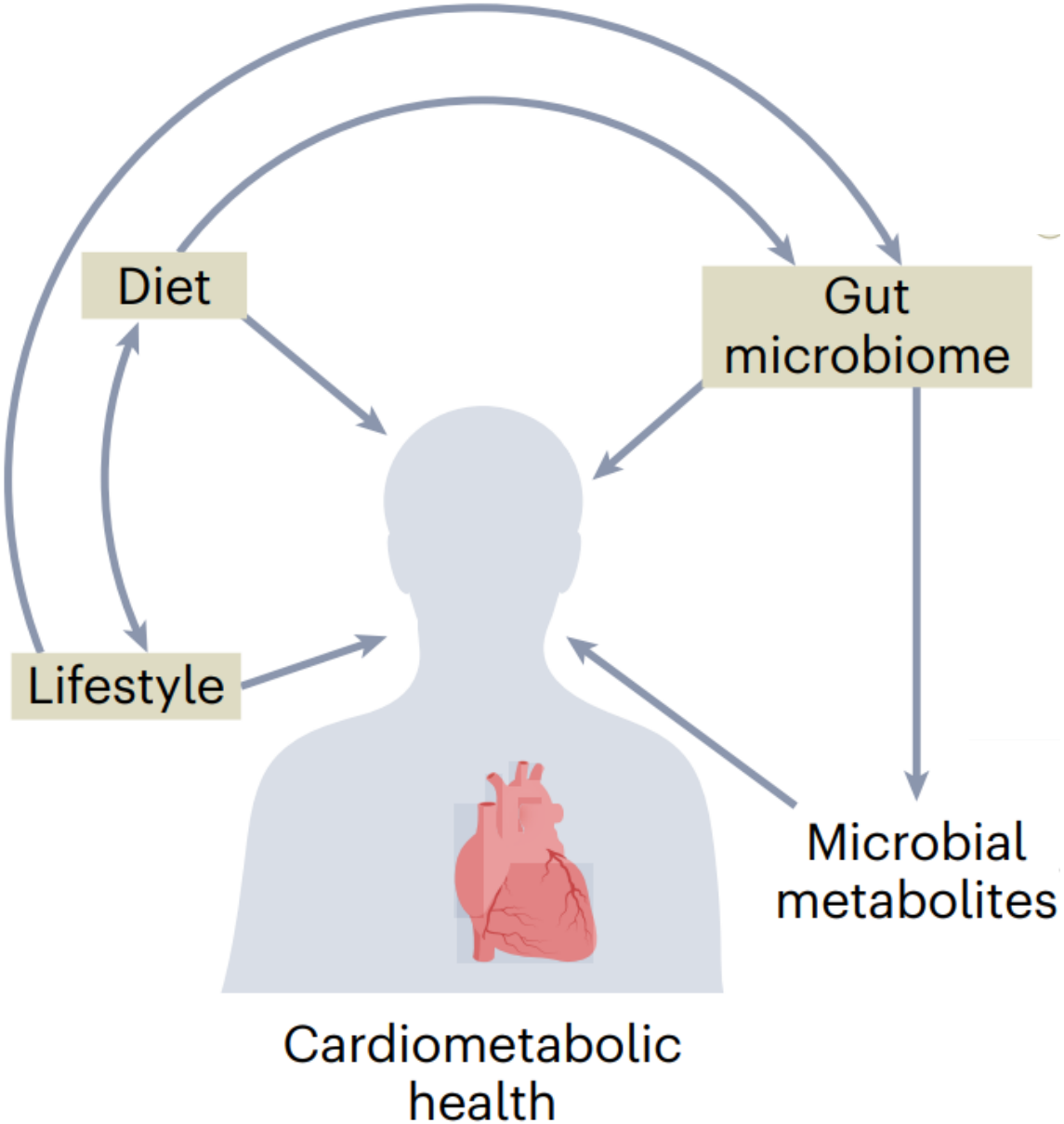
elde

Ik heb de hele podcast af geluisterd, en de professor leek me heel deskundig, maar ik zag mezelf niet dagelijks bloed en poep in envelopjes proppen en op de post doen.

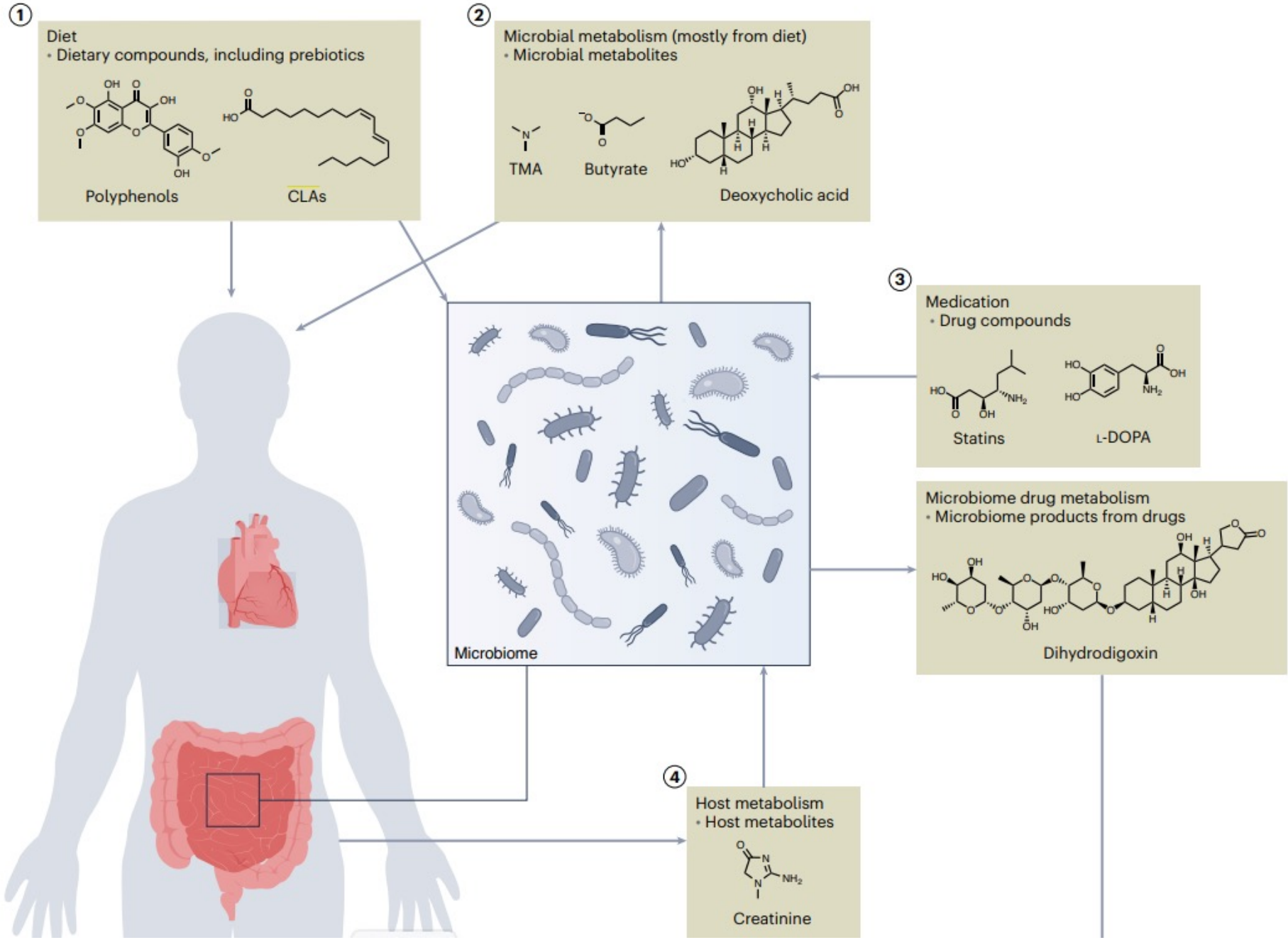
Helemaal aan het eind had hij toch nog een algemene tip: minimaal dertig soorten plantaardig voedsel per week. Dat lijkt veel, maar koffie en thee tellen mee, net als bijvoorbeeld nootjes of de schimmel uit blauwe kaas. Bier en chips noemde hij niet, maar die zijn ook plantaardig dus ik zit voorlopig snor.

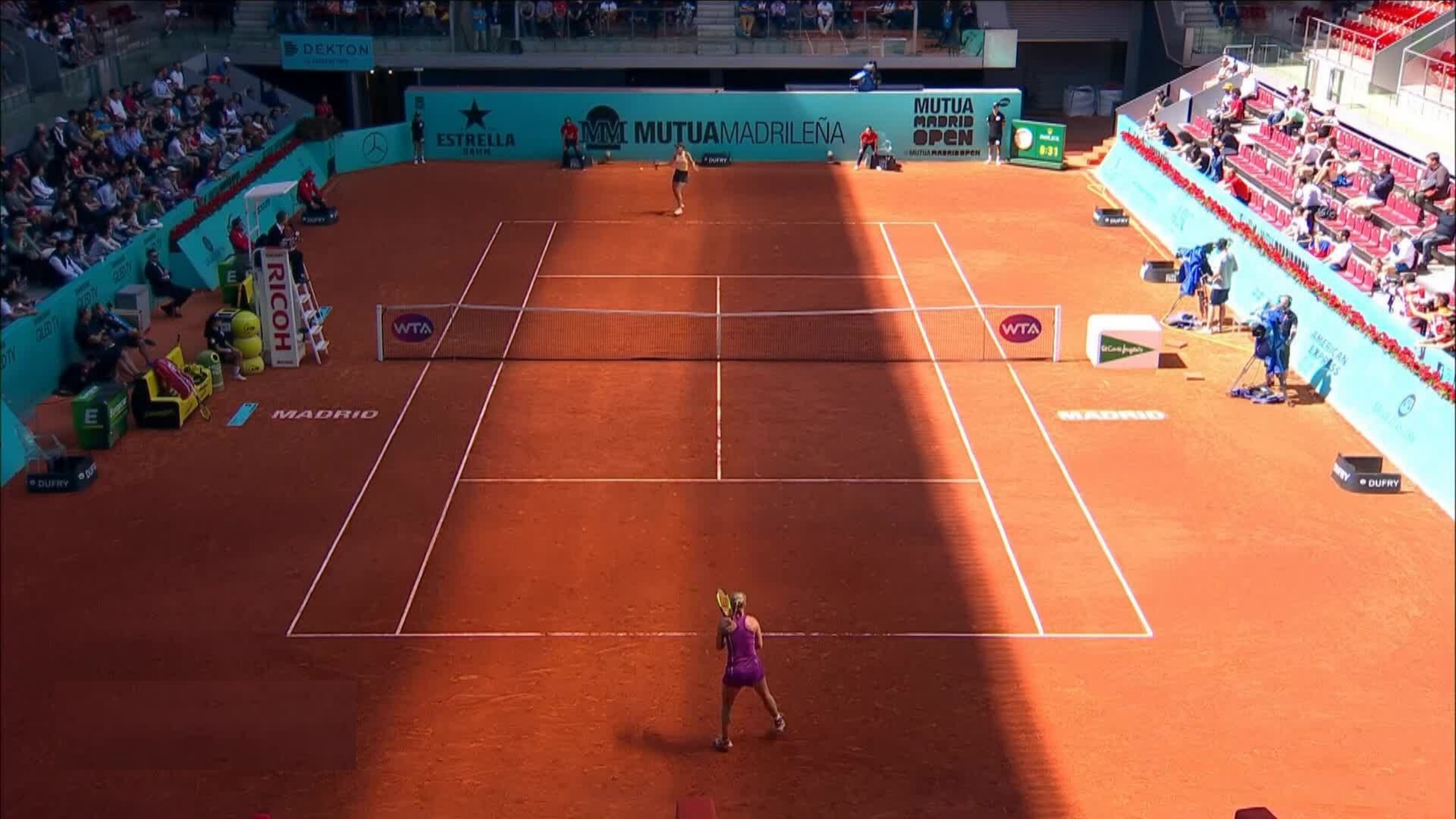
t.vanluyn@volkskrant.nl

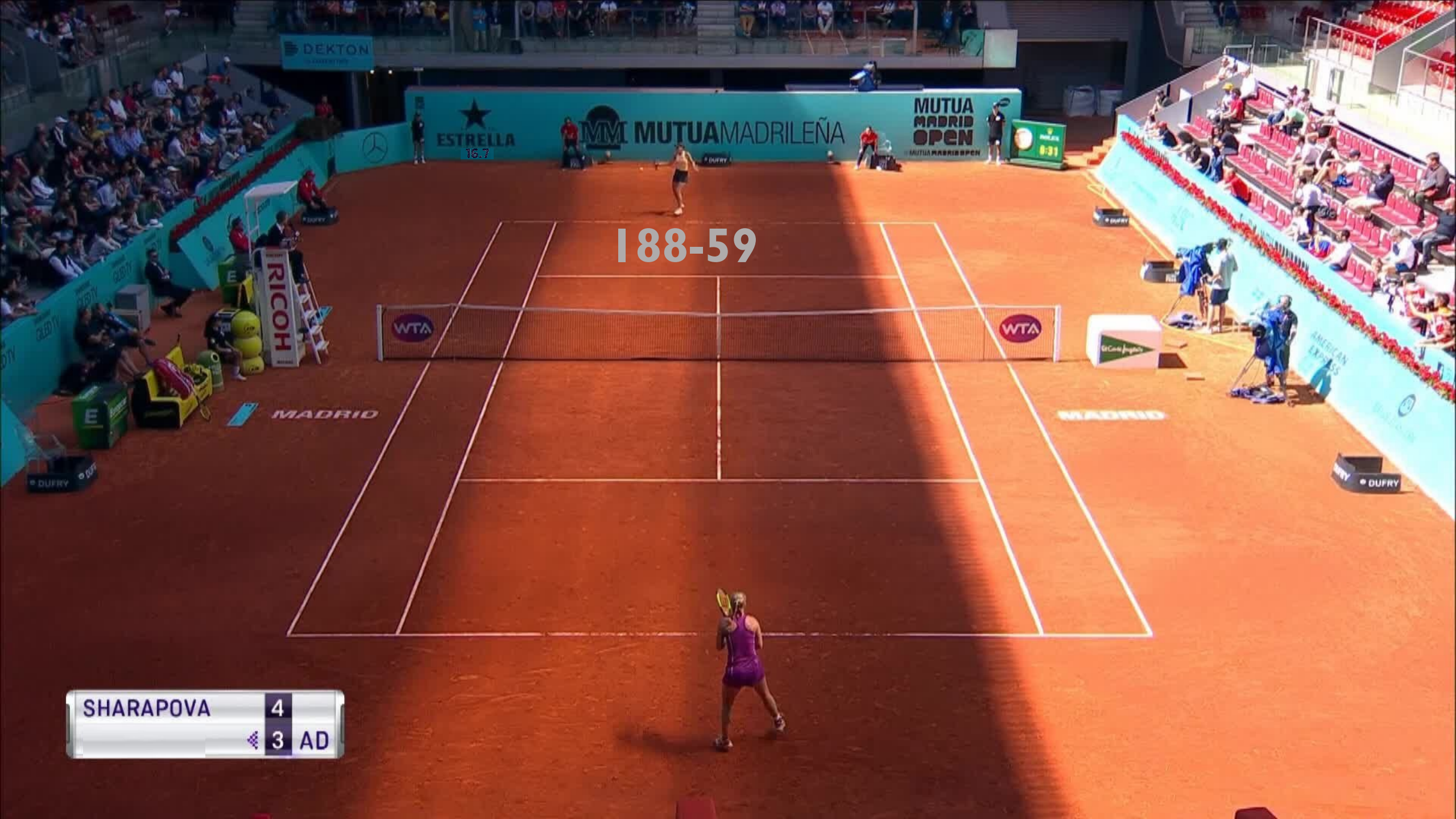
https://www.theguardian.com/lifeandstyle/2022/may/15/go-with-your-gut-tim-spector-power-of-microbiome



https://doi.org/10.1038/s41591-023-02260-4


1
Diet
• Dietary compounds, including prebiotics
Polyphenols
CLAs
2
Microbial metabolism (mostly from diet)
• Microbial metabolites
TMA
Butyrate
Deoxycholic acid
3
Medication
• Drug compounds
Statins
L-DOPA
Microbiome
Microbiome drug metabolism
• Microbiome products from drugs
Dihydrodigoxin
4
Host metabolism
• Host metabolites
Creatinine

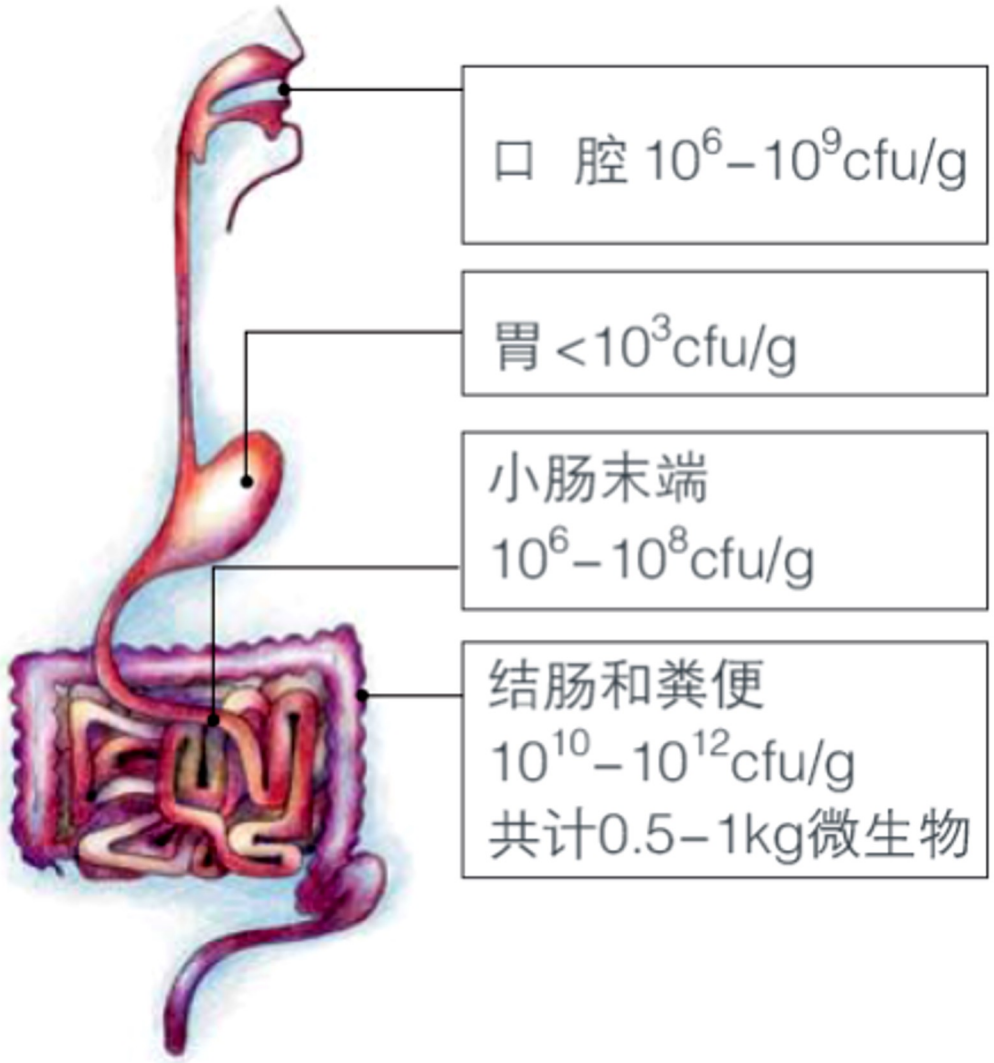

DEKTON
ESTRELLA DAMM
MUTUAMADRILEÑA
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RICOH
WTA
WTA
MADRID
MADRID
DUFRY
DUFRY


188-59
SHARAPOVA 4
3 AD
MUTUAMADRILEÑA
MUTUA MADRID OPEN
ESTRELLA
RICOH
MADRID
DUFRY
WTA

Achromobacter spp, Acidaminococc ermentans, Acinetobacter calcoaceticus, Actinomyces spp, Actinomyces viscosus, Actinomyces slundii, Aeromonas spp, Aggregatibacter actinomycetem-comitans, Anaerobiospirillum spp, Alcali es faecalis, Arachnia propionica, Bacillus spp, Bacteroides spp, Bacteroides gingivalis, Bacteroides fra , Bacteroides intermedius, Bacteroides melanino-genicus, Bacteroides pneumosintes, Bacterione otii, **Bifidobacterium spp**, Buchnera aphidicola, Butyriviberio fibrosolvens, Campyloba Campylobacter coli, Campylobacter sputorum, Campylobacter upsaliensis, Candida a a spp, Clostridium spp, Citrobacter freundii, Clostridium difficile, Clostric , Cor bacterium spp, Cutibacterium acnes, Eikenella corrodens, Enterobacter cloa occus , Enterococcus faecalis, Entero-coccus faecium, Escherichia coli, Eubacterium sp erium lavobacterium spp, Fusobacterium spp, Fusobacterium nucleatum, Gordonia p, Haemophilus para-influenzae, Haemophilus paraphrophilus, **Lactobacillus spp**, L salis, Methano-brevibacter smithii, Morganella morganii, Mycobacteria spp, Mycoplas cus spp, Mycoplasma spp, Mycobacterium chelonae, Neisseria spp, Neisseria sic ptococ spp, Peptostreptococcus spp, Plesiomonas shigelloides, Porphyromonas gingivalis, ionibac m spp, Providencia spp, Pseudomonas aeruginosa, Ruminococcus bromii, Rothia de iosa, -coccus spp, Sarcina spp, Staphylococcus aureus, Staphylococcus epidermidis, Strepto cus an s, Streptococcus mutans, Streptococcus oralis, Streptococcus pneumoniae, Strepto us sobrinus, Streptococcus viridans, Torulopsis glabrata, Treponema denticola, Treponema refring eillonella spp, Vibrio spp, Vibrio sputorum, Wolinella succinogenes. Yersinia enterocolitica



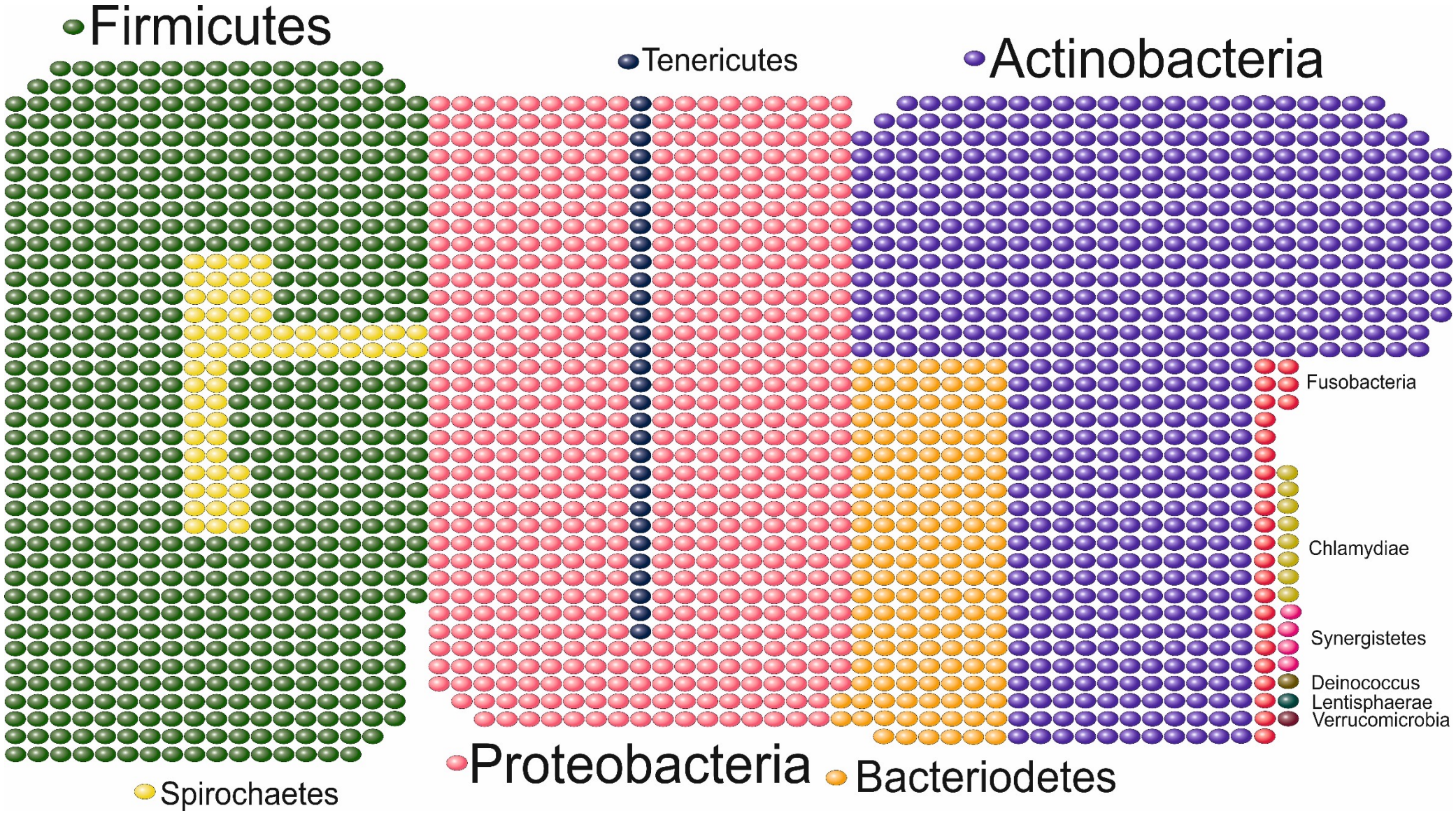
Darmbacterien: aantallen



1.000.000.000

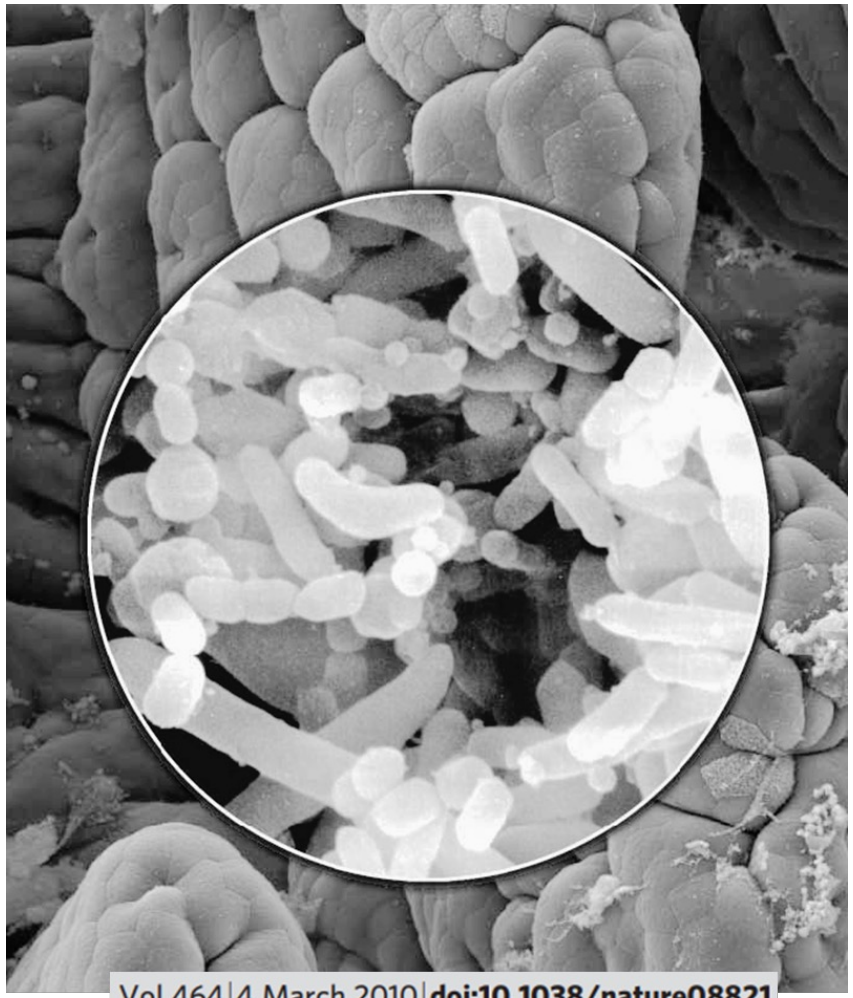
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2172 different bacteria



Microbiome: unique but alike





Vol 464|4 March 2010|doi:10.1038/nature08821

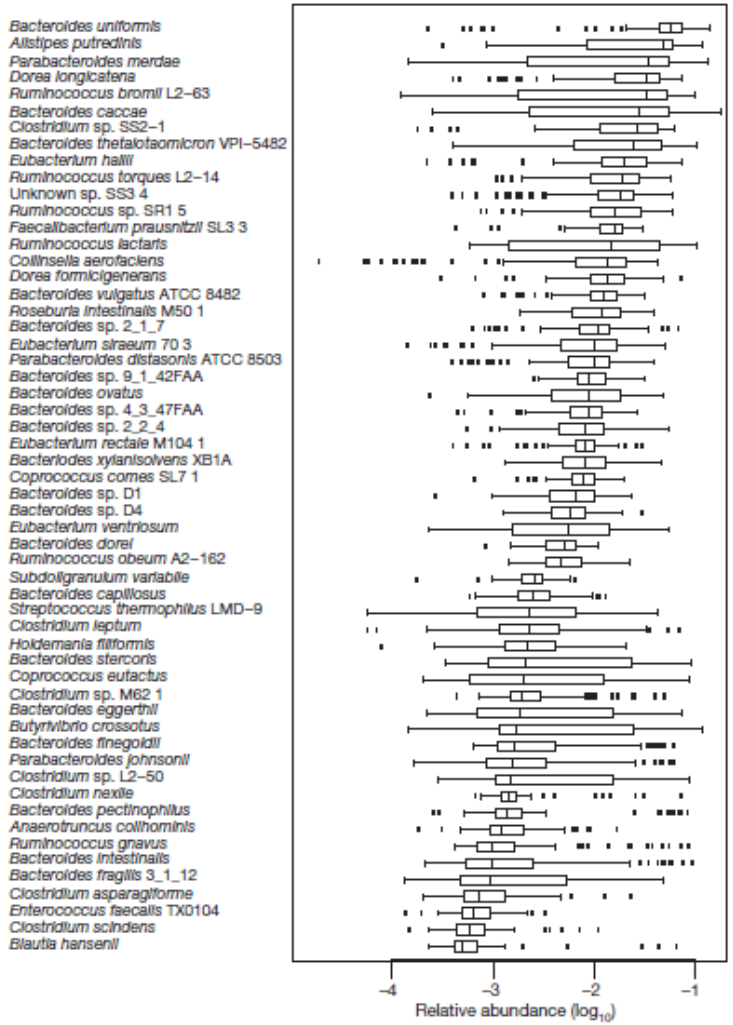
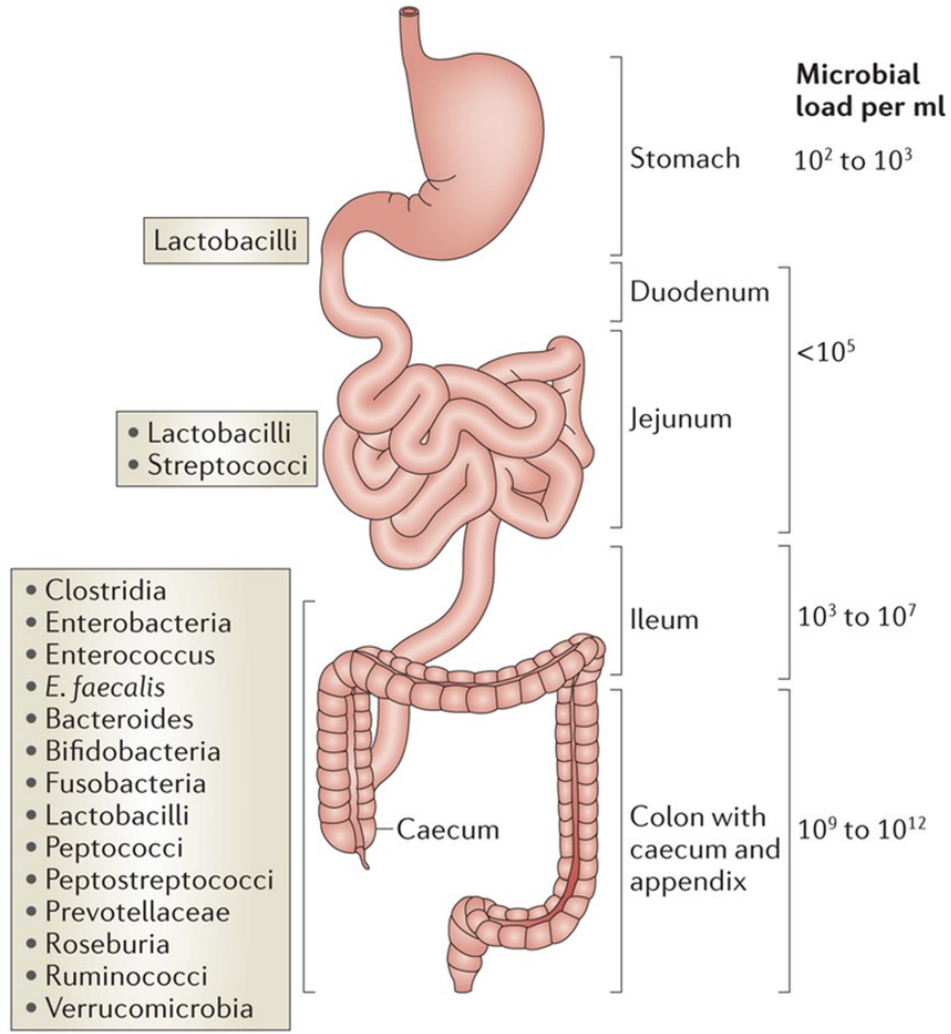


Figure 3 | Relative abundance of 57 frequent microbial genomes among individuals of the cohort. See Fig. 2c for definition of box and whisker plot.

structuur, functie en diversiteit
van het gezonde menselijke microbioom



Nature Reviews | Immunology

UCR
University College Research








SCIENTIFIC AMERICAN
June 2012
ScientificAmerican.com
Your Inner Ecosystem

HOW DO WE GET OUR MICROBIOME?

BIRTH:

A newborn gets its microbes from:

- its mother's birth canal
- skin of its mother and other care-givers



BREAST MILK:

Breast milk has been fine-tuned over millions of years to provide:

- nutrients, vitamins, and antibodies
- diverse microbes to populate the baby's gut



ENVIRONMENT:

For the rest of the baby's life, it will continuously encounter new microbes from:

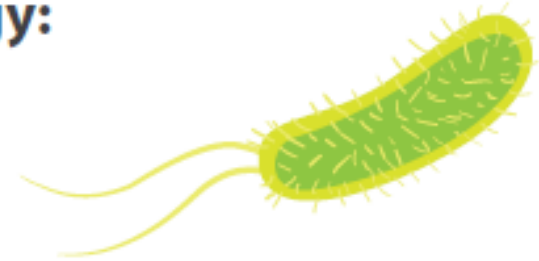
- soil and water
- people, pets, plants
- new and diverse foods



Learn more about your microbiome

American Academy of Microbiology:
http://bit.ly/HumanMicrobiome

AMERICAN SOCIETY FOR MICROBIOLOGY



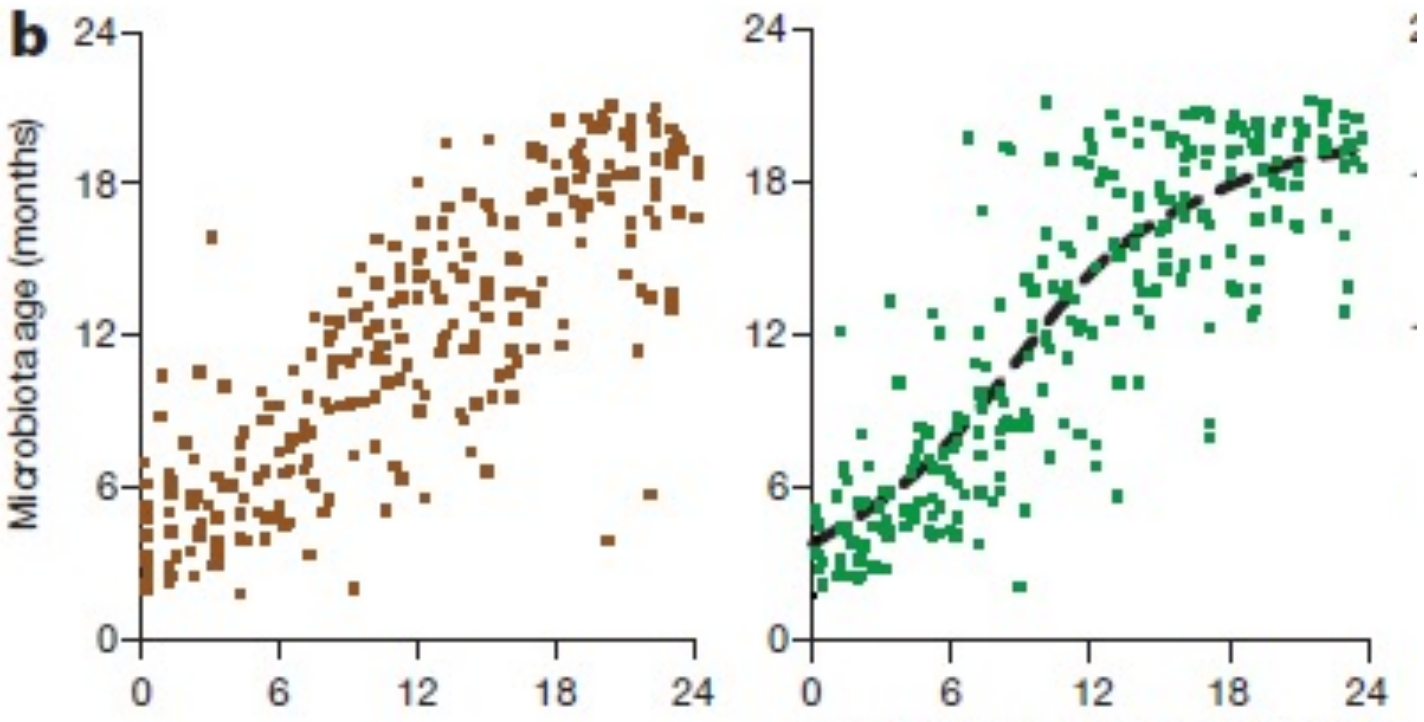
Normal development gutmicrobiota

a

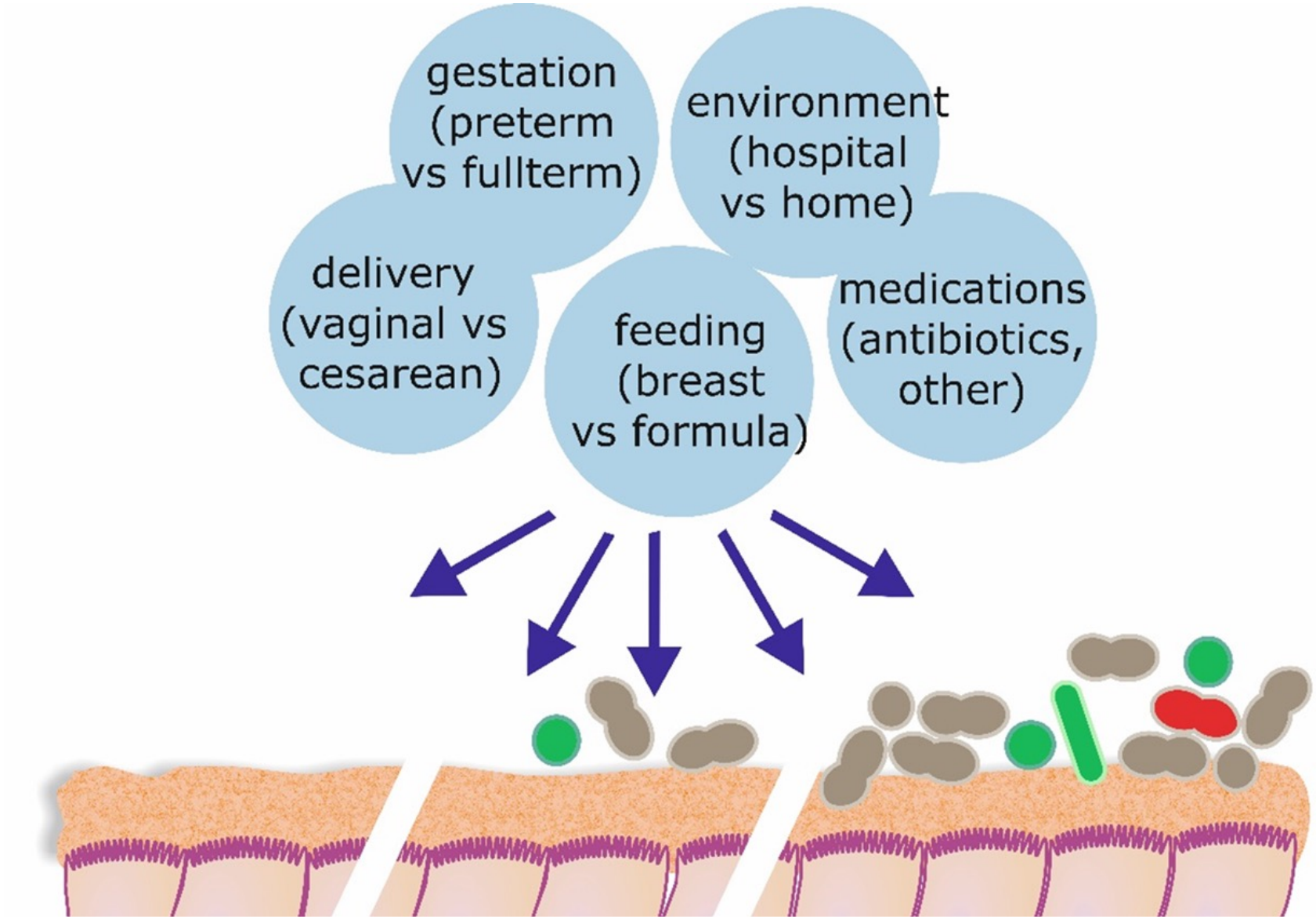
Increasing importance in accuracy of model

Rank	OTU ID	Taxonomic annotation
1	326792	*Faecalibacterium prausnitzii*
2	189827	*Ruminococcus* sp. 5 1 39BFAA
3	470663	*Lactobacillus ruminis*
4	191687	*Dorea longicatena*
5	72820	*Bifidobacterium longum*
6	194745	*Ruminococcus* sp. 5 1 39BFAA
7	15141	*Lactobacillus mucosae*
8	561483	*Bifidobacterium* sp.
9	217996	*Staphylococcus* sp.
10	364234	*Ruminococcus* sp. 5 1 39BFAA
11	287510	*Catenibacterium mitsuokai*
12	261912	*Dorea formicigenerans*
13	361809	*Ruminococcus torques*
14	108747	*Streptococcus thermophilus*
15	533785	*Bifidobacterium* sp.
16	9514	*Haemophilus parainfluenzae*
17	561636	*Streptococcus* sp.
18	312461	*Clostridium* sp.
19	470139	*Clostridium ramosum*
20	181834	*Clostridium* sp.
21	148099	*Weissella cibaria*
22	469873	*Bifidobacterium* sp.
23	185951	*Clostridiales* sp.
24	212619	*Ruminococcaceae* sp.

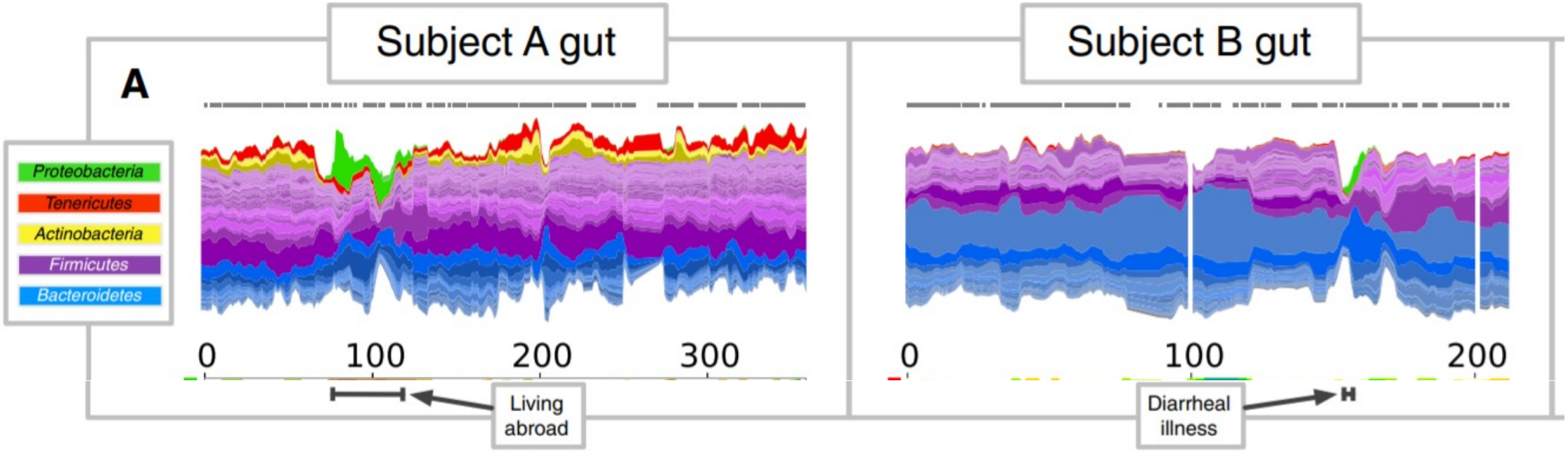
b



doi:10.1038/nature13421


gestation (preterm vs fullterm)
environment (hospital vs home)
delivery (vaginal vs cesarean)
feeding (breast vs formula)
medications (antibiotics, other)

Stable gut microbiota composition?



David *et al. Genome Biology* 2014, **15**:R89
http://genomebiology.com/2014/15/7/R89

MICROBIOTA

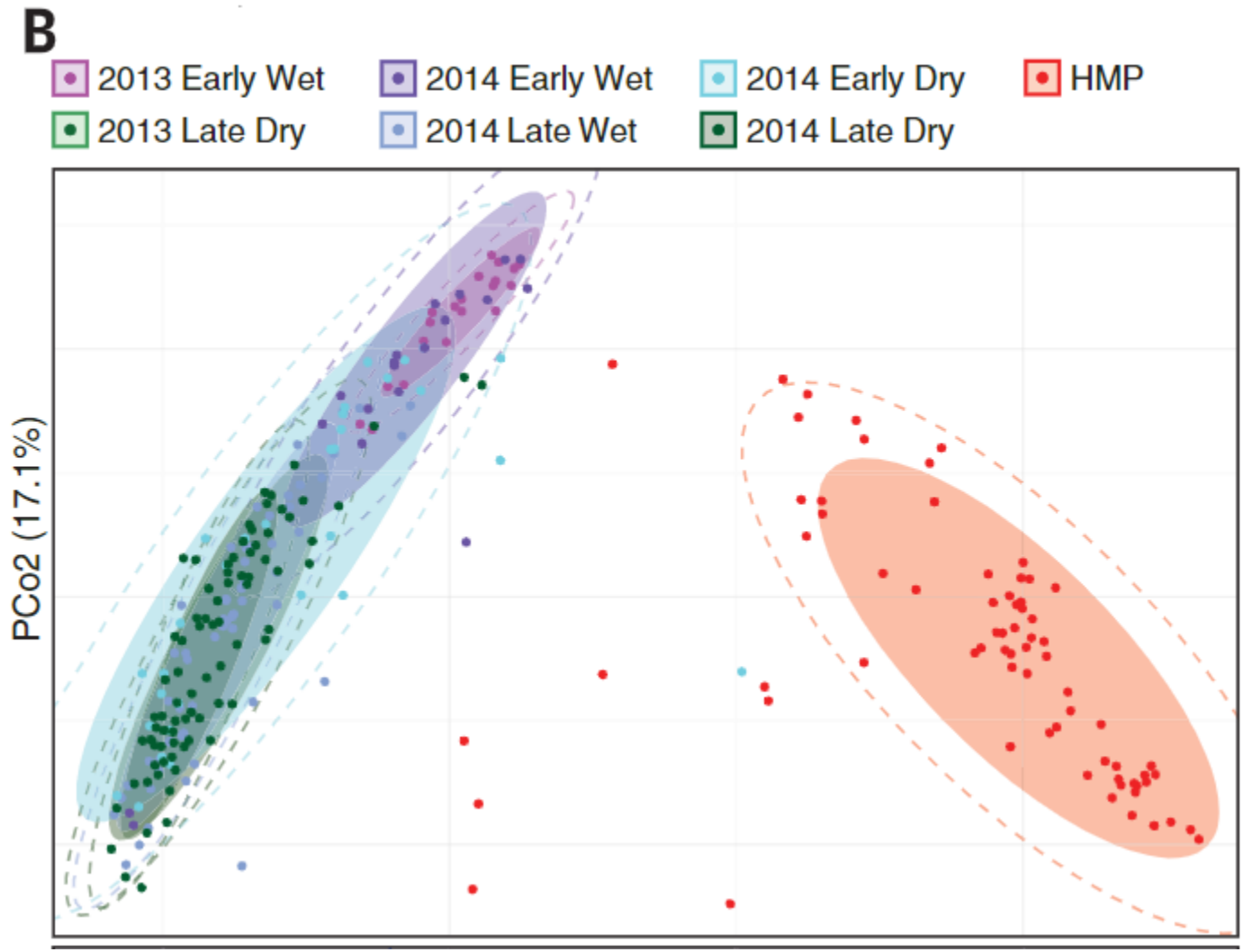
Seasonal cycling in the gut microbiome of the Hadza hunter-gatherers of Tanzania

Samuel A. Smits,[1]* Jeff Leach,[2,3]* Erica D. Sonnenburg,[1] Carlos G. Gonzalez,[4] Joshua S. Lichtman,[4] Gregor Reid,[5] Rob Knight,[6] Alphaxard Manjurano,[7] John Changalucha,[7] Joshua E. Elias,[4] Maria Gloria Dominguez-Bello,[8] Justin L. Sonnenburg[1]†

Although humans have cospeciated with their gut-resident microbes, it is difficu
infer features of our ancestral microbiome. Here, we examine the microbiome pr
of 350 stool samples collected longitudinally for more than a year from the Had
hunter-gatherers of Tanzania. The data reveal annual cyclic reconfiguration of th
microbiome, in which some taxa become undetectable only to reappear in a subs
season. Comparison of the Hadza data set with data collected from 18 populatio
in 16 countries with varying lifestyles reveals that gut community membership
corresponds to modernization: Notably, the taxa within the Hadza that are the r
seasonally volatile similarly differentiate industrialized and traditional populatio
These data indicate that some dynamic lineages of microbes have decreased in
prevalence and abundance in modernized populations.



in the taxonomic representation of bacteria within the two Hadza data sets, which, independent


B
2013 Early Wet
2014 Early Wet
2014 Early Dry
HMP
2013 Late Dry
2014 Late Wet
2014 Late Dry
PCo2 (17.1%)

Science

$15
29 APRIL 2016
sciencemag.org

AAAS



SPECIAL ISSUE

MICROBIOTA AT WORK

MICROBIOME

Population-based metagenomics analysis reveals markers for gut microbiome composition and diversity

Alexandra Zhernakova,[1,2]* Alexander Kurilshikov,[3,4]† Marc Jan Bonder,[1]† Ettje F. Tigchelaar,[1,2]† Melanie Schirmer,[5,6] Tommi Vatanen,[5,7] Zlatan Mujagic,[2,8] Arnau Vich Vila,[9] Gwen Falony,[10,11] Sara Vieira-Silva,[10,11] Jun Wang,[10,11] Floris Imhann,[9] Eelke Brandsma,[12] Soesma A. Jankipersadsing,[1] Marie Joossens,[10,11,13] Maria Carmen Cenit,[1,14,15] Patrick Deelen,[1,16] Morris A. Swertz,[1,16] LifeLines cohort study, Rinse K. Weersma,[9] Edith J. M. Feskens,[2,17] Mihai G. Netea,[18] Dirk Gevers,[5]‡ Daisy Jonkers,[8] Lude Franke,[1] Yurii S. Aulchenko,[4,19,20,21] Curtis Huttenhower,[5,6] Jeroen Raes,[10,11,13] Marten H. Hofker,[12] Ramnik J. Xavier,[5,22,23,24] Cisca Wijmenga,[1]*§ Jingyuan Fu[1,12]*§

Welke drank (slechts 1) heeft een negatief effect op darm microbiota?









World Journal of Gastroenterology

Review

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World J Gastro
Published onlir

Brain-gu

International Journal of Molecular Sciences

nutrients

MDPI

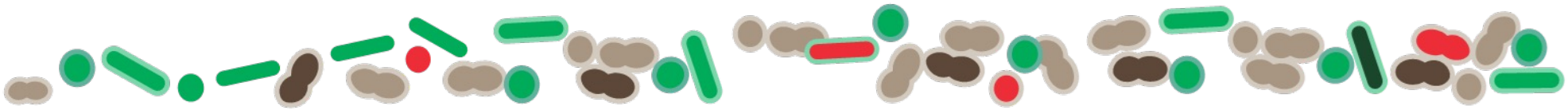
microorganisms

MDPI

Communication

The Microbiota–Gut–Brain Axis Heart Shunt Part I: The French Paradox, Heart Disease and the Microbiota

gut–lung axis



The French paradox



The NEW ENGLAND JOURNAL of MEDICINE

REVIEW ARTICLE

Elizabeth G. Phimister, Ph.D., *Editor*

The Human Intestinal Microbiome in Health and Disease

Susan V. Lynch, Ph.D., and Oluf Pedersen, M.D., D.M.Sc.

Glossary

Biomarker sequencing: The process of cataloguing microbes in a mixed-species community through analysis of sequence variation in a single ubiquitous gene.

Holobiont: The totality of organisms in a given ecosystem (e.g., the shared human and microbial ecosystem); also called a superorganism.

Metabolome: The complete set of small-molecule chemicals found in a biologic sample.

Metagenome: All the genetic material present in an environmental sample, consisting of the genomes of many individual organisms.

Methanogenic archaea: Methane-producing microbes of the ancient Archaea kingdom.

Microbiome: The collection of all genomes of microbes in an ecosystem.

Microbiota: The microbes that collectively inhabit a given ecosystem.

Pathobionts: Typically benign endogenous microbes with the capacity, under altered ecosystem conditions, to elicit pathogenesis.

Prebiotics: Nutritional substrates that promote the growth of microbes that confer health benefits in the host.

Probiotics: Live microbes that confer health benefits when administered in adequate amounts in the host.

Synbiotics: Formulations consisting of a combination of prebiotics and probiotics.

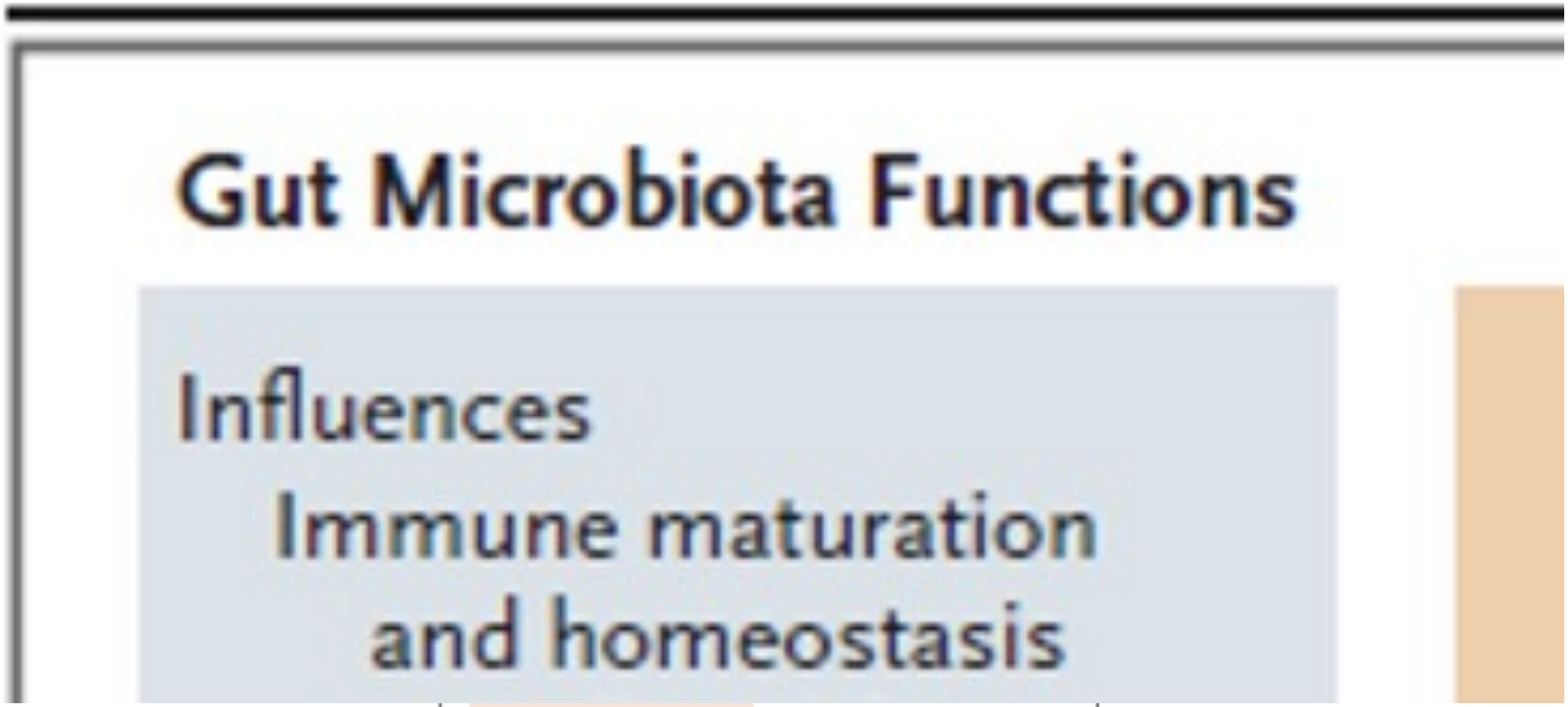


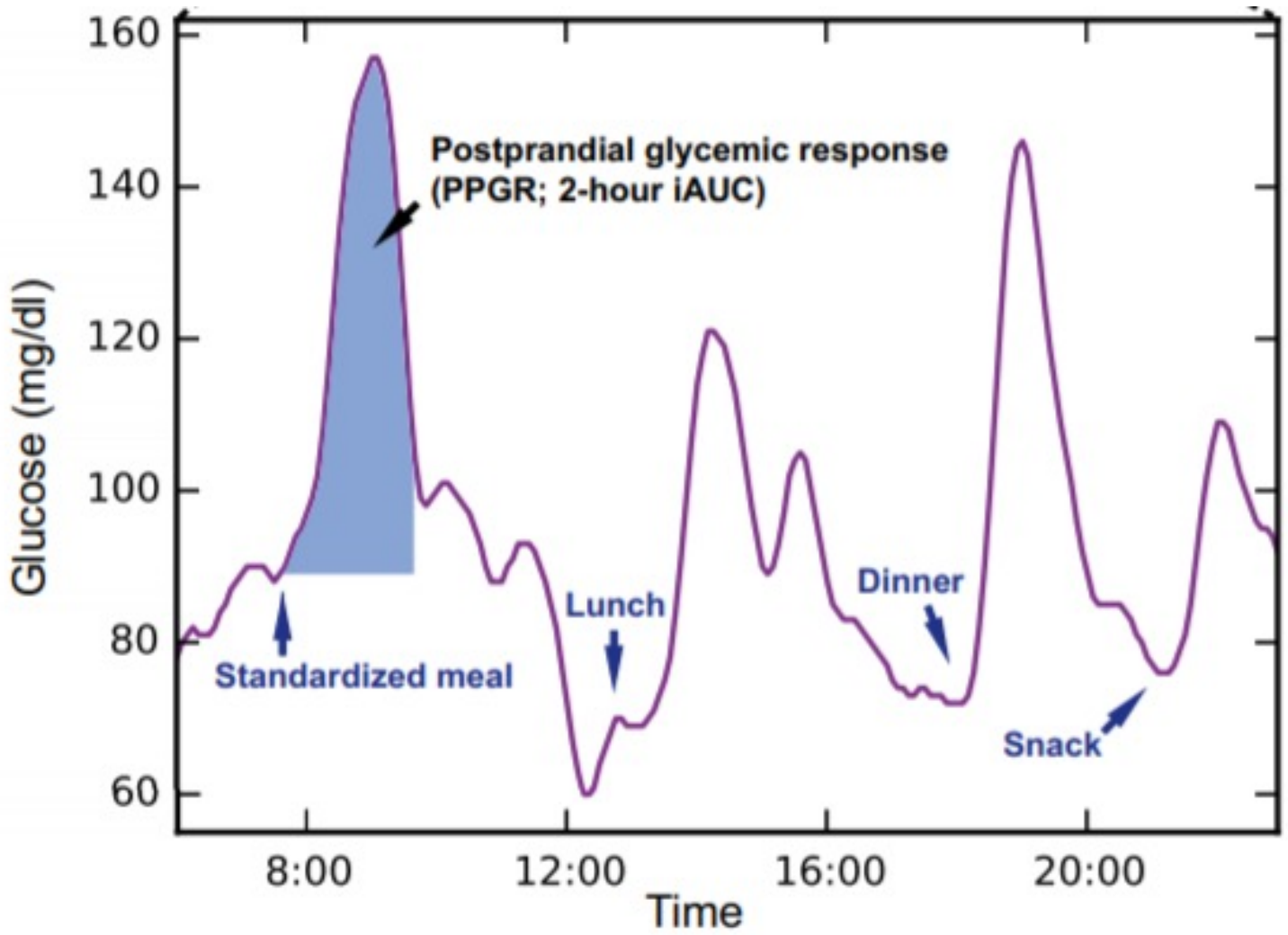
Figure 1. Some Functions of the Gut Microbiota and Disease Associations.



Gut Microbiota Functions	Disease Indications
Influences Immune maturation and homeostasis Host cell proliferation Vascularization Neurologic signaling Pathogen burden Intestinal endocrine functions Bone density Energy biogenesis	Neurologic Psychiatric Respiratory Cardiovascular Gastrointestinal Hepatic Autoimmune Metabolic Oncologic
Biosynthesis Vitamins Steroid hormones Neurotransmitters	
Metabolism Branched-chain and aromatic amino acids Dietary components Bile salts Drugs Xenobiotics	

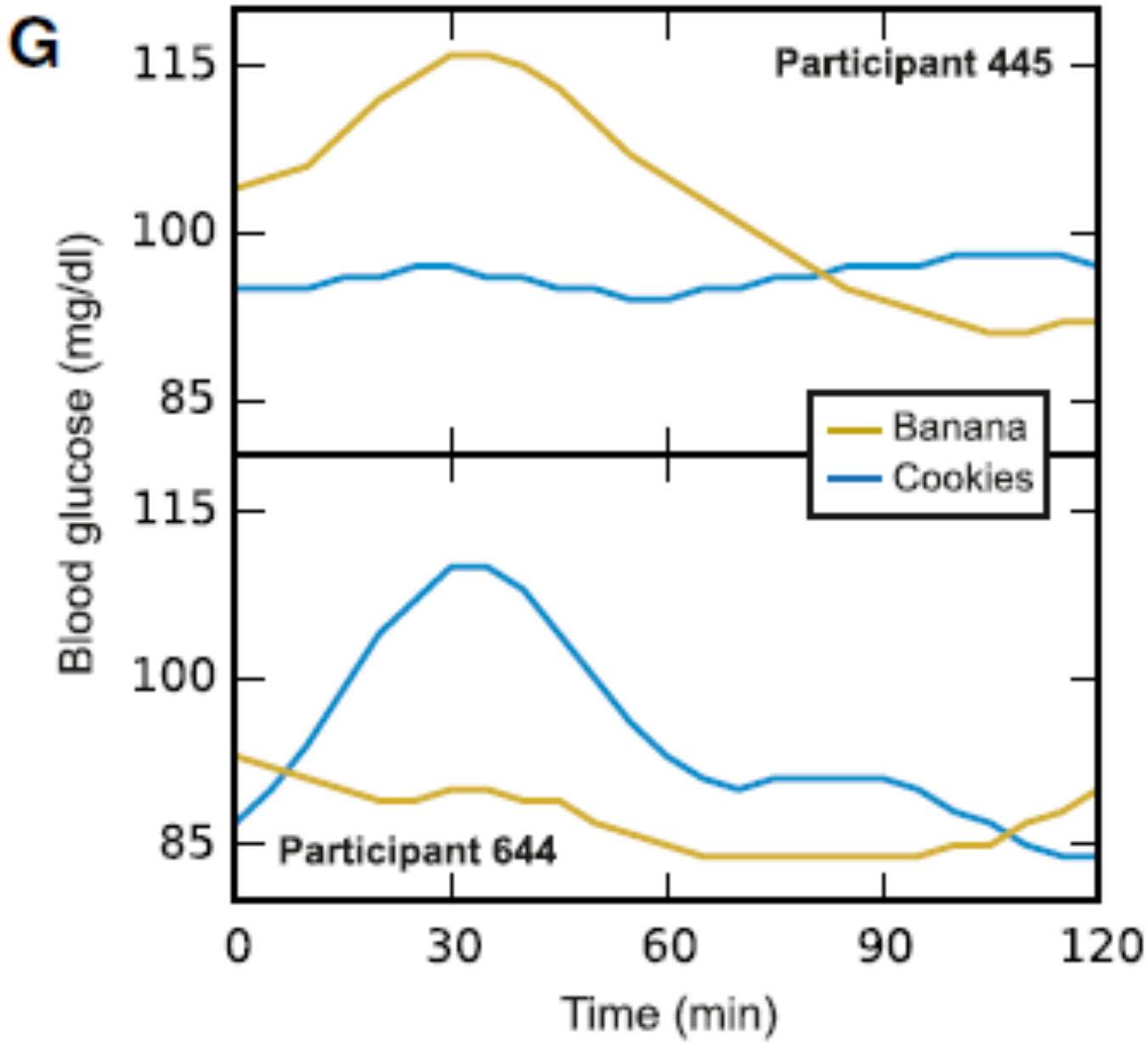
Figure 1. Some Functions of the Gut Microbiota and Disease Associations.



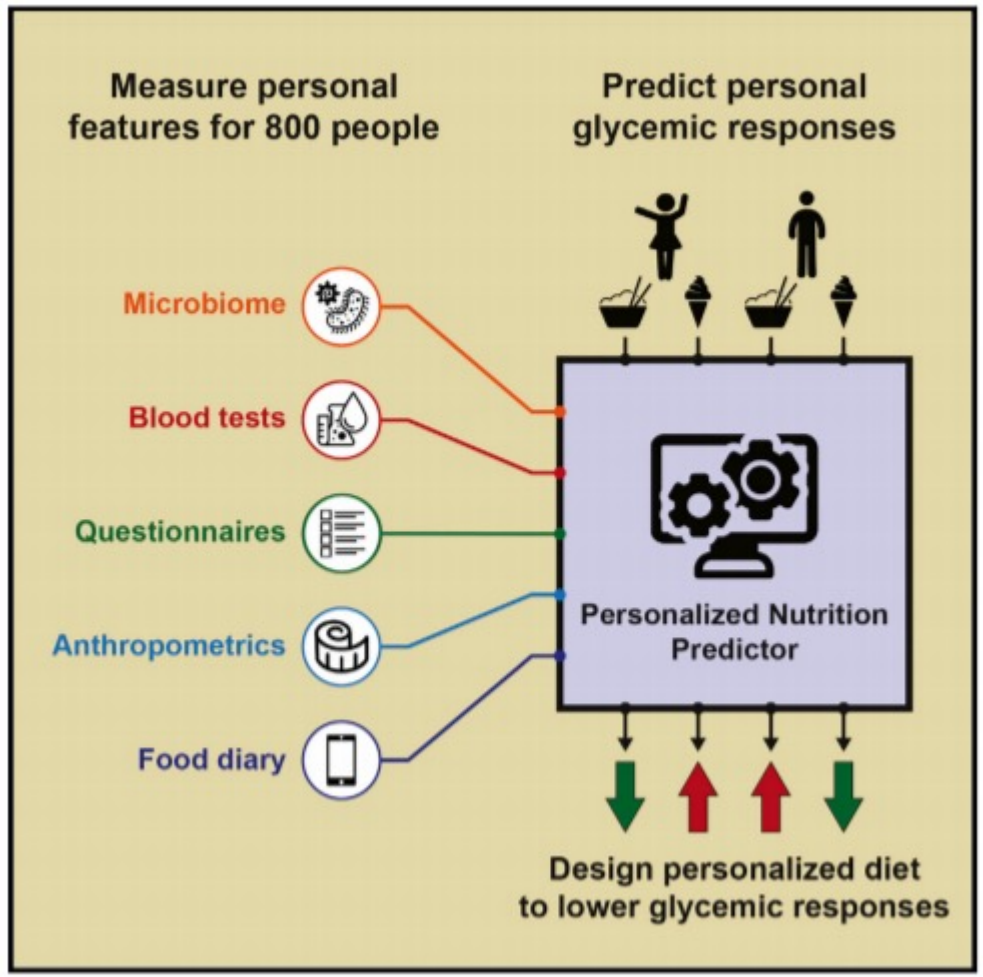


Cell *163*, 1079–1094, November 19, 2015

Personal Glycemic Response



Zeevi et al., 2015, Cell *163*, 1079–1094
November 19, 2015 ©2015 Elsevier Inc.
http://dx.doi.org/10.1016/j.cell.2015.11.001



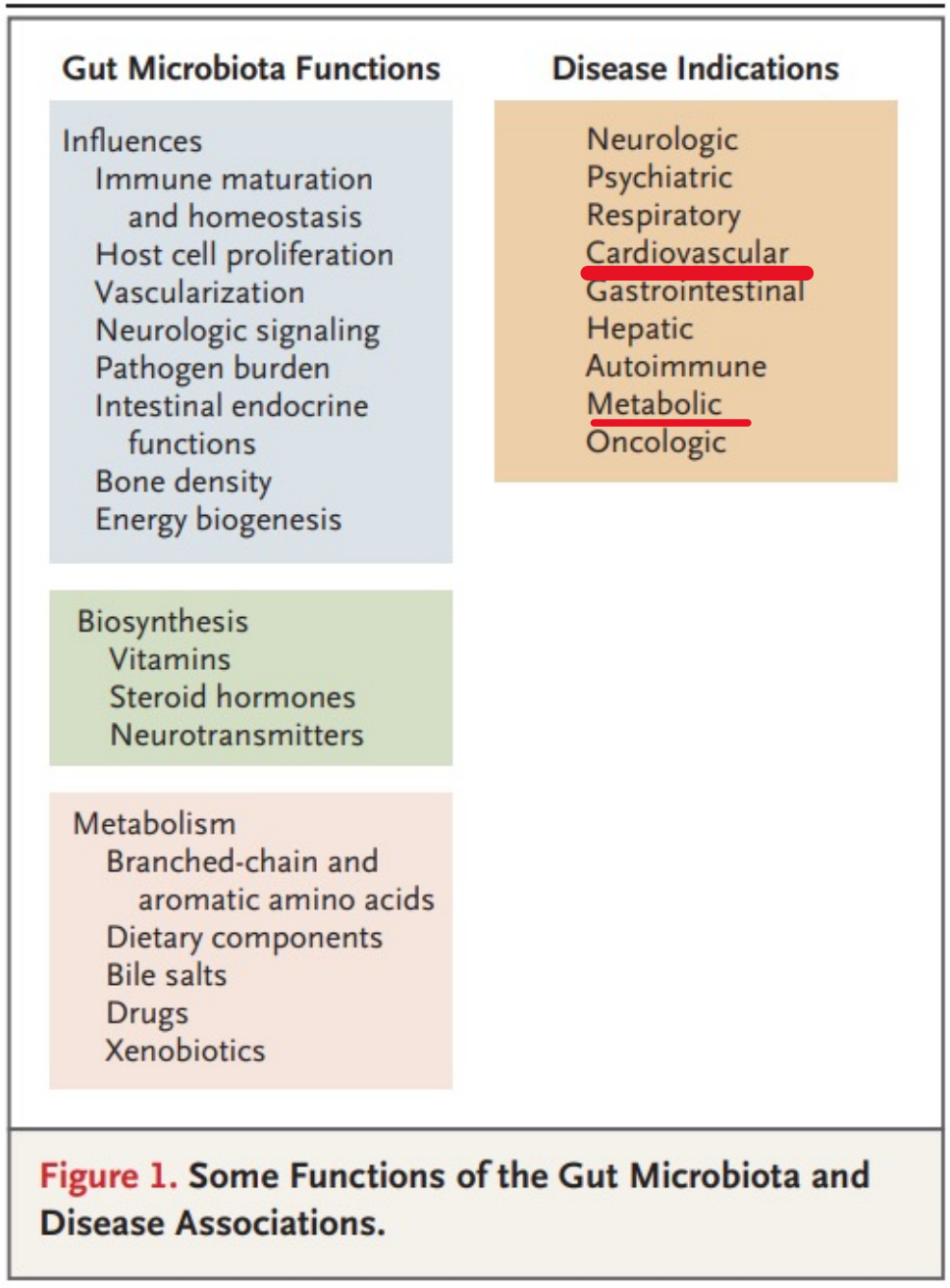


Figure 1. Some Functions of the Gut Microbiota and Disease Associations.



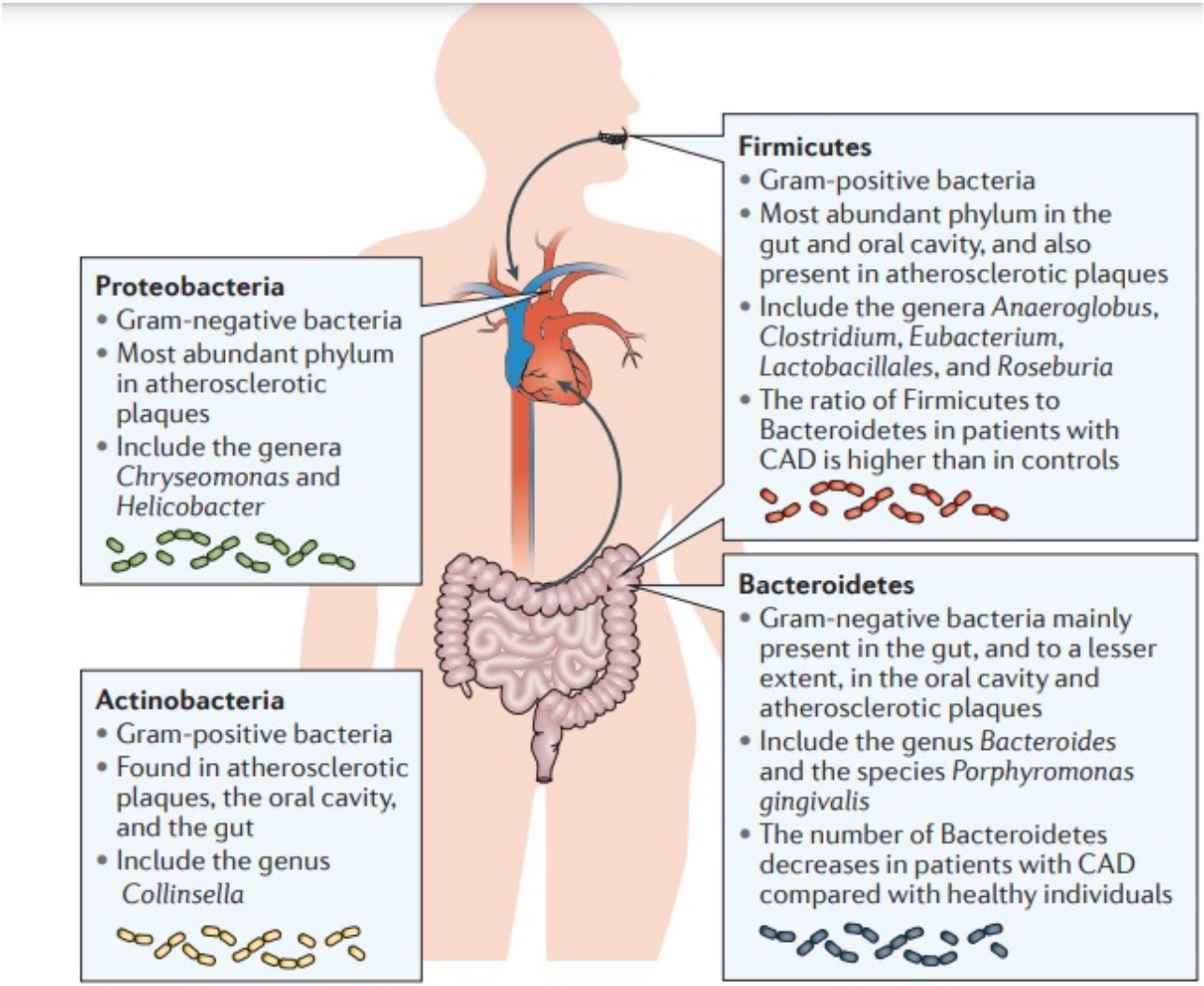


Figure 1 | **Body sites of microbiota that influences atherosclerosis.** Bacterial DNA detected in atherosclerotic plaques might derive from bacteria residing in the oral cavity or the gut. The description of the dominant phylum in each body habitat is based on a previous publication[6]. Firmicutes is the most abundant phyla in the gut and oral cavity,

nrcardio.2016.183.pdf

NEWS & VIEWS

PHYSIOLOGY

Obesity and gut flora

Matej Bajzer and Randy J. Seeley

**The intestinal bacteria in obese humans and mice differ from those in le
involved in how we regulate body weight, and are they a factor in the obe**

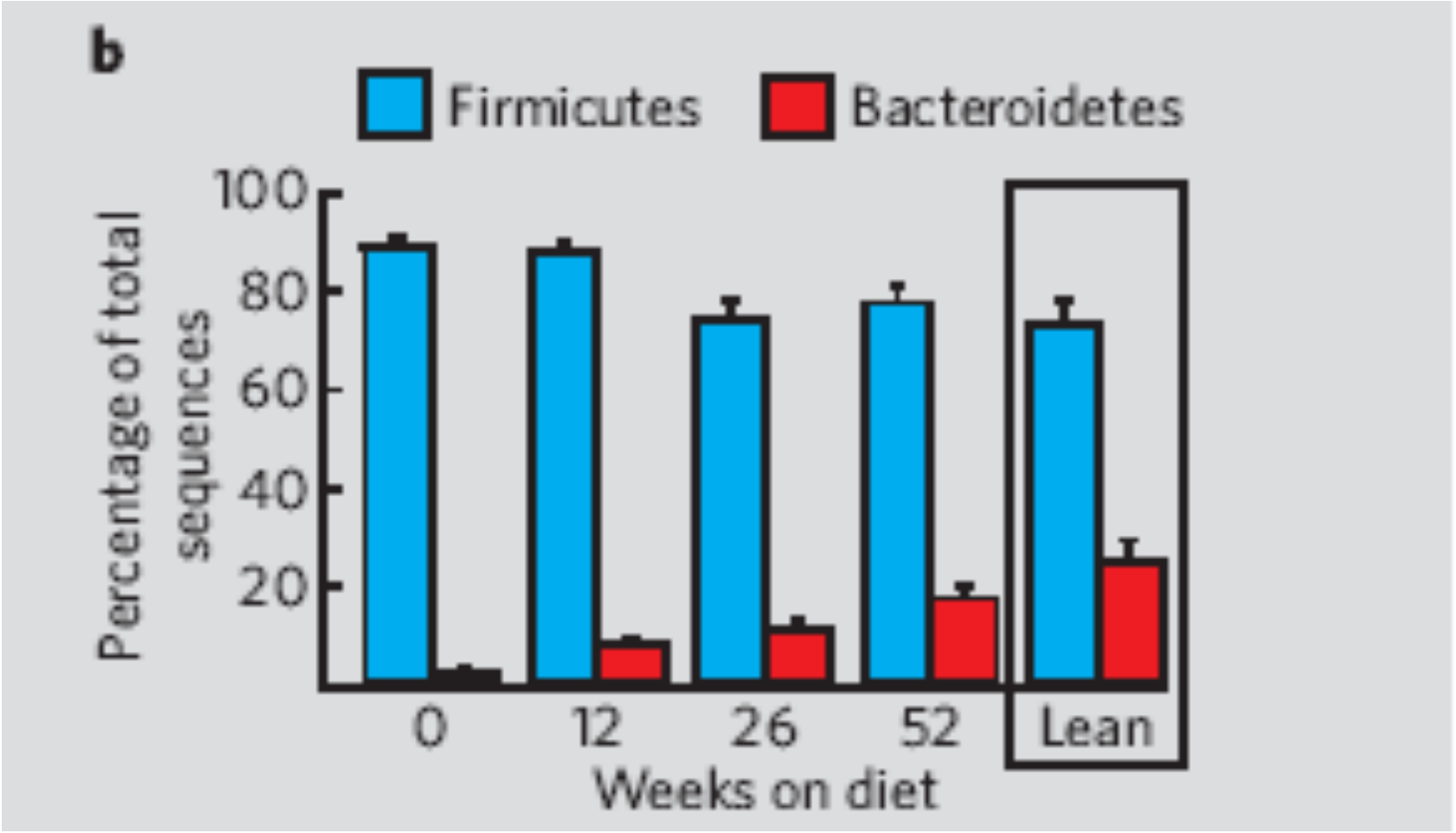


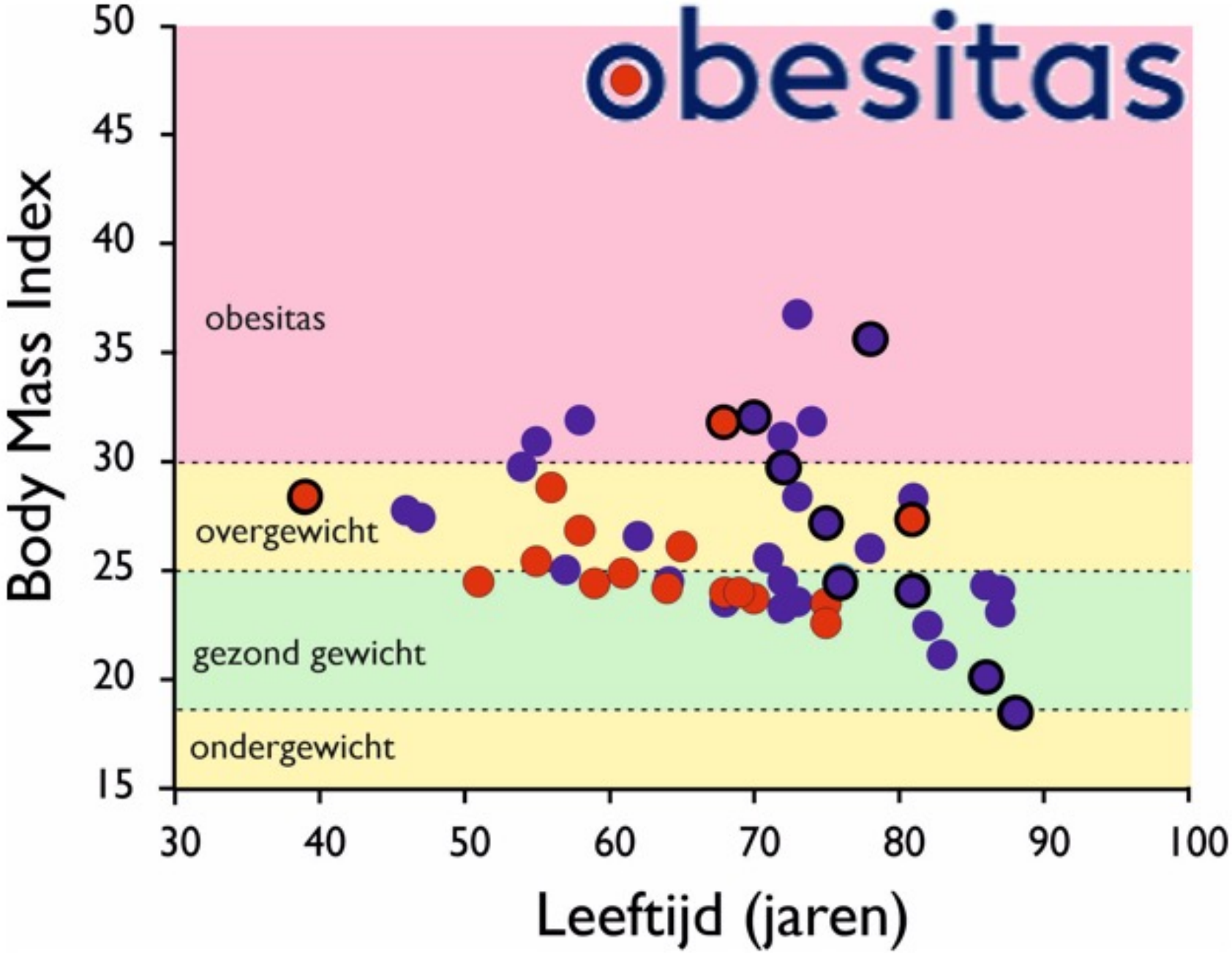
Much has been said and written about the sequencing of the human genome, and the research avenues that it has opened up. But our own genome is not the only one with which we need to be concerned. In particular, trillions of bacteria — collectively referred to as the microbiota — reside in our gastrointestinal tracts (Fig. 1), and each brings its own genome to this genetic party.

Reports by Gordon and colleagues[1,2] on

assess the relative abundance of various types of bacterium. The two predominant populations of microbiota in both the mouse and the human gut are members of the bacterial groups known as the Firmicutes and the Bacteroidetes (Box 1, overleaf). The authors[1] studied a small number of obese humans, and found that the proportion of the genetic material from Firmicutes was higher than the proportion in lean individuals. Moreover, when obese indi-

obese humans have less bacteriodetes




obesitas
Body Mass Index
50
45
40
35
30
25
20
15
obesitas
overgewicht
gezond gewicht
ondergewicht
30
40
50
60
70
80
90
100
Leeftijd (jaren)

Idee voor een bedrijfje?



United States Of America

Total population: 322 000 000

Income group: High

Prevalence of diabetes and related risk factors

	males	females	total
Diabetes	9.8%	8.3%	9.1%
Overweight	74.1%	65.3%	69.6%
Obesity	33.7%	36.3%	35.0%
Physical inactivity	27.6%	42.1%	35.0%

World Health Organization – Diabetes country profiles, 2016.

http://www.who.int/diabetes/country-profiles/usa_en.pdf

Netherlands

Total population: 16 925 000

Income group: High

Prevalence of diabetes and related risk factors

	males	females	total
Diabetes	7.0%	5.3%	6.1%
Overweight	67.2%	52.6%	59.8%
Obesity	23.2%	20.6%	21.9%
Physical inactivity	16.0%	19.7%	17.9%

World Health Organization – Diabetes country profiles, 2016.

http://www.who.int/diabetes/country-profiles/usa_en.pdf

Microbiota and SCFA in Lean and Overweight Healthy Subjects

Andreas Schwiertz[1], David Taras[2], Klaus Schäfer[2], Silvia Beijer[3], Nicolaas A. Bos[3], Christiane Donus[4] and Philip D. Hardt[4]

Table 3 Fecal microbiota composition of lean (n = 30), overweight (n = 35), and obese subjects (n = 33)





OBESITY | VOLUME 18 NUMBER 1 | JANUARY 2010

Microbiota and SCFA in Lean and Overweight Healthy Subjects

Andreas Schwiertz[1], David Taras[2], Klaus Schäfer[2], Silvia Beijer[3], Nicolaas A. Bos[3], Christiane Donus[4] and Philip D. Hardt[4]

Table 3 Fecal microbiota composition of lean (*n* = 30), overweight (*n* = 35), and obese subjects (*n* = 33)

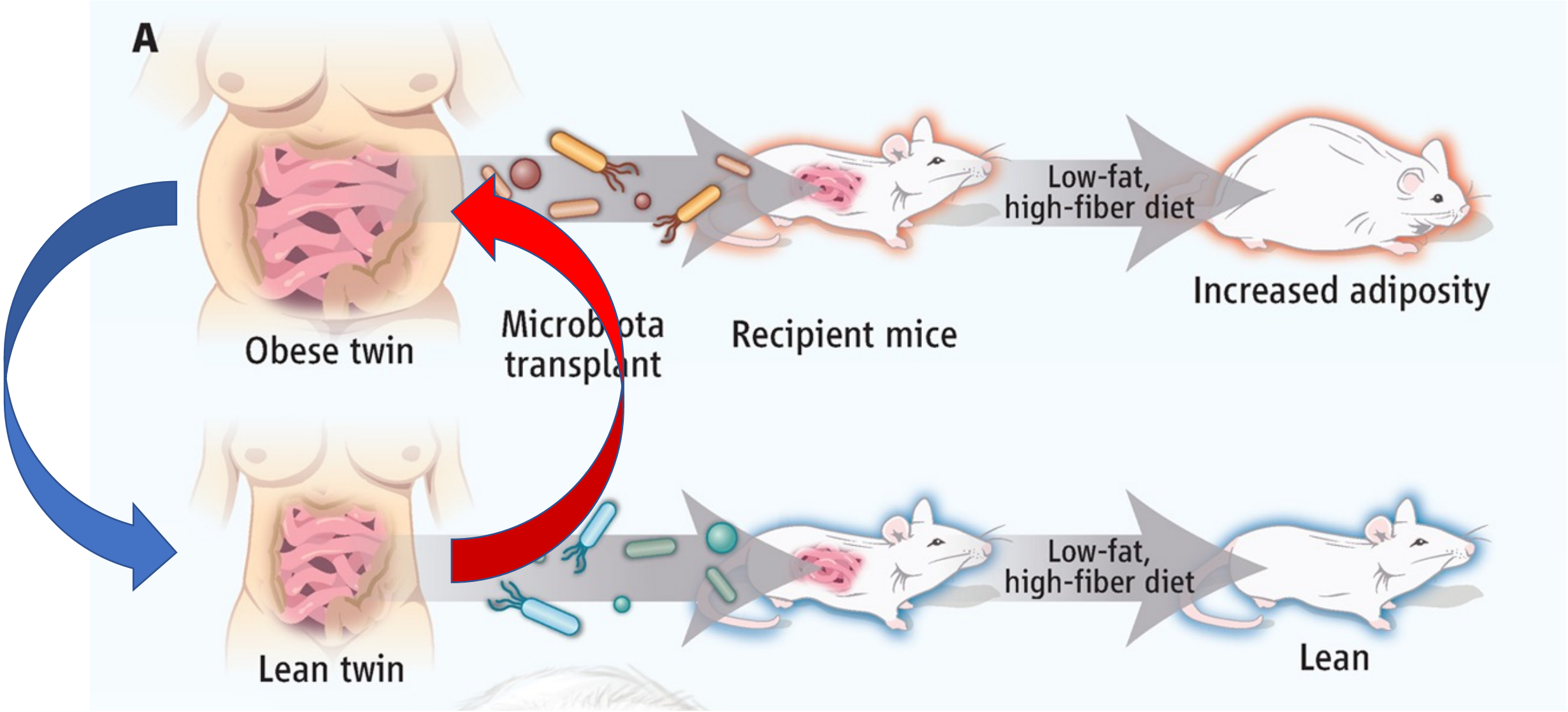
	BMI		
Population	<25	25–30	>30
Proportion of Firmicutes (%)	73.1	47.7[a]	51.0[a]
Proportion of Bacteroidetes (%)	22.9	46.8[b]	45.0[b]
Ratio Firmicutes/ Bacteroidetes	3.3	1.1[a]	1.2[a]




INDEPENDENTLY OWNED
ROYAL BLUE
BEST QUALITY ALWAYS
STORE
APPLIANCE
REPAIRING
Reliance



1 week: +2,5 kilo


A
Obese twin
Microbiota transplant
Recipient mice
Low-fat, high-fiber diet
Increased adiposity
Lean twin
Low-fat, high-fiber diet
Lean



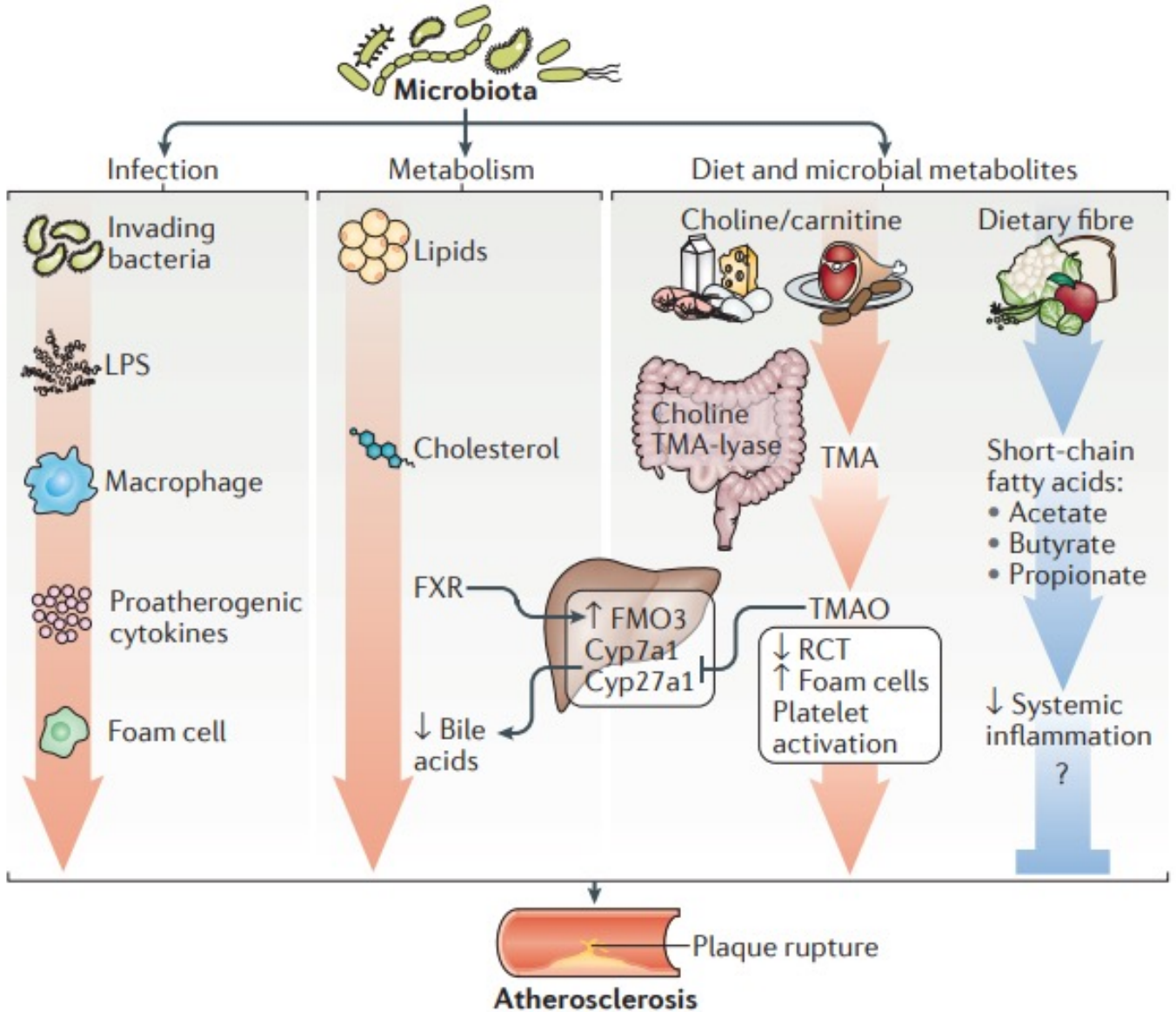
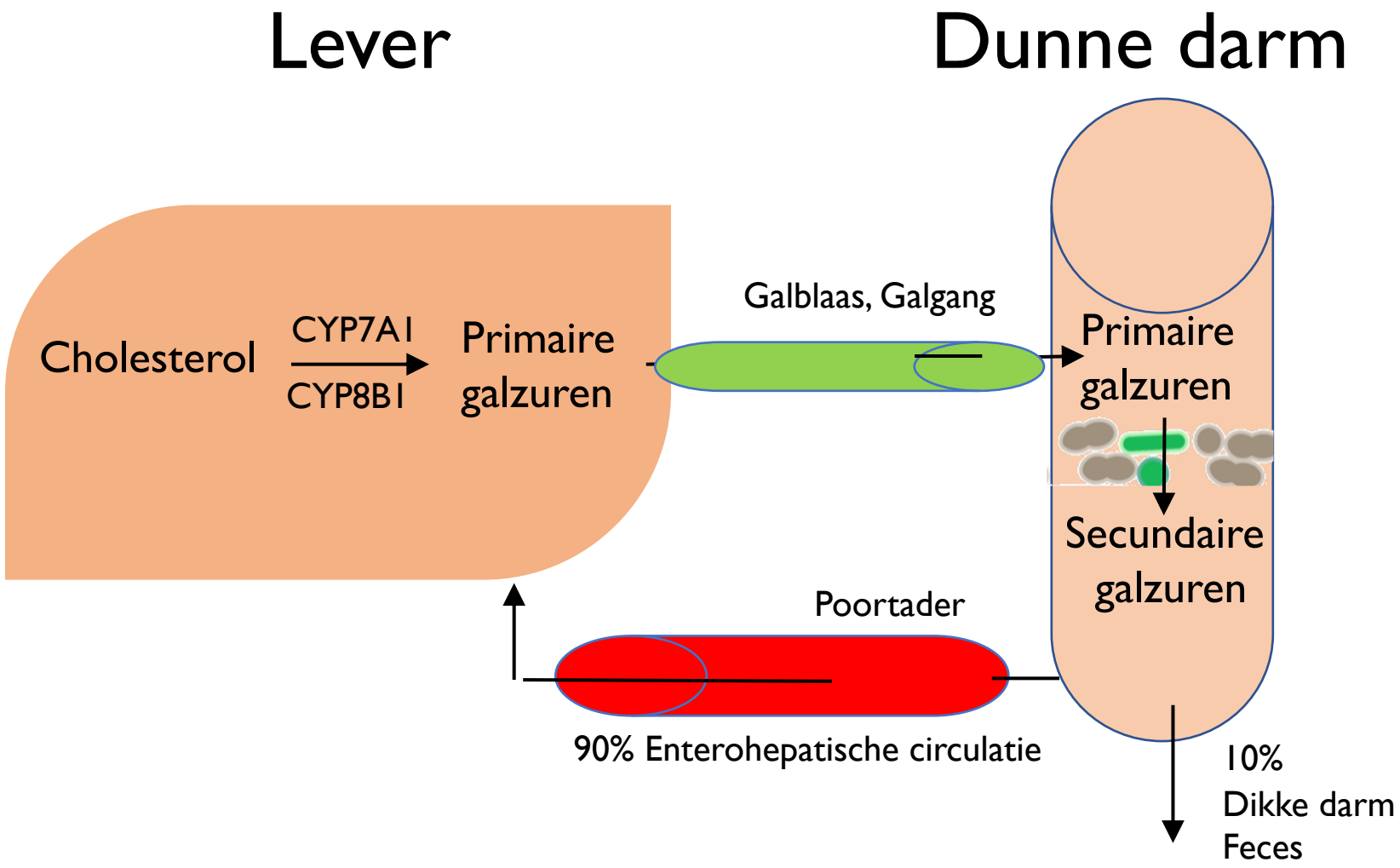
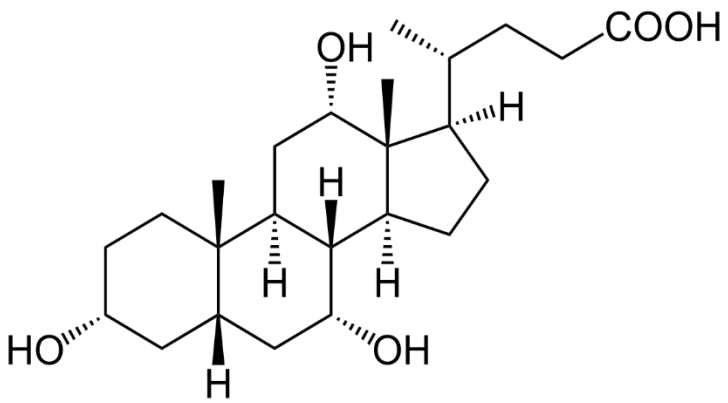


Figure 2 | **Microbiota-related pathways in atherosclerosis.** Microbiota can affect

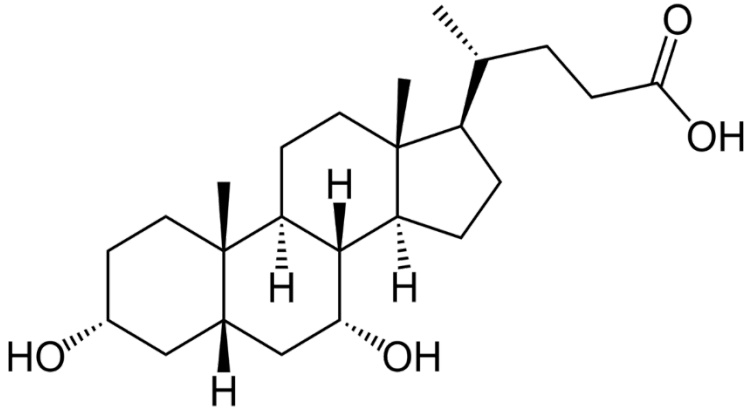
nrcardio.2016.183.pdf


Lever
Dunne darm
Cholesterol
CYP7A1
CYP8B1
Primaire galzuren
Galblaas, Galgang
Primaire galzuren
Secundaire galzuren
Poortader
90% Enterohepatische circulatie
10%
Dikke darm
Feces

Primaire galzouten

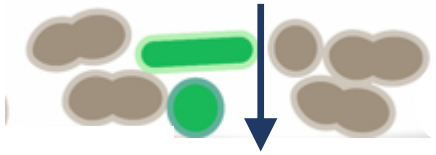


Cholinezuur (CA)



Chenodeoxycholinezuur (CDCA)

7-α dehydroxylering



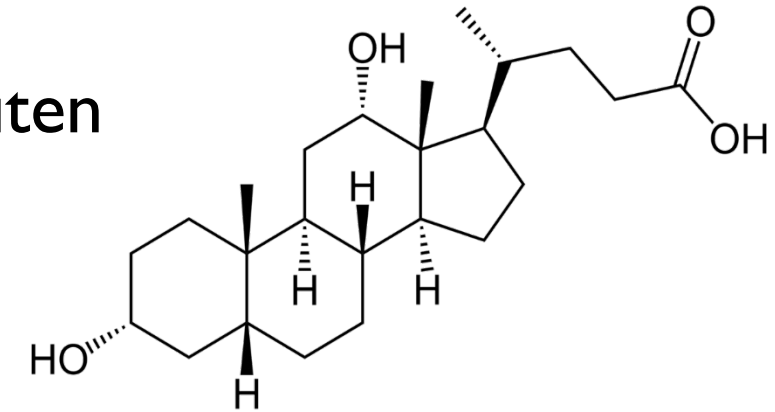


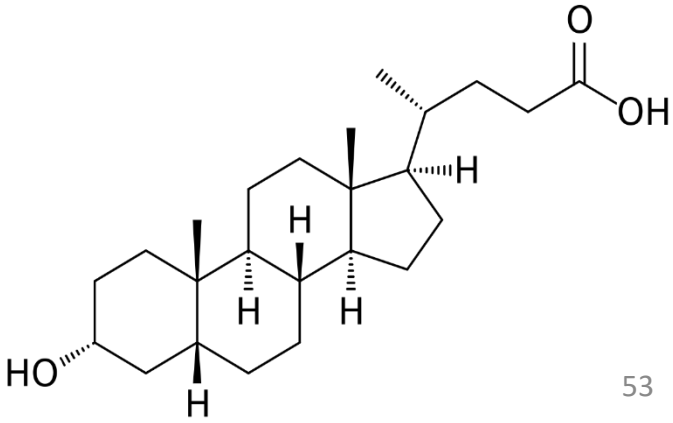


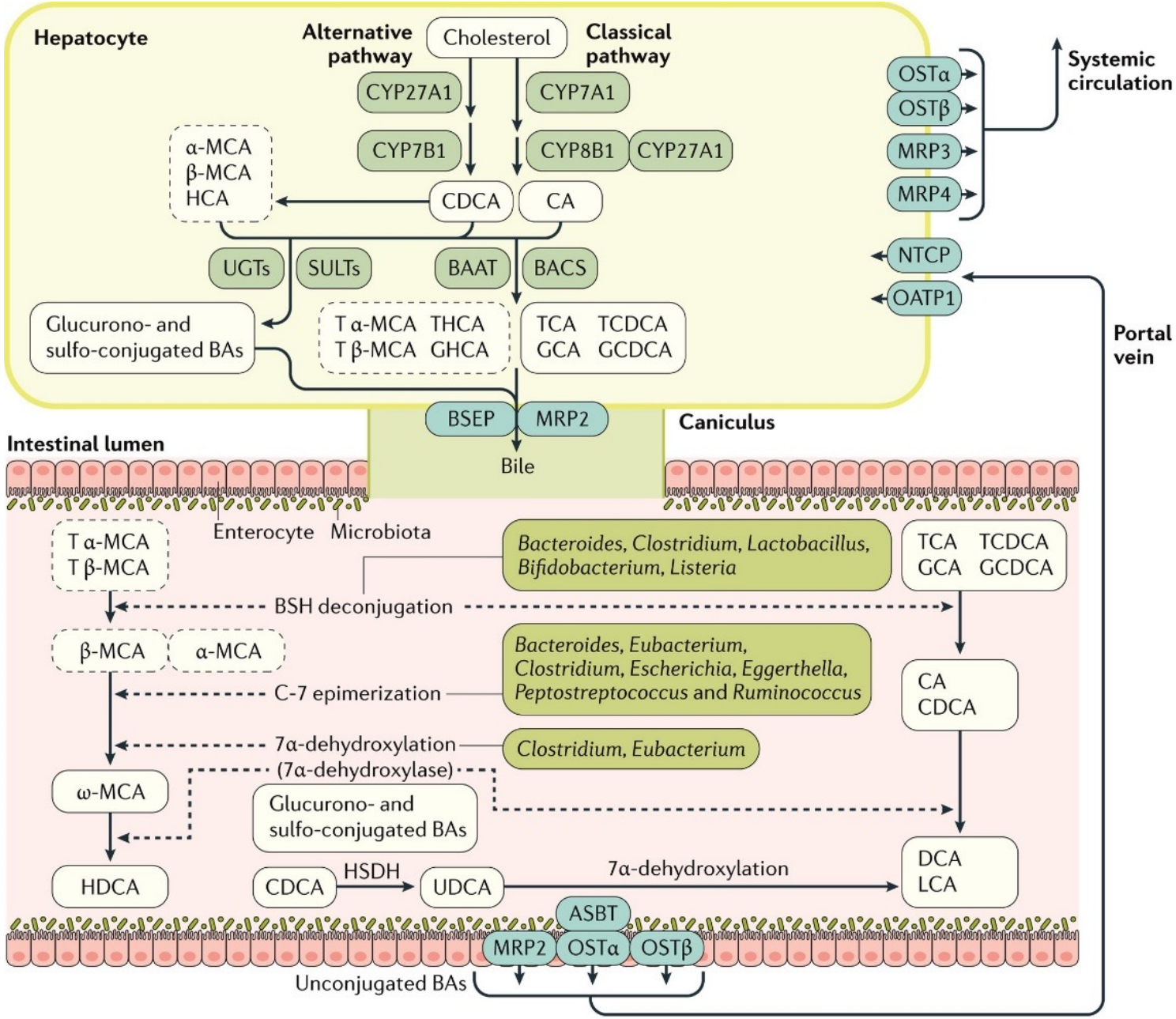
Deoxycholinezuur (DCA)

Litocholinezuur (LCA)

Secundaire galzouten



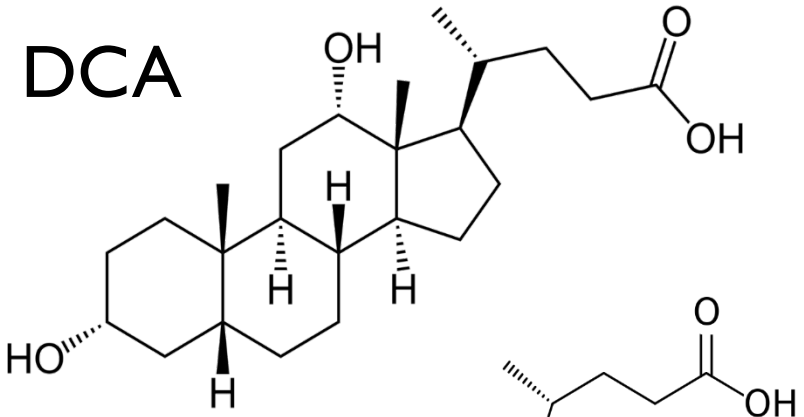




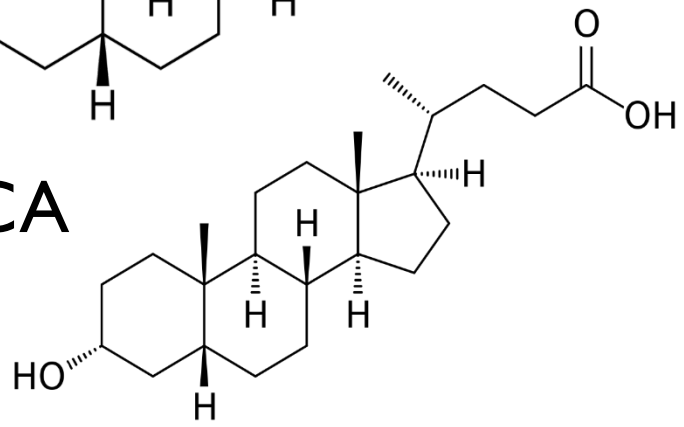
Nature Reviews | Gastroenterology & Hepatology

Secundary bile acids: cardiovascular

DCA



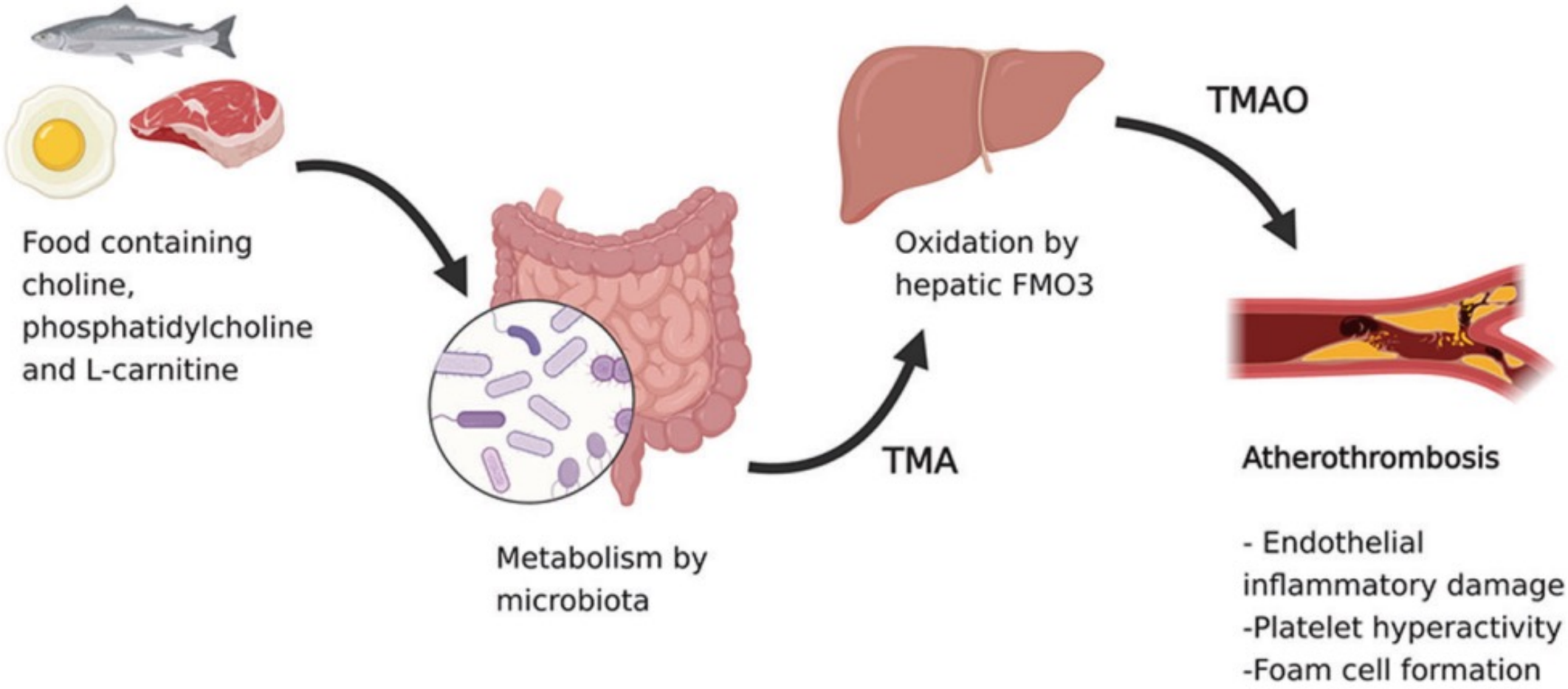
LCA



- Increase cholesterol levels
- Promote foam cell formation
- Increase the size of the atherosclerotic plaque

NB: Primary bile acids are cardio-protective

trimethylamine-N-oxide: TMAO



ATHEROSCLEROSIS AND PRODUCTS OF THE MICROBIOTA

Studies have shown that gut microbiota metabolism of dietary phosphatidylcholine and L-carnitine produces trimethylamine, which subsequently undergoes flavin monooxygenase 3–dependent oxidation to trimethylamine-*N*-oxide (TMAO); elevated circulating levels of TMAO appear to be a strong risk factor for atherosclerosis in humans and animals.[55,56] A study of a mouse model

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REVIEW ARTICLE

OPEN ACCESS Check for updates

Gut microbiota-derived trimethylamine N-oxide is associated with the risk of all-cause and cardiovascular mortality in patients with chronic kidney disease: a systematic review and dose-response meta-analysis

Yachun Li[a,b], Hongmei Lu[a,b], Jing Guo[a,b], Meiling Zhang[a,b], Huijuan Zheng[a,b], Yuning Liu[a,b] and Weijing Liu[a,b,c]

[a]Dongzhimen Hospital, Beijing University of Chinese Medicine, Beijing University of Chinese Medicine, Beijing, P.R. China; [b]Key Laboratory of Chinese Internal Medicine of Ministry of Education and Beijing, Beijing, P.R. China; [c]Zhanjiang Key Laboratory of Prevention and Management of Chronic Kidney Disease, Guangdong Medical University, Zhanjiang, Guangdong, P.R. China

ABSTRACT

Background: Trimethylamine N-oxide (TMAO) derived from gut microbiota causes kidney-heart damage in chronic kidney disease (CKD) patients. However, it is controversial whether CKD patients with higher TMAO are associated with a higher risk of death. We aimed to assess the correlation between circulating TMAO concentration and the risk of all-cause and cardiovascular death in CKD patients of different dialysis statuses and different races by dose-response analyses, and the underlying mechanisms were also explored by analyzing the correlations of TMAO with glomerular filtration rate (GFR) and inflammation.

Method: PubMed, Web of Science, and EMBASE were systematically searched up to 1 July 2022. A total of 21 studies involving 15,637 individuals were included. Stata 15.0 was used to perform the meta-analyses and dose-response analyses with extracted data. Subgroup analyses were conducted to recognize possible sources of heterogeneity.

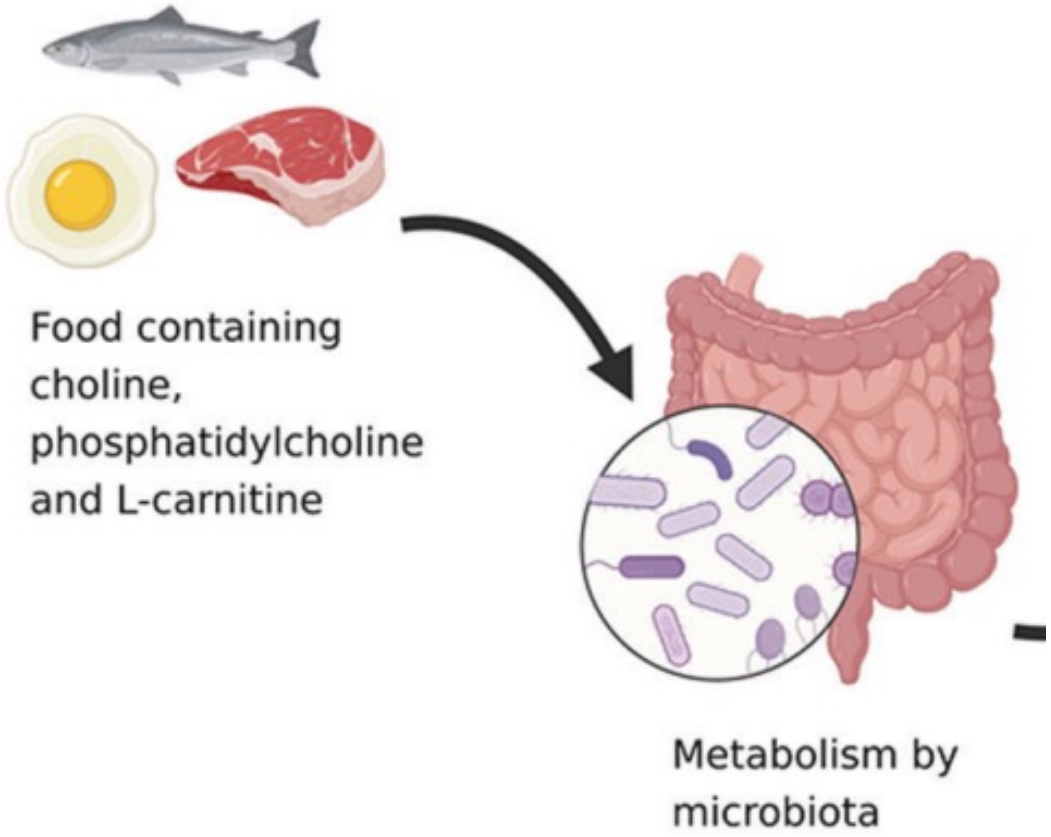
ARTICLE HISTORY

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Revised 10 April 2023
Accepted 13 May 2023

KEYWORDS

Trimethylamine N-oxide; chronic kidney disease; all-cause mortality; cardiovascular mortality

trimethylamine-N-oxide: TMAO

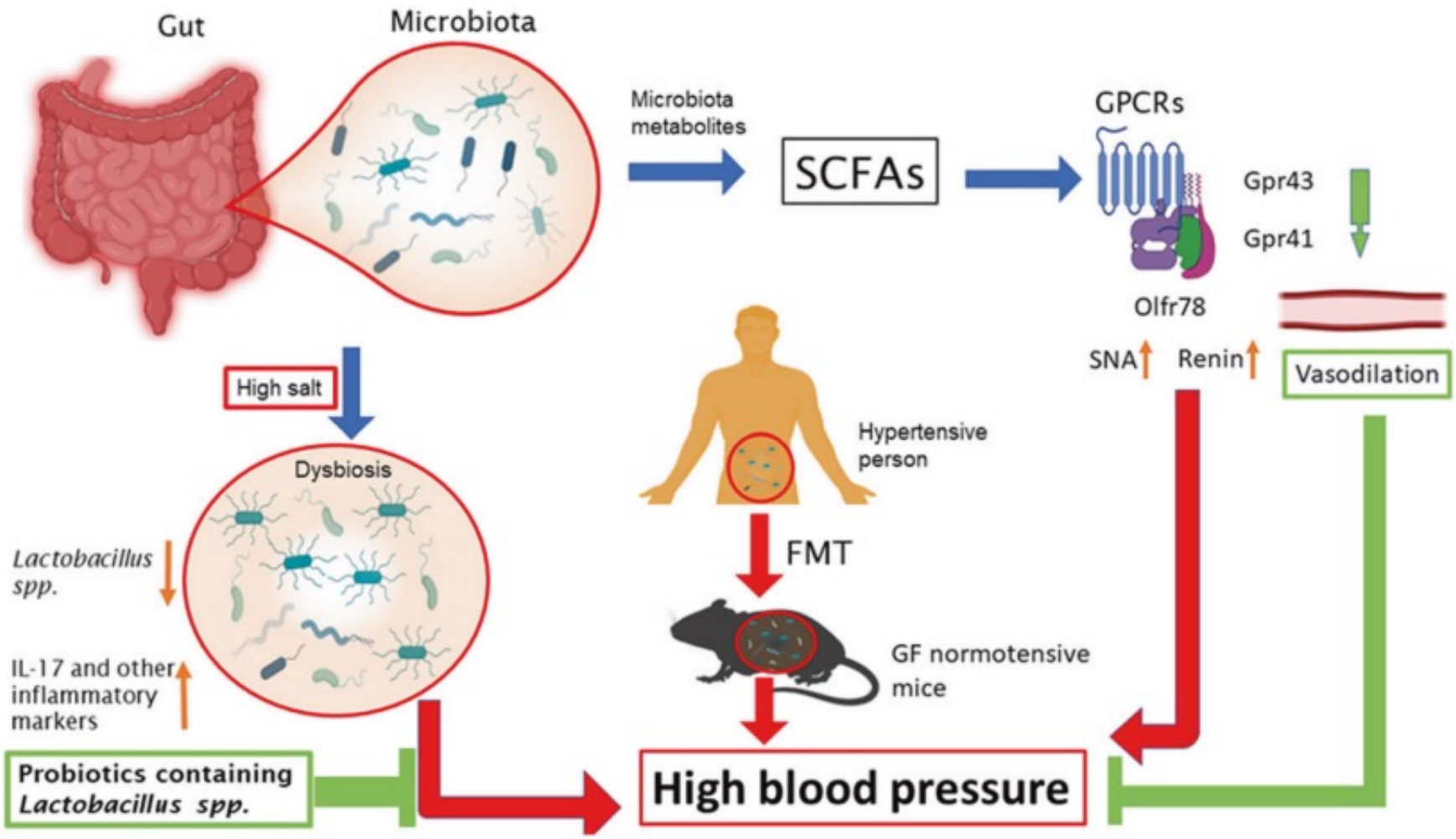


- Clostridia, Enterobacteriaceae, Eubacteriaceae species
- Degradation of nutrients found in foods of animal origin, including carnitine, choline and lecithin



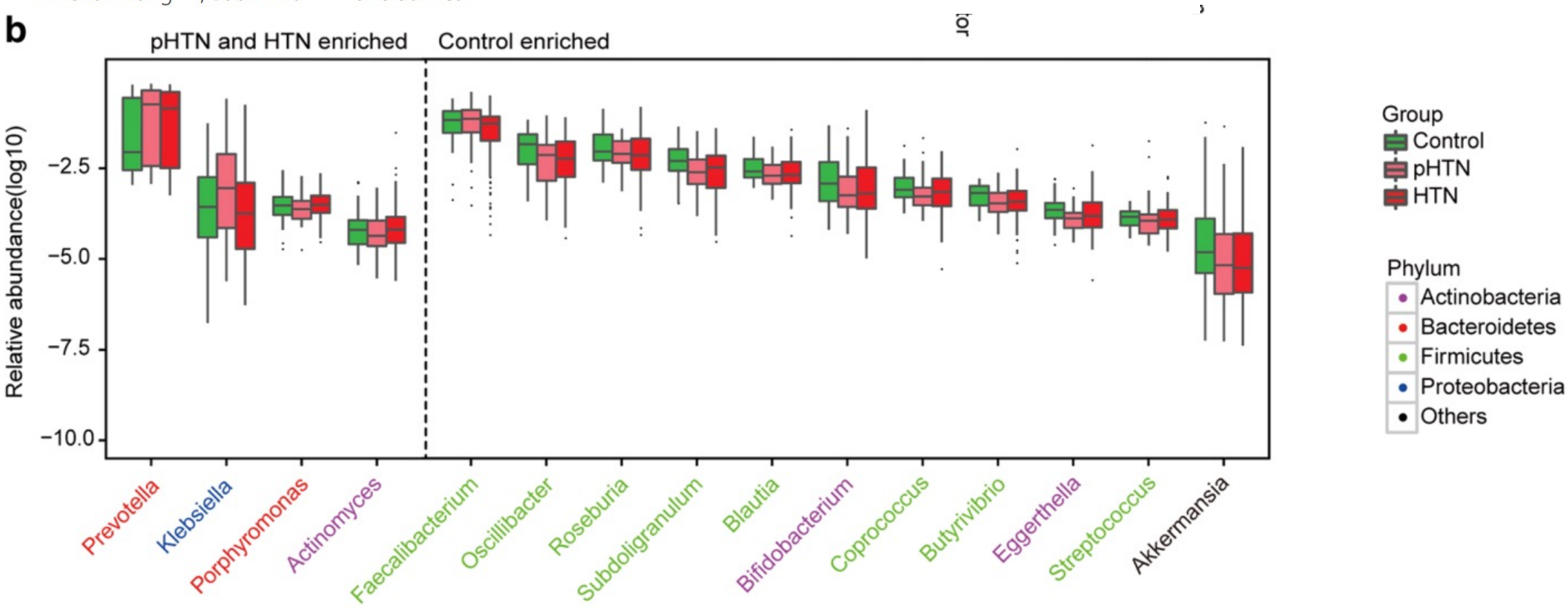
Hypertension

S.K. Masenga et al.



Gut microbiota dysbiosis contributes to the development of hypertension

Jing Li[1,2,3†], Fangqing Zhao[4†], Yidan Wang[1†], Junru Chen[5†], Jie Tao[6†], Gang Tian[7], Shouling Wu[8], Wenbin Liu[5], Qinghua Cui[9], Bin Geng[1], Weili Zhang[1], Ryan Weldon[10], Kelda Auguste[10], Lei Yang[11], Xiaoyan Liu[11], Li Chen[10,12,13], Xinchun Yang[2,3*], Baoli Zhu[14,15*] and Jun Cai[1*]

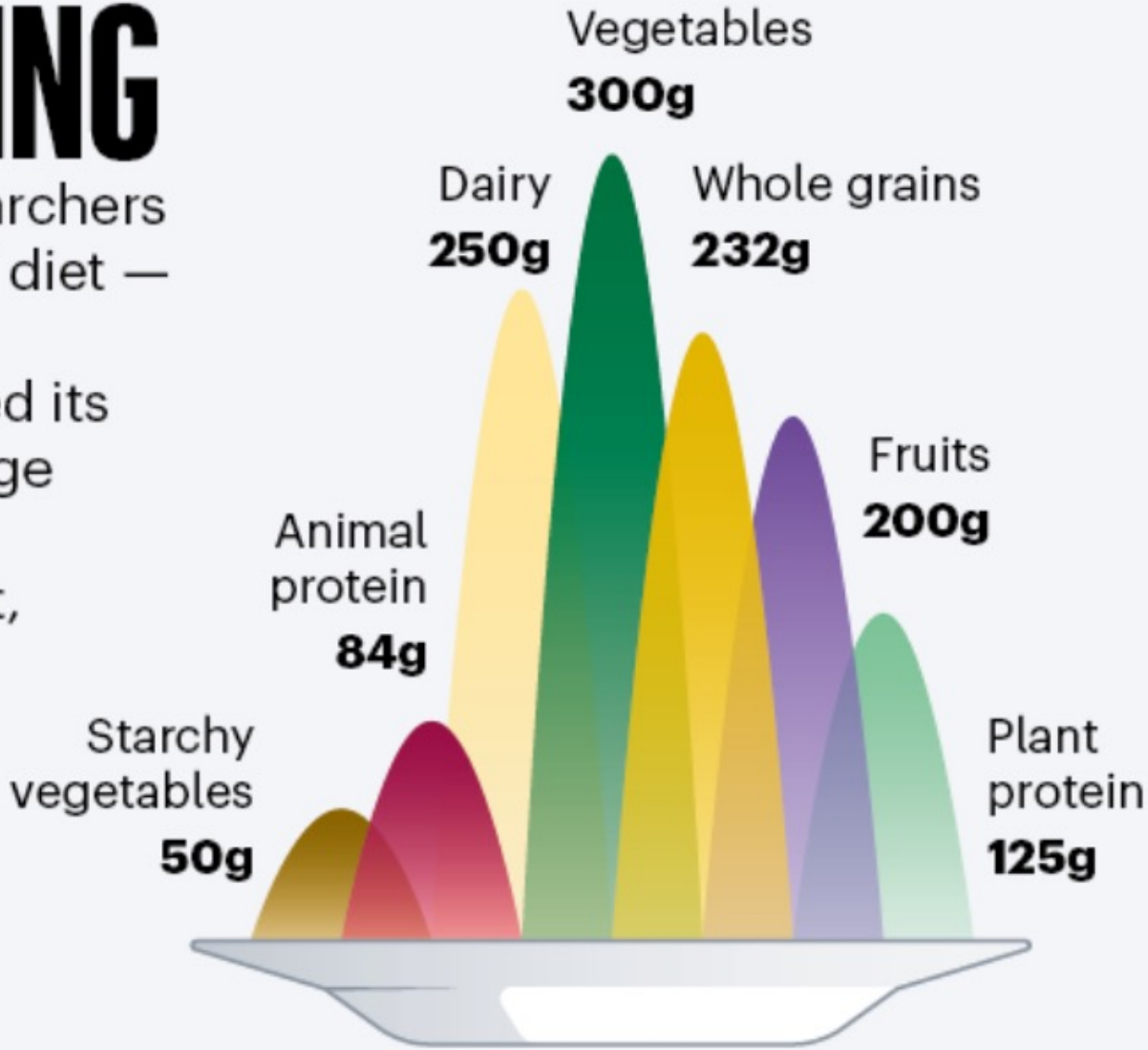



D 303
TOUTES DIRECTIONS
Cimetière
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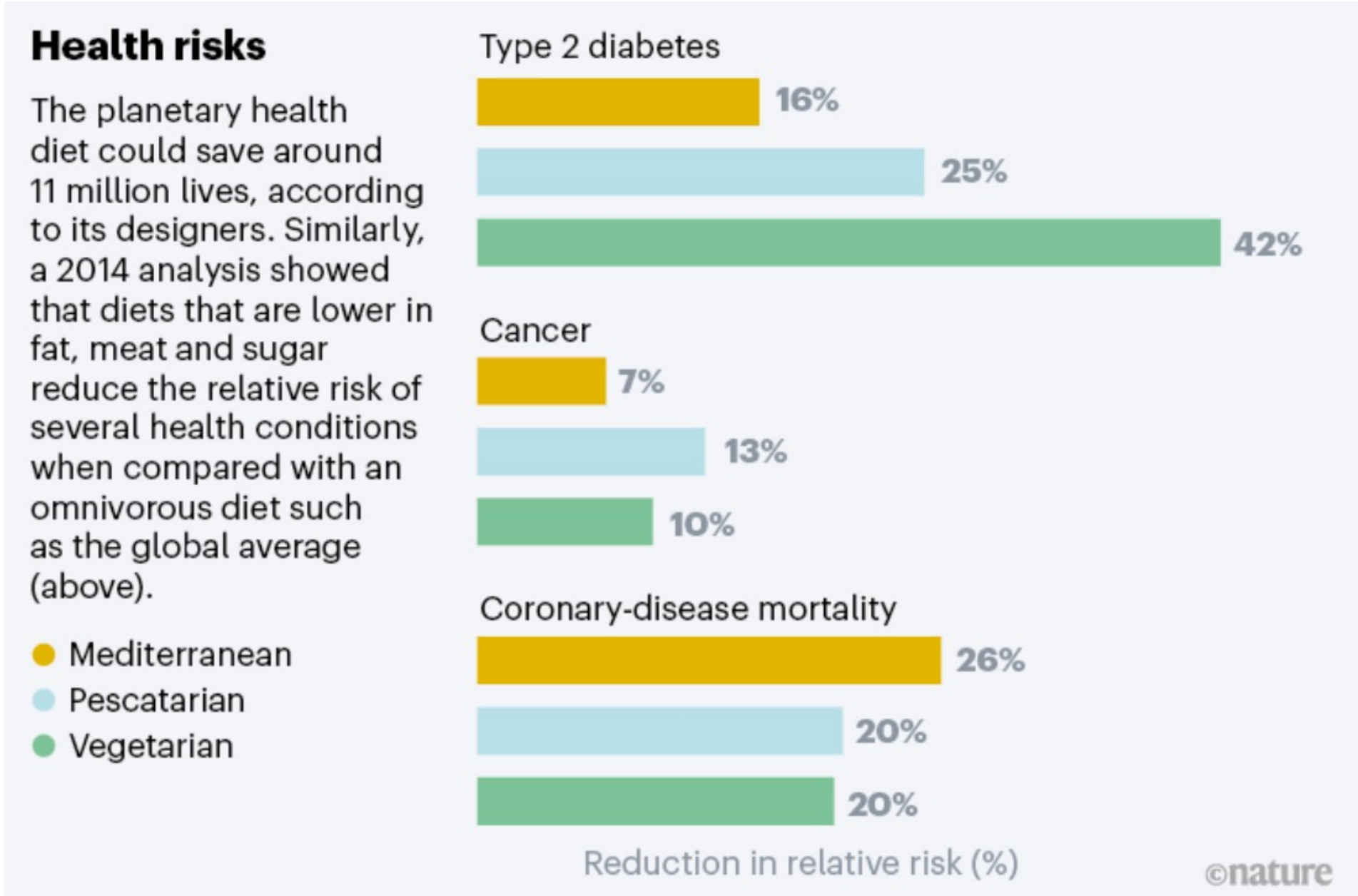
HEALTHY EATING

A commission of food researchers devised a 'planetary health' diet — meant to be nutritious and sustainable — and compared its composition with the average diets in different regions. Further studies showed that, in many regions, following the proposed diet would be prohibitively expensive.

By Kerri Smith
Design by Jasiek Krzysztofiak



https://www-nature-com.proxy.library.uu.nl/articles/d41586-021-03565-5

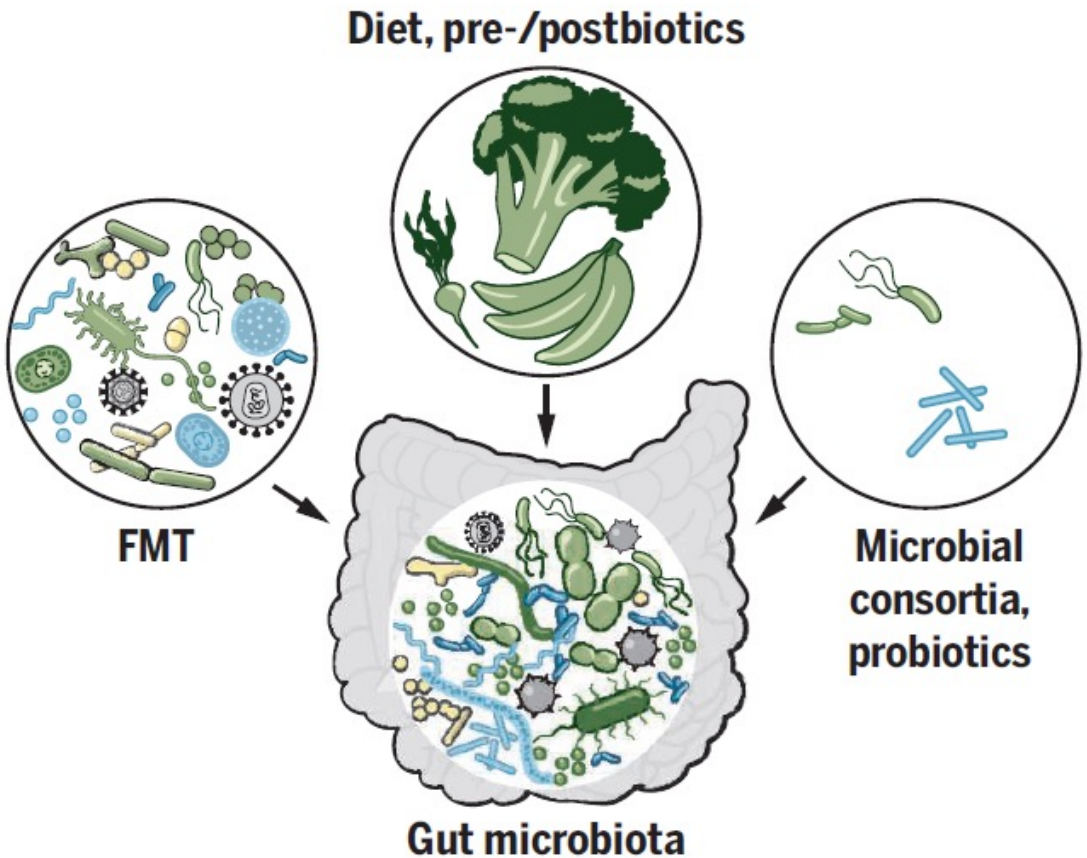


https://www-nature-com.proxy.library.uu.nl/articles/d41586-021-03565-5

Modulating gut microbes

Strategies to alter gut microbiota

Fecal microbiota transplant (FMT) involves transfer of fecal microbiota from a donor to another individual. Alternatively, microbial consortia (targeted formulations used to augment host microbiota) are being developed. Diet, prebiotics, and postbiotics can also influence the microbial community.



Unsuccessful

Open Access Article

Regular Consumption of Cocoa and Red Berries as a Strategy to Improve Cardiovascular Biomarkers via Modulation of Microbiota Metabolism in Healthy Aging Adults

by Joaquín García-Cordero [1], Alba Martinez [1], Carlos Blanco-Valverde [1], Alicia Pino [1], Verónica Puertas-Martín [2,3], Ricardo San Román [2] and Sonia de Pascual-Teresa [1,*]

[1] Departamento de Metabolismo y Nutrición, Instituto de Ciencia y Tecnología de Alimentos y Nutrición (ICTAN-CSIC), C/José Antonio Novais, 10, 28040 Madrid, Spain

[2] Hospital 12 de Octubre, 28041 Madrid, Spain

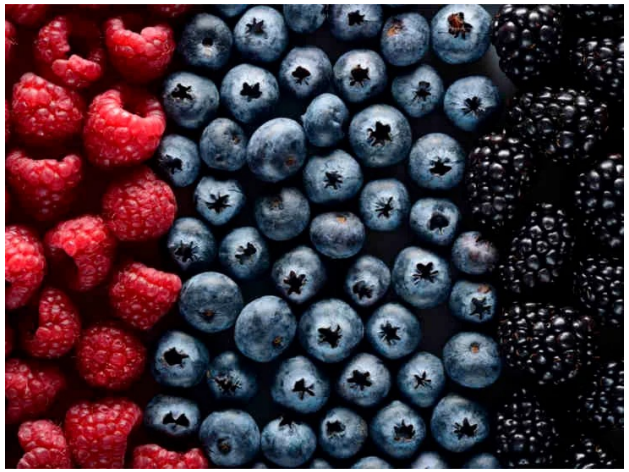
[3] Facultad de Educación, Universidad Internacional de la Rioja, 26006 Logroño, Spain

[*] Author to whom correspondence should be addressed.

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Microbiota management

stress
(maagdarm) infectie
antibotica

gezonde microbiota







dysbiose





prebiotica



probiotica



feces trans-
plantatie



live micro-organisms which, when administered in adequate amounts, confer a health benefit on the host

FAO/WHO 2001

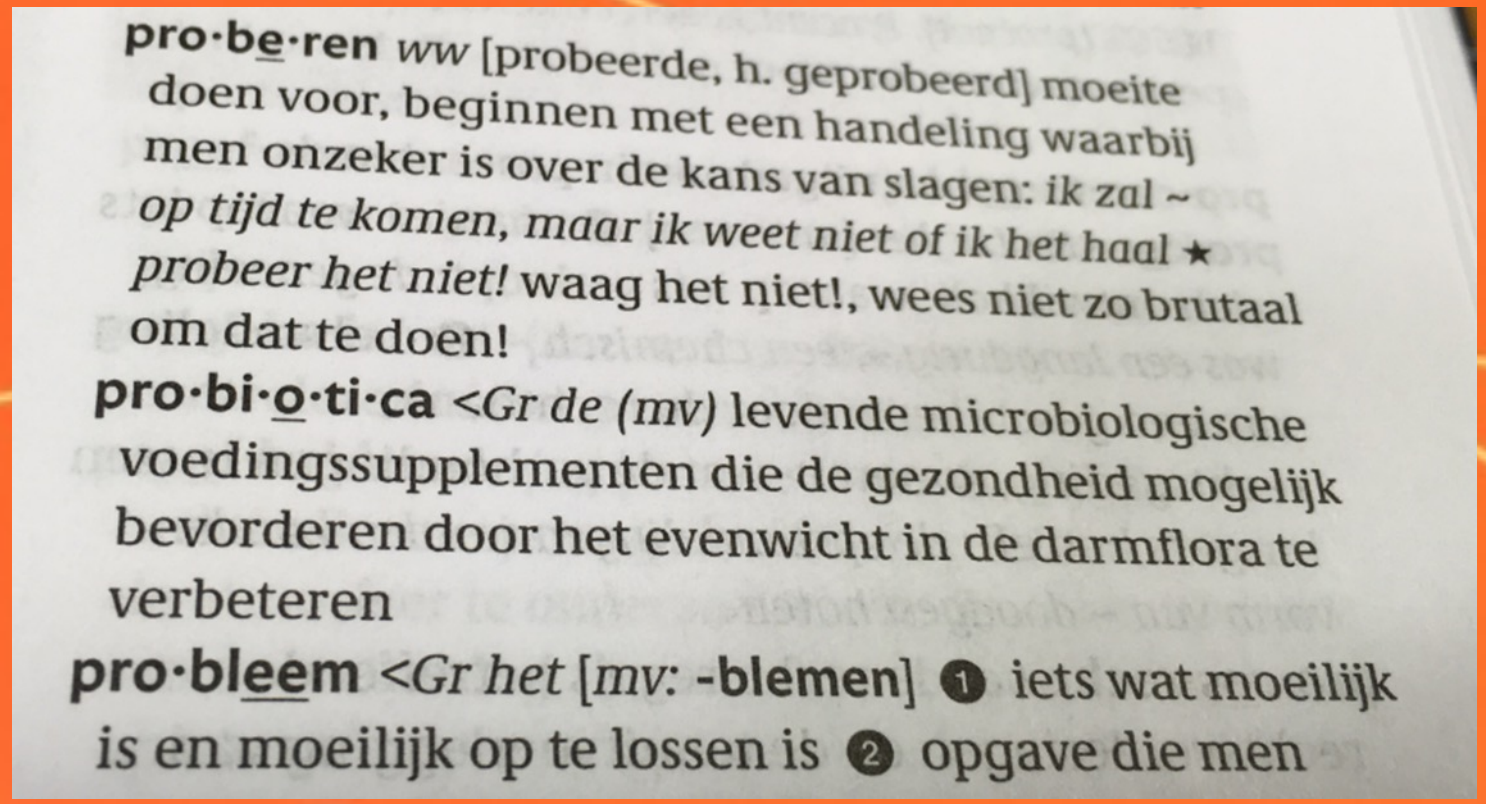
Groot Woordenboek

pro·bi·o·ti·ca <*Gr de (mv)* levende microbiologische voedingssupplementen die de gezondheid mogelijk bevorderen door het evenwicht in de darmflora te verbeteren

Nederlands

prisma

Groot Woordenboek



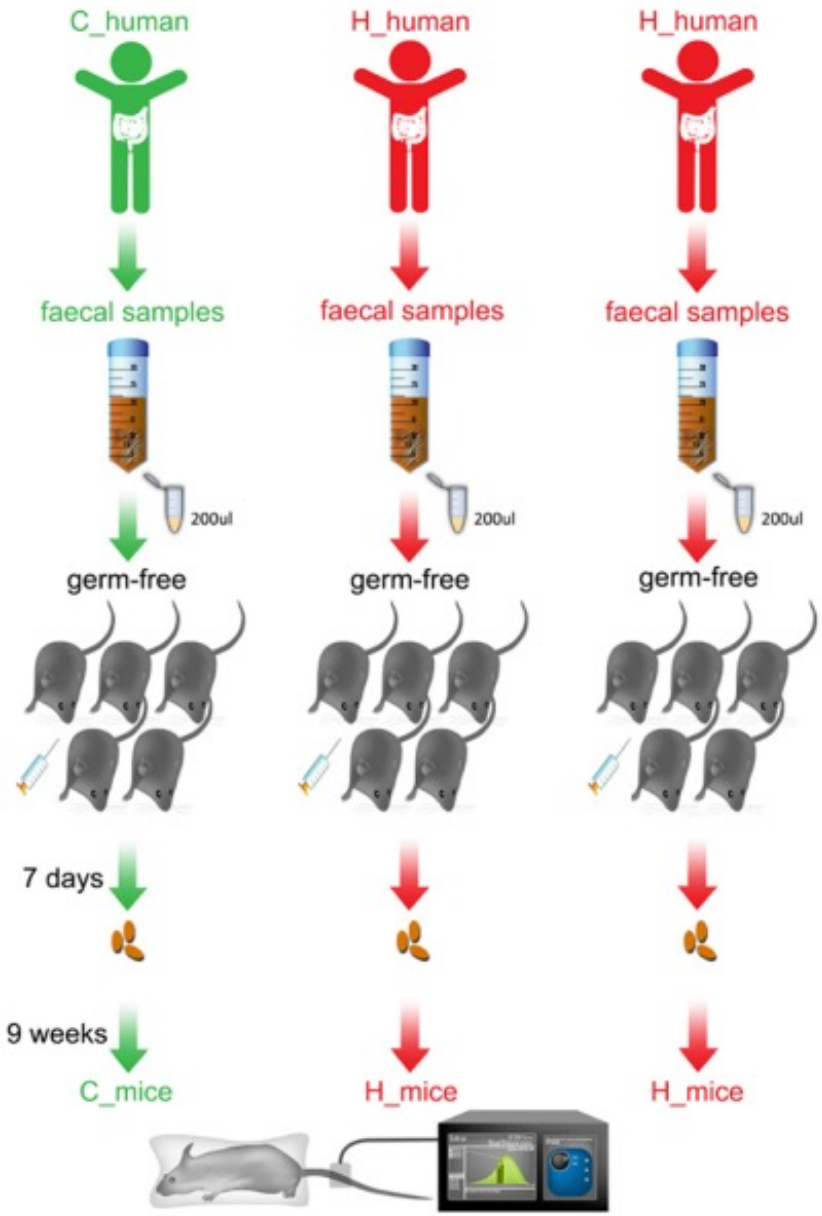
pro·be·ren *ww* [probeerde, h. geprobeerd] moeite doen voor, beginnen met een handeling waarbij men onzeker is over de kans van slagen: *ik zal ~ op tijd te komen, maar ik weet niet of ik het haal* ★ *probeer het niet!* waag het niet!, wees niet zo brutaal om dat te doen!

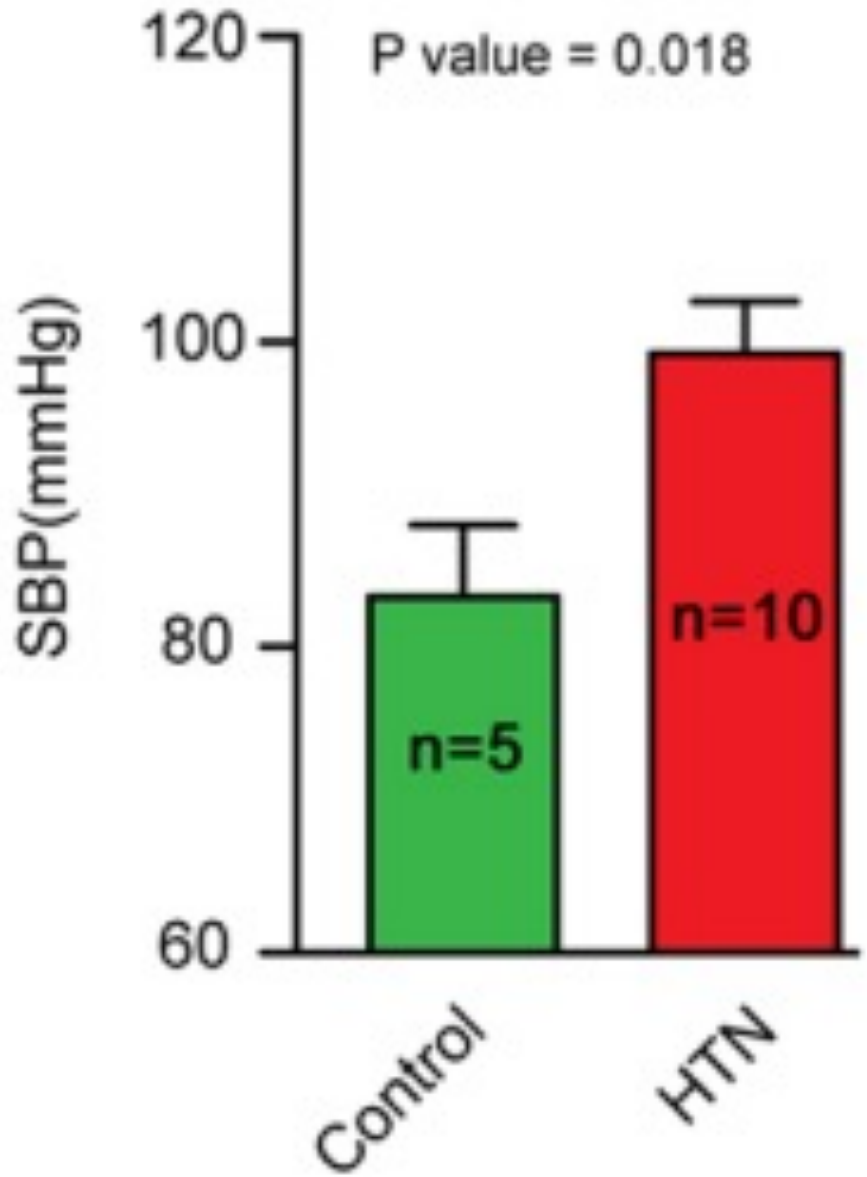
pro·bi·o·ti·ca <*Gr de (mv)* levende microbiologische voedingssupplementen die de gezondheid mogelijk bevorderen door het evenwicht in de darmflora te verbeteren

pro·bleem <*Gr het* [*mv:* **-blemen**] ❶ iets wat moeilijk is en moeilijk op te lossen is ❷ opgave die men

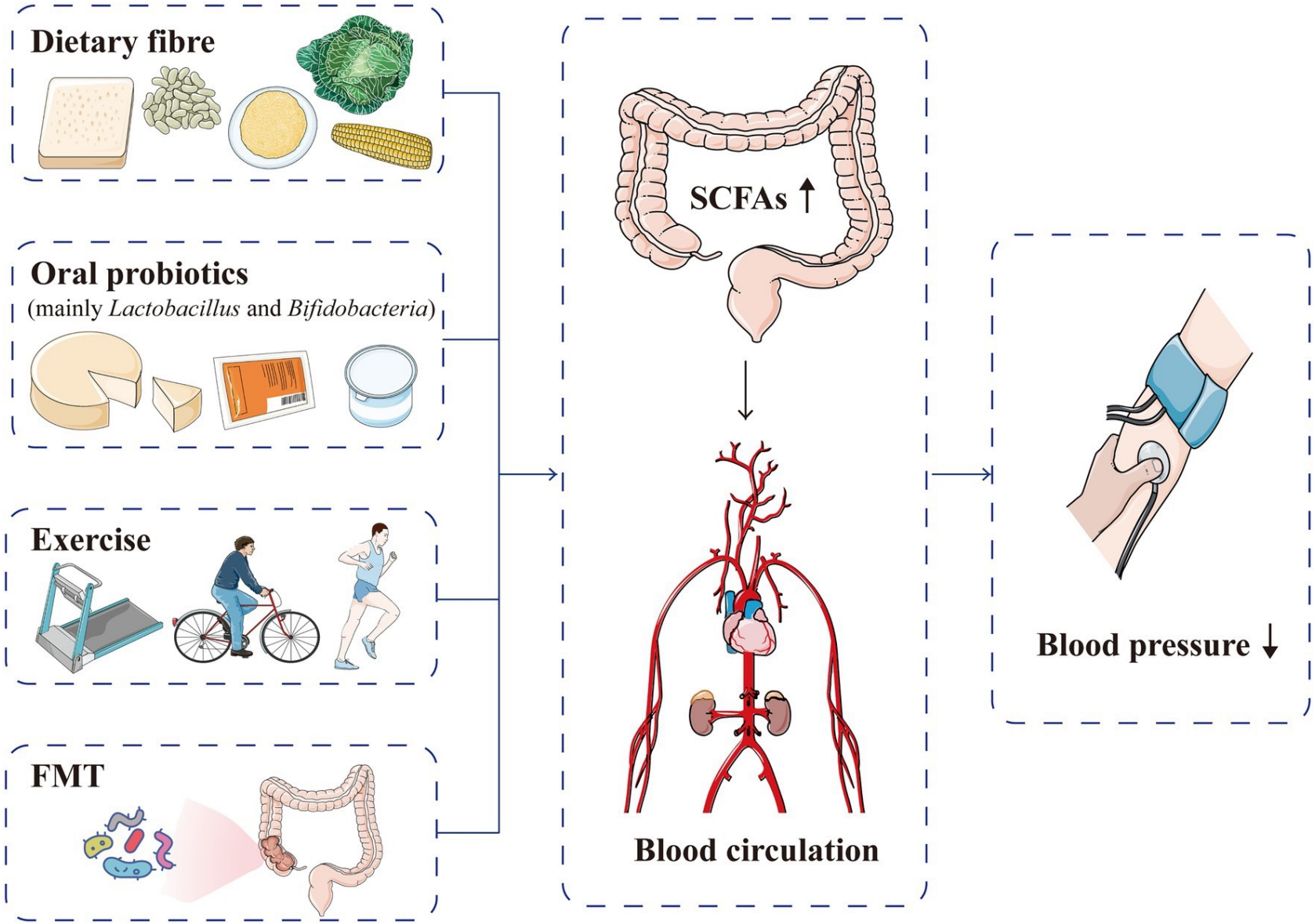
Nederlands

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Li *et al. Microbiome* (2017) 5:14

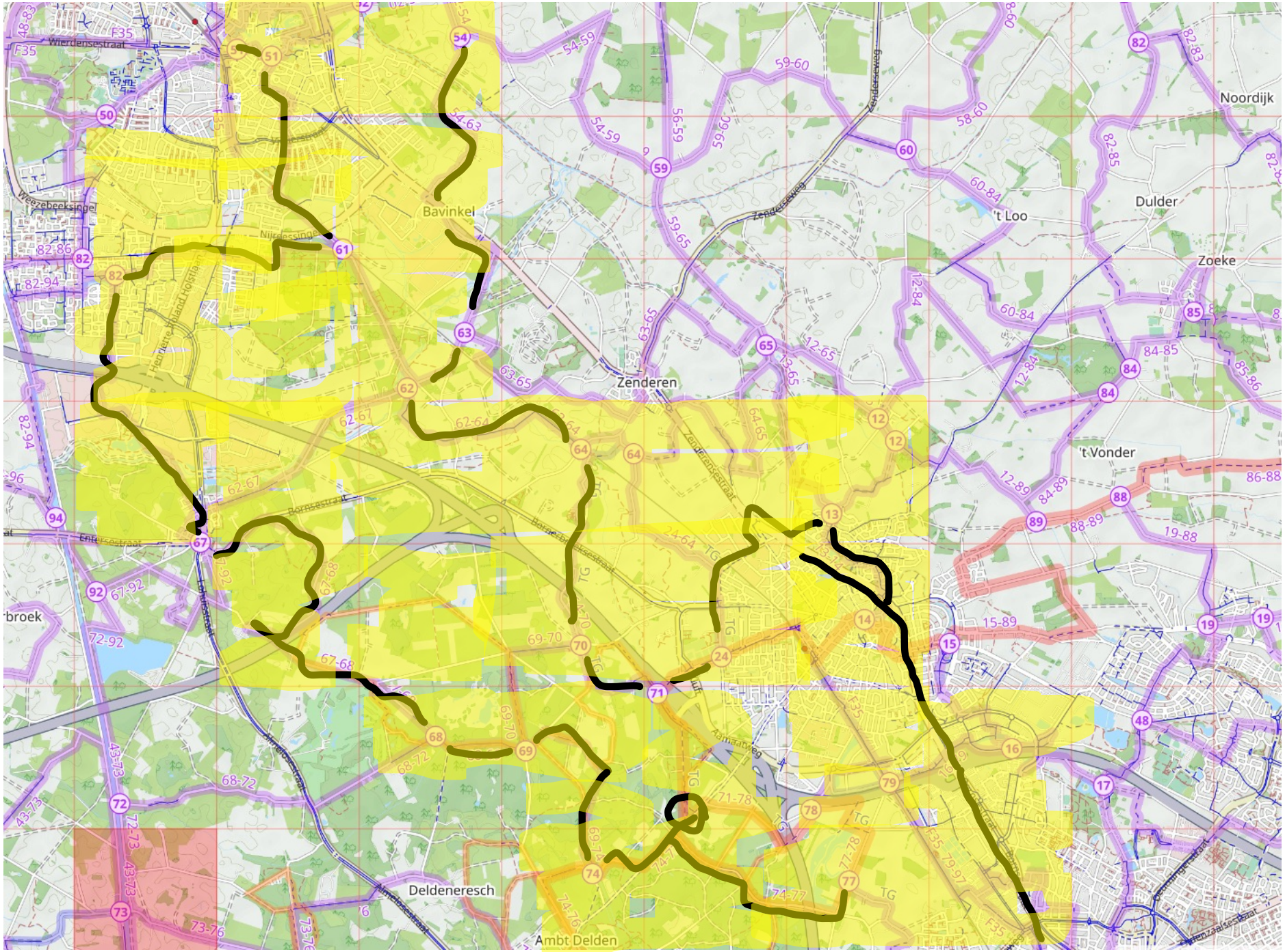

Dietary fibre
Oral probiotics
(mainly *Lactobacillus* and *Bifidobacteria*)
Exercise
FMT
SCFAs ↑
Blood circulation
Blood pressure ↓



Damaged Guts

Damaged Guts by PizzaDude.dk


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Bavinkel
Zenderen
Noordijk
Dulder
't Loo
Zoeke
't Vonder
Deldeneresch
Ambt Delden
Wierdensestraat
Weezebeeksingel
Nijverdalseweg
Zenderenseweg
Zenderenseestraat
Borneseestraat
Enschedestraat
Hengelosestraat
Almelosestraat
Aamaabweg
Hermelerstraat
Hollandhoistraat