MİKROBİYOTA NEREDEYİZ??

Prof. Dr. Ener Çağrı DİNLEYİCİ
Eskişehir Osmangazi Üniversitesi Tıp Fakültesi
Çocuk Sağlığı ve Hastalıkları Anabilim Dalı

KLİMİK
15 MART 2019, ANTALYA

ener çağrı dinleyici

ESKİŞEHİR OSMANGAZİ ÜNİVERSİTESİ 1970

PROBAGE STUDY GROUP

Pediatrik Probiyotik Prebiyotik Derneği

MİKROBİYOTA

ener çağrı dinleyici

29 Nisan2018

5 Ekim 2018

MİKROBİYOTA ÇALIŞMALARI

ener çağrı dinleyici

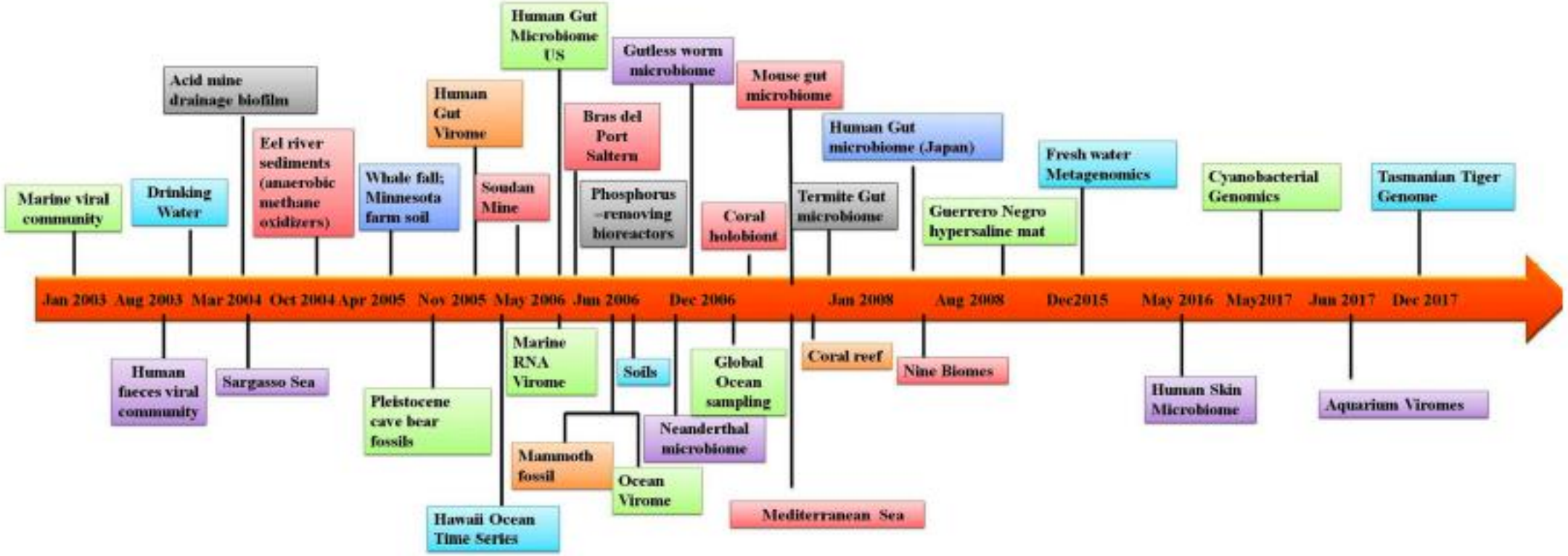

FIGURE 1 | Timeline of the sequence-based metagenomic projects showing the variety of the environmental samples.

Malla et al. Froniters Immunology 2019.

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Microbiome
IN NUMBERS

100 Trillion
symbiotic microbes live in and on every person and make up the human microbiota

The human body has more microbes than there are stars in the milky way

95%
of our microbiota is located in the GI tract

150:1
The genes in your microbiome outnumber the genes in our genome by about 150 to one

The surface area of the **GI tract** is the same size as 2 tennis courts

You have **1.3X** more microbes than human cells

>10,000
Number of different microbial species that researchers have identified living in and on the human body

2kg The gut microbiota can weigh up to 2Kg

Microbiome Ireland
Interfacing Food & Medicine

The microbiome is more medically accessible and manipulable than the human genome

90% It is thought that of disease can be linked in some way back to the gut and health of the microbiome

5:1
Viruses:Bacteria in the gut microbiota

2.5 The number of times your body's microbes would circle the earth if positioned end to end

Each individual has a unique gut **microbiota**, as personal as a fingerprint

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frontiers in Immunology

REVIEW
published: 07 January 2019
doi: 10.3389/fimmu.2018.02868

Check for updates

Exploring the Human Microbiome: The Potential Future Role of Next-Generation Sequencing in Disease Diagnosis and Treatment

Muneer Ahmad Malla[1], Anamika Dubey[2], Ashwani Kumar[2], Shweta Yadav[1], Abeer Hashem[3,4] and Elsayed Fathi Abd_Allah[5]*

HEDEF SAĞLIKLI MİKROBİYOTA

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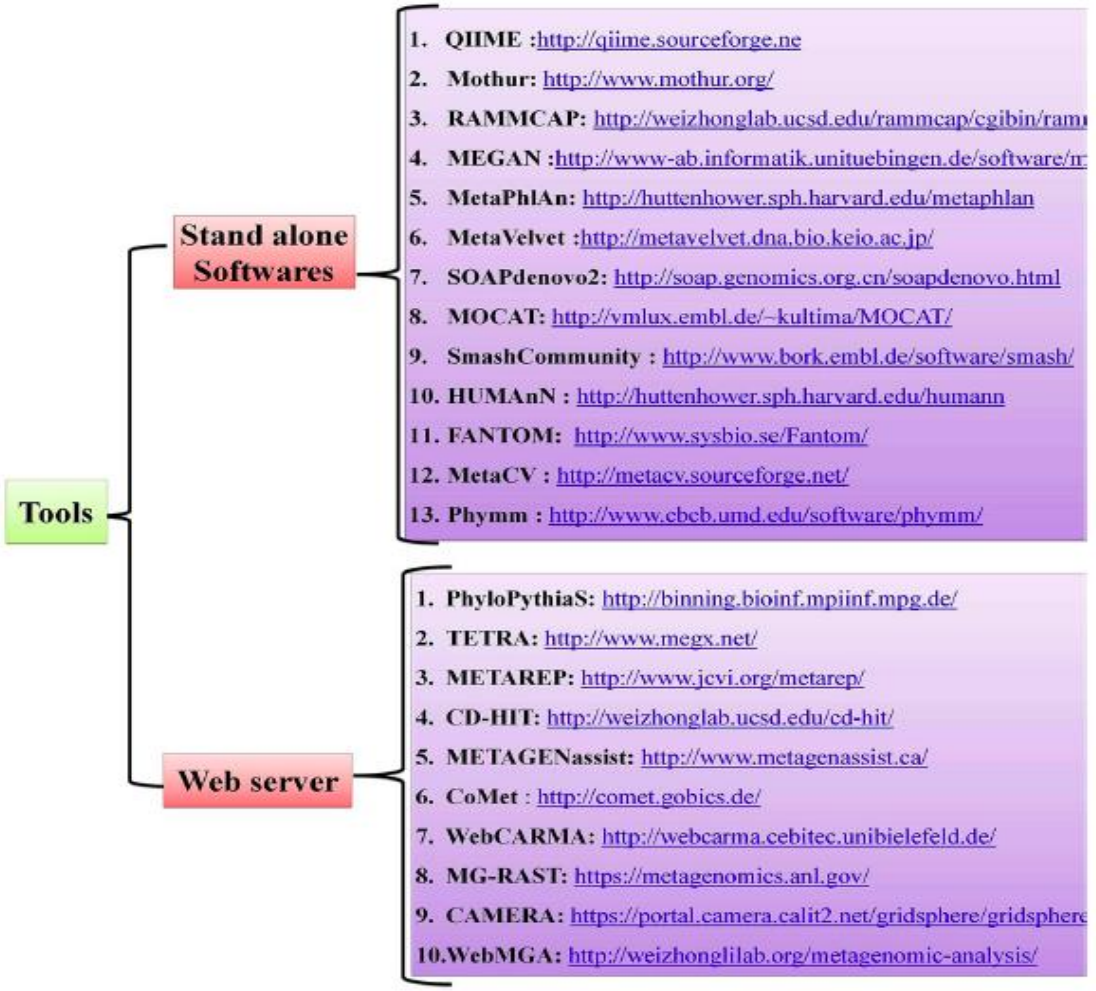

FIGURE 2 | Tools and web servers related to gut microbiome studies.

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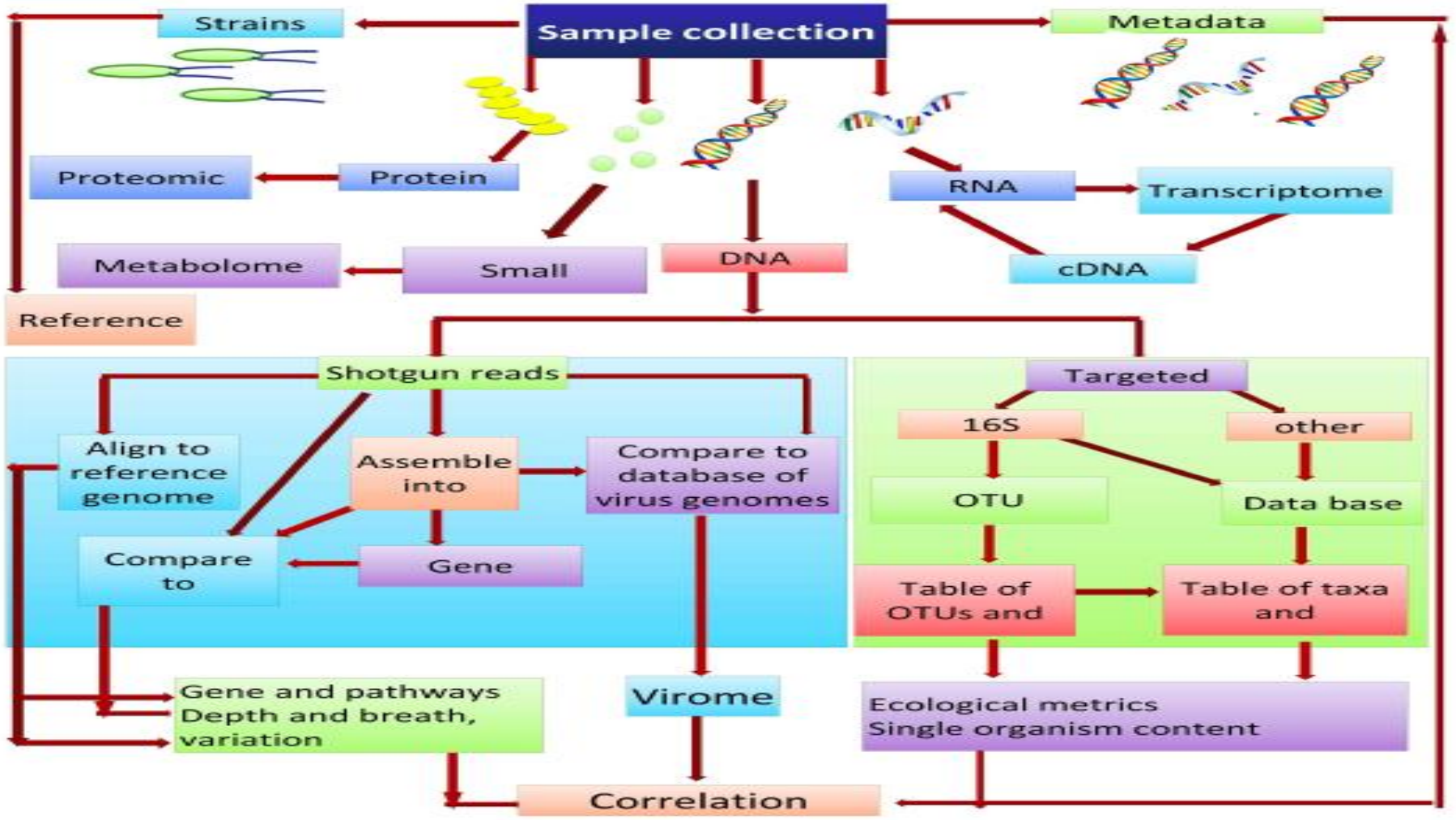

Malla et al. Froniters Immunology 2019.

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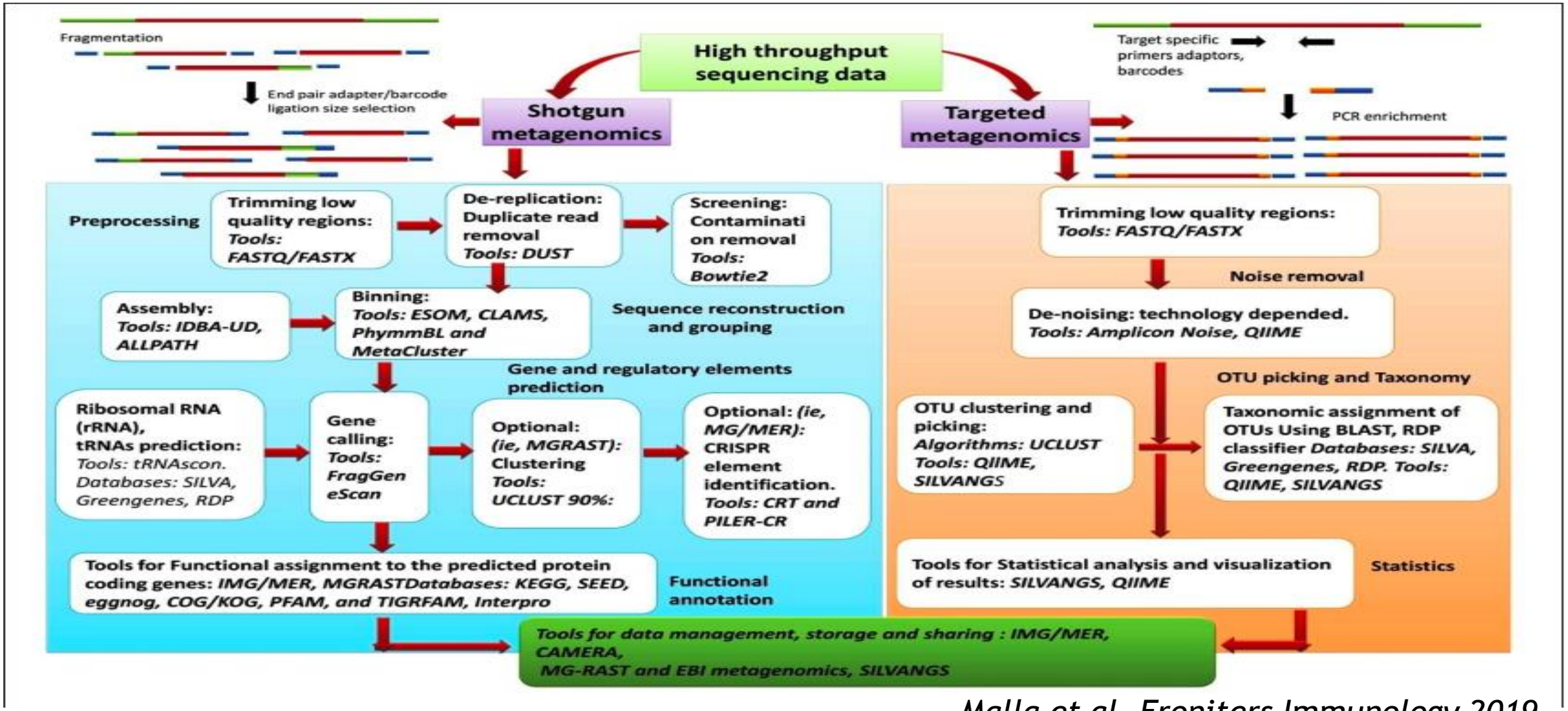

Malla et al. Froniters Immunology 2019.

MİKROBİYOTA ANALİZ?

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Digestive Diseases and Sciences
https://doi.org/10.1007/s10620-018-5299-6

INVITED REVIEW

Clinician Guide to Microbiome Testing

Christopher Staley[1,2] · Thomas Kaiser[1,2] · Alexander Khoruts[2,3]

Received: 16 July 2018 / Accepted: 19 September 2018

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AMERICAN GUT

What it does: This crowd funded research project sequences 16S rRNA — an RNA subunit that's purportedly helpful for identifying bacteria and archaea (single-cell microorganisms). Results are shared anonymously in open repositories to help further microbiome research around the world.

Price: $99

Where to find it: AmericanGut.org

What you get: A report on which bacteria and archaea are present, and how your microbiome compares to the 10,000-plus others in the project database. You'll also receive information on how your diet and lifestyle might contribute to your microbiome makeup.

Notes: It takes four to six weeks to receive your testing kit, and up to three months to get results — by which point your microbiome may have changed significantly, depending on any changes in your diet or lifestyle.

BIOHM

What it does: Sequences the genes of both the bacteria and fungi in your gut at a genus and species level. A candida specific test is also available.

Price: $135

Where to find it: BiohmHealth.com

What you get: A profile of your gut makeup, and comparison to normal levels of bacterial strains from the NIH Human Microbiome Project and/or fungal strains from Case Western Reserve University School of Medicine.

Notes: For an additional fee, you can receive diet and lifestyle recommendations from a registered nutritionist. Biohm also sells their own line of probiotics.

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DAYTWO

What it does: Geared toward people with diabetes and prediabetes, DayTwo uses a stool test to sequence the DNA of your microbiome, and a blood test to measure HbA1C, which provides an idea of blood sugar levels on average.

Price: $349

Where to find it: DayTwo.com

What you get: A profile of your microbiome composition and diversity, and a Personalized Nutrition App dedicated to helping you manage your blood sugar levels via customized advice on foods to avoid and meal and snack recommendations.

Notes: The tests and personalized plans are based on a five-year clinical research project licensed from Weizmann Institute of Science.

THRYVE

What it does: Like American Gut, it uses 16S rRNA sequencing to sequence your microbiome down to a species level.

Price: $105

Where to find it: ThryveInside.com

What you get: A rundown of which healthy bacteria are low and which pathogens are high, and a "wellness score" based on how your results compare to data from the American Gut Project. You'll also get personalized daily dietary and supplement recommendations.

Notes: Thryve sells probiotics ($42/bottle) for gut health, general health, weight management, and immune support, which they deliver on ice in the summer.

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UBIOME

What it does: Sequences the DNA of your gut microbes to identify pathogens associated with conditions like Irritable Bowel Syndrome (IBS) and Crohn's Disease.

Price: $89-$399

Where to find it: uBiome.com

What you get: You'll get a breakdown of the pathogens and commensal bacteria in your microbiome, how your biome compares to the company's database of 150,000+ samples, and an overview of how well it's functioning.

Notes: uBiome also offers SmartGut, a physician-ordered test that might be covered by insurance. Your doctor will receive a clinical report on your microbiome and possible links to specific infections and gut conditions.

VIOME

What it does: Uses metatranscriptomic analysis to sequence all the RNA in your stool and identify all living gut microorganisms (bacteria, viruses, bacteriophages, archaea, fungi, yeast, parasites, etc.) at a species and strain level.

Price: $399

Where to find it: Viome.com

What you get: A gut score (health of your microbiome), metabolic score (fitness and nutrition level), and body score (overall shape and lifestyle choices) based on your results and findings from peer-reviewed articles.

Notes: Viome also measures the metabolites your microbes produce after you've eaten, then offers personalized food and nutrition plans for minimizing production of harmful metabolites and maximizing production of beneficial ones.

microoorganisms

MDPI

Review

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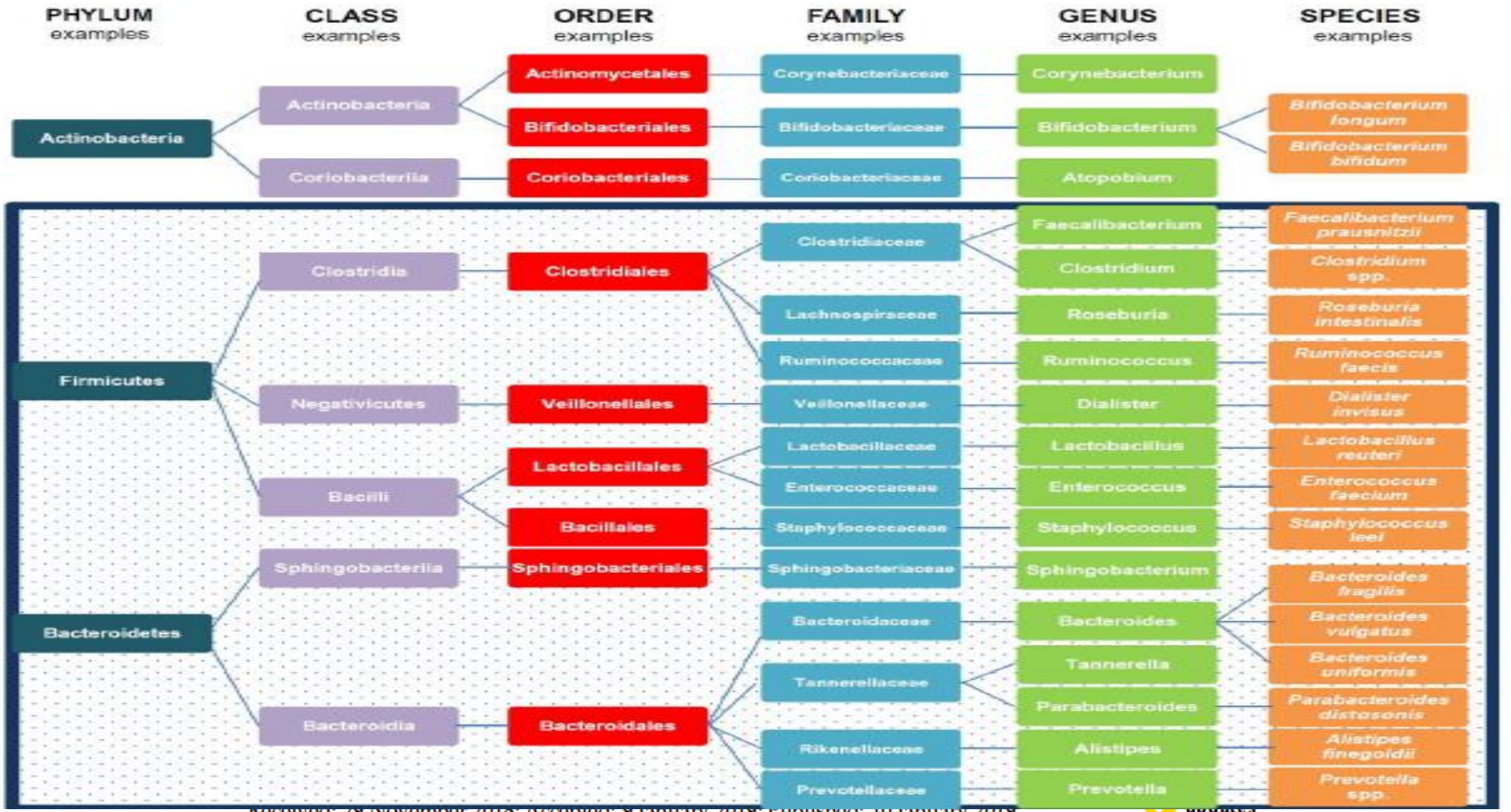

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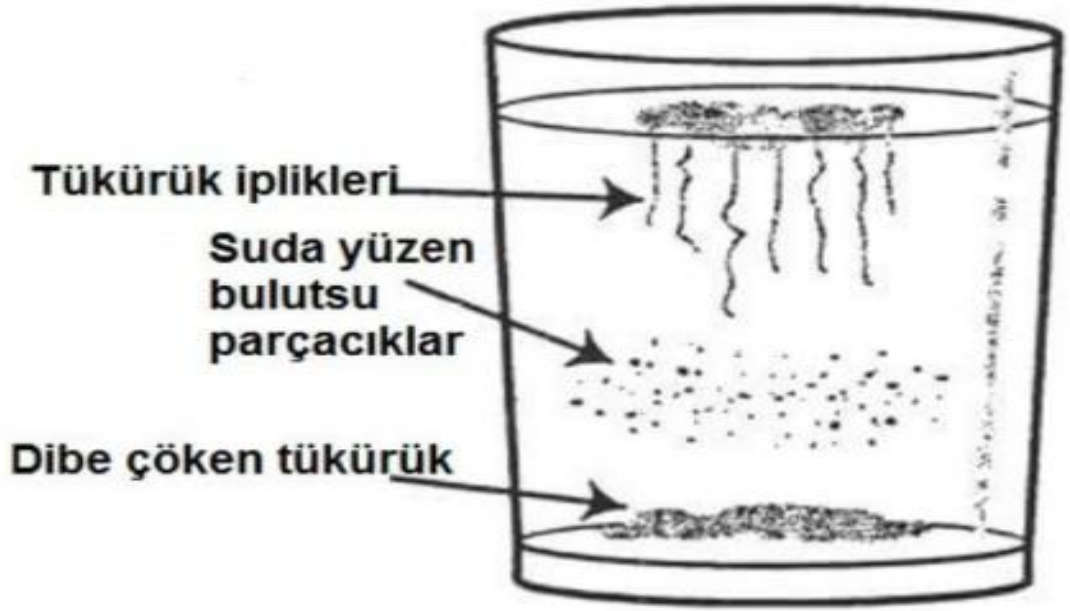
ANALİZ?

ener çağrı dinleyici

MİKROBİYOTA
GAYTADA CANDIDA ARTIŞI??



Bağırsaklarınızda Kandida (Candida albicans) maya mantarının arttığını basit bir test yardımıyla anlayabilirsiniz. Sabah uyandığınızda aç karnına, dişlerinizi fırçalamadan ve ağzınızı çalkalamadan önce, cam bardağı 2/3'ü kadar içme suyu ile doldurun ve suya tükürün. Bunu 15 dakika izleyin. Eğer tükürük suyun üstünde kalıyorsa, sağlıklı bağırsak florasına sahipsiniz demek oluyor. Eğer tükürük dibe çöküyorsa, saçak gibi aşağıya iniyorsa veya kar yağmış gibi oluyorsa ya da suya rakı konmuş gibi bulanıyorsa kandida maya mantarı bağırsak floranızı bozmuş anlamına geliyor.

MİKROBİYOTA
CANDIDA?

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Cell

Log in

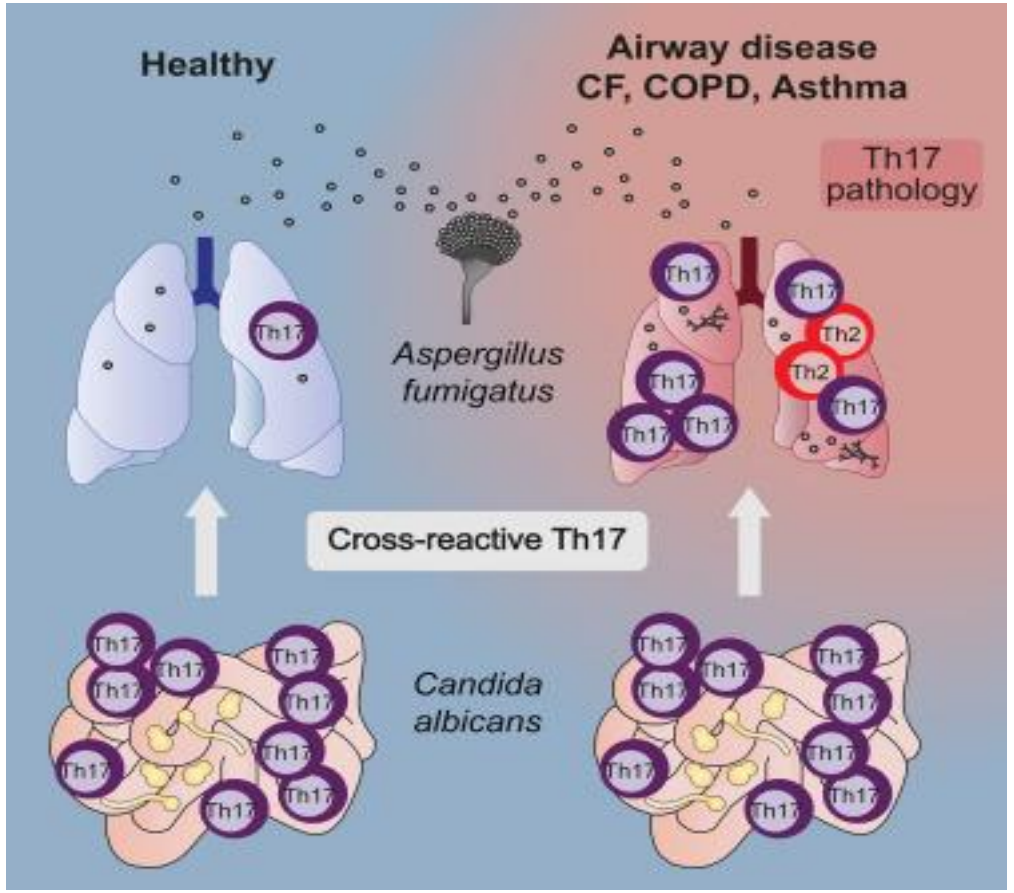
ARTICLE | VOLUME 176, ISSUE 6, P1340-1355.E15, MARCH 07, 2019

Purchase

Human Anti-fungal Th17 Immunity and Pathology Rely on Cross-Reactivit against *Candida albicans*

Petra Bacher • Thordis Hohnstein • Eva Beerbaum • Marie Röcker • Matthew G. Blango • Svenja Kaufmann • Jobst Röhmel • Patience Eschenhagen • Claudia Grehn • Kathrin Seidel • Volker Rickerts • Laura Lozza • Ulrik Stervbo • Mikalai Nienen • Nina Babel • Julia Milleck • Mario Assenmacher • Oliver A. Cornely • Maren Ziegler • Hilmar Wisplinghoff • Guido Heine • Margitta Worm • Britta Siegmund • Jochen Maul • Petra Creutz • Christoph Tabeling • Christoph Ruwwe-Glösenkamp • Leif E. Sander • Christoph Knosalla • Sascha Brunke • Bernhard Hube • Olaf Kniemeyer • Axel A. Brakhage • Carsten Schwarz • Alexander Scheffold 25 • Show less • Show footnotes

Published: February 21, 2019 • DOI: https://doi.org/10.1016/j.cell.2019.01.041 • Check for updates



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2019
IN VIVO? IN VITRO? IN FIMO?

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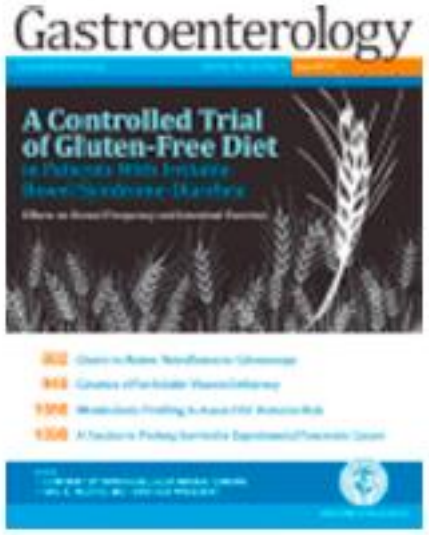
Accepted Manuscript



"*In Fimo*": A Term Proposed for Excrement Examined Experimentally

Aadra P. Bhatt, Luca Grillo, Matthew R. Redinbo

PII: S0016-5085(18)35403-9
DOI: https://doi.org/10.1053/j.gastro.2018.11.070
Reference: YGAST 62318

To appear in: *Gastroenterology*
Accepted Date: 29 November 2018

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2019

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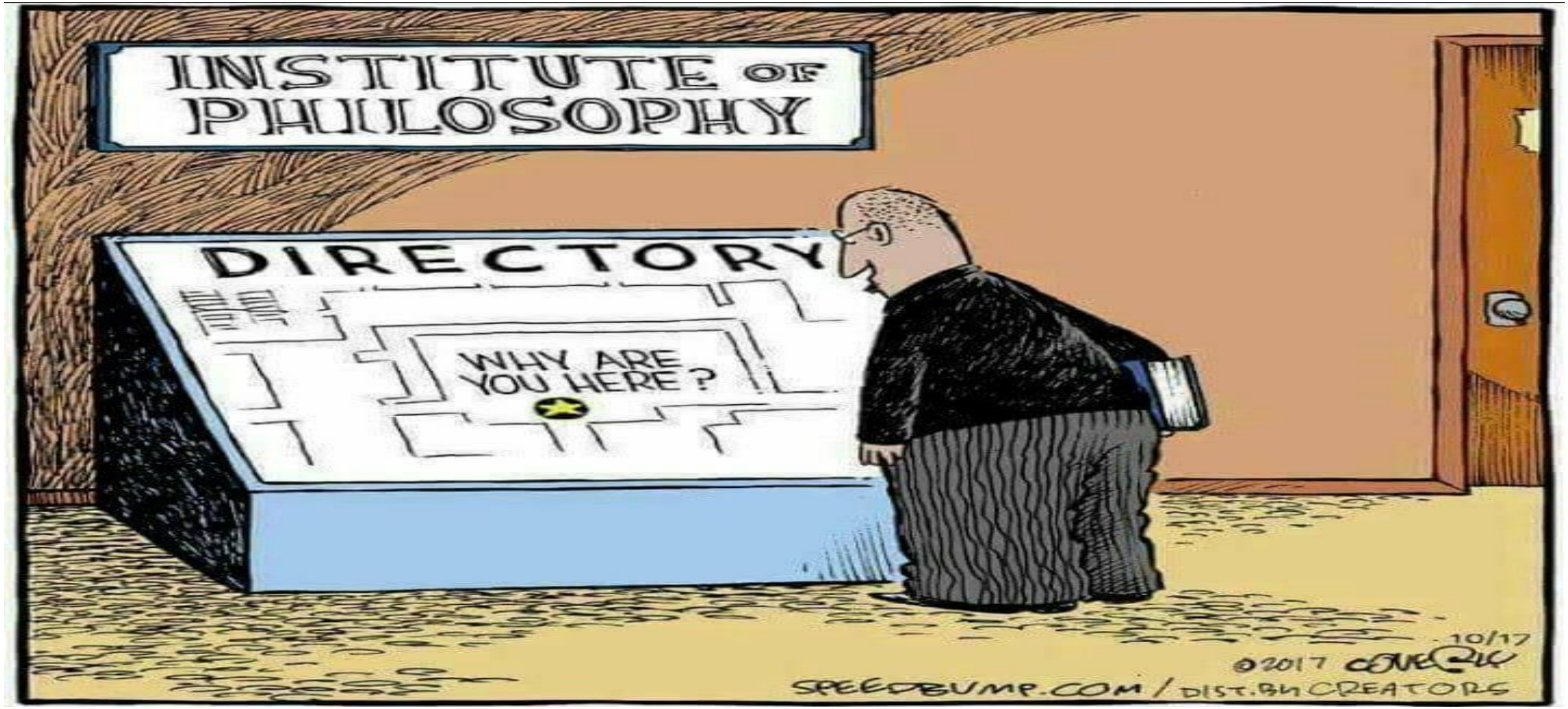

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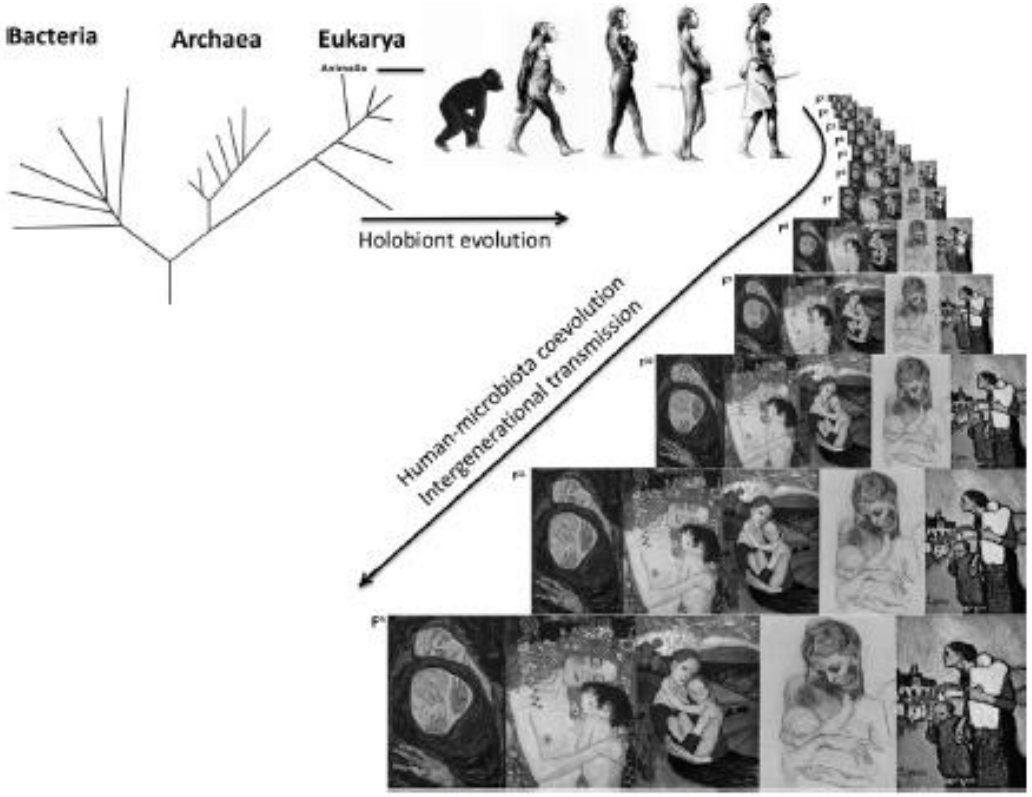

Figure 1 Evolution of the holobiont and vertical transmission through human generations.

Role of the microbiome in human development

Maria Gloria Dominguez-Bello,[1] Filipa Godoy-Vitorino,[2] Rob Knight,[3] Martin J Blaser[4]

Dominguez-Bello MG, *et al*. *Gut* 2019;**0**:1–7. doi:10.1136/gutjnl-2018-317503

B Traditional farming or fishing population

Microbial Diversity : High
Enriched Taxa: *Prevotella, Succinovibrio, Treponema, Ruminococcus, Bacteroides* [Clostridiaceae, Rickenellaceae, Bacteroidetes, Firmicutes, Proteobacteria & Spirochaetes]
Depleted Taxa: Low abundance of *Prevotella* compared to ancient population

A Remote hunter gatherer population

Microbial Diversity: Very High
Enriched Taxa: *Prevotella, Succinovibrio, Treponema, Cyanobacteria,* Tenericutes, *Clostridium, Catenibacterium, Eubacterium, Lachnospira, Salmonella* [Enterococcaceae, Firmicutes, Proteobacteria, Spirochaetes, Clostridiaceae & Euryarchaeota]
Depleted Taxa: Lachnospiraceae, Bacteroidales

C Western (US/European) urban industrialized population

Microbial Diversity : Low
Enriched Taxa: *Bacteroides, Bifidobacterium, Ruminococcus, Blautia, Dorea* [Actinobacteria, Firmicutes, Rickenellaceae]
Depleted Taxa: *Prevotella, Xylanibacter* & *Treponema*

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2019

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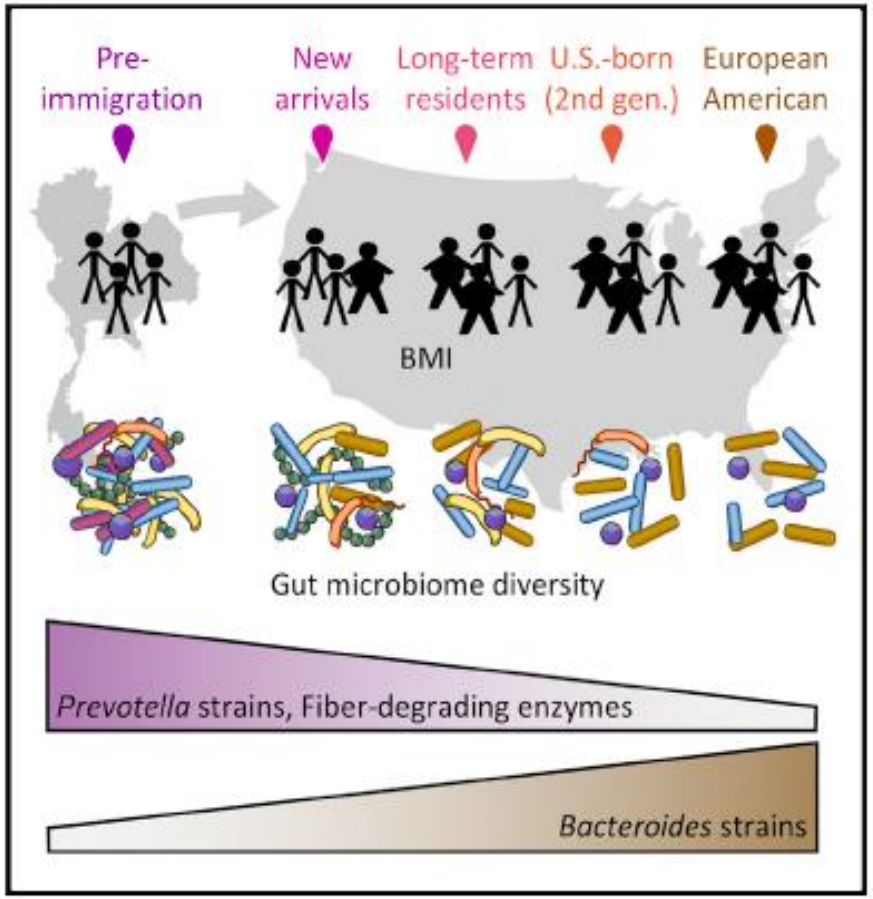
Cell

US Immigration Westernizes the Human Gut Microbiome

Graphical Abstract



Authors

Pajau Vangay, Abigail J. Johnson, Tonya L. Ward, ..., Puma C. Kashyap, Kathleen A. Culhane-Pera, Dan Knights

Correspondence

dknights@umn.edu

In Brief

Migration from a non-western nation to the United States is found to be associated with a loss in gut microbiome diversity and function in a manner that may predispose individuals to metabolic disease.

Vangay et al., 2018, Cell 175, 962–972
November 1, 2018
https://doi.org/10.1016/j.cell.2018.10.029

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2019

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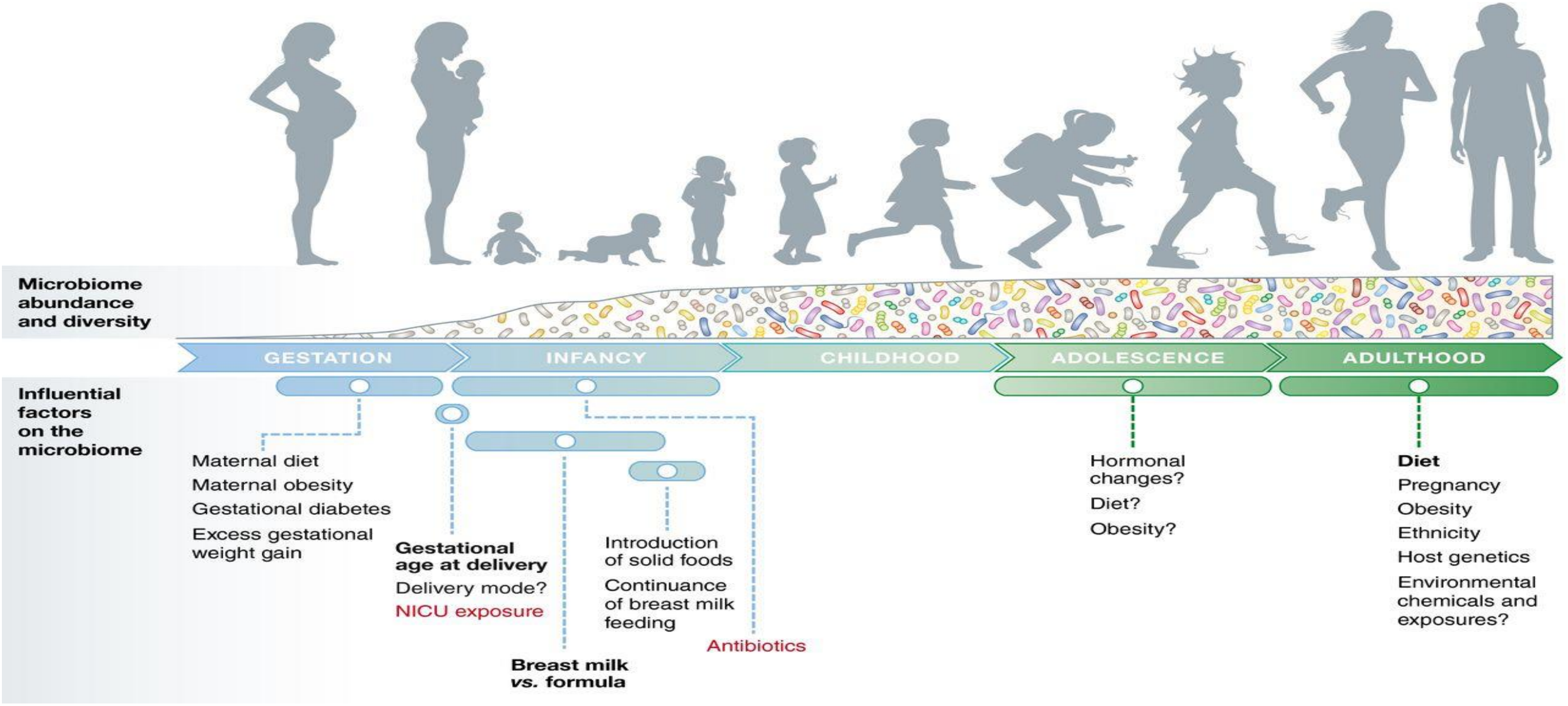

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2019

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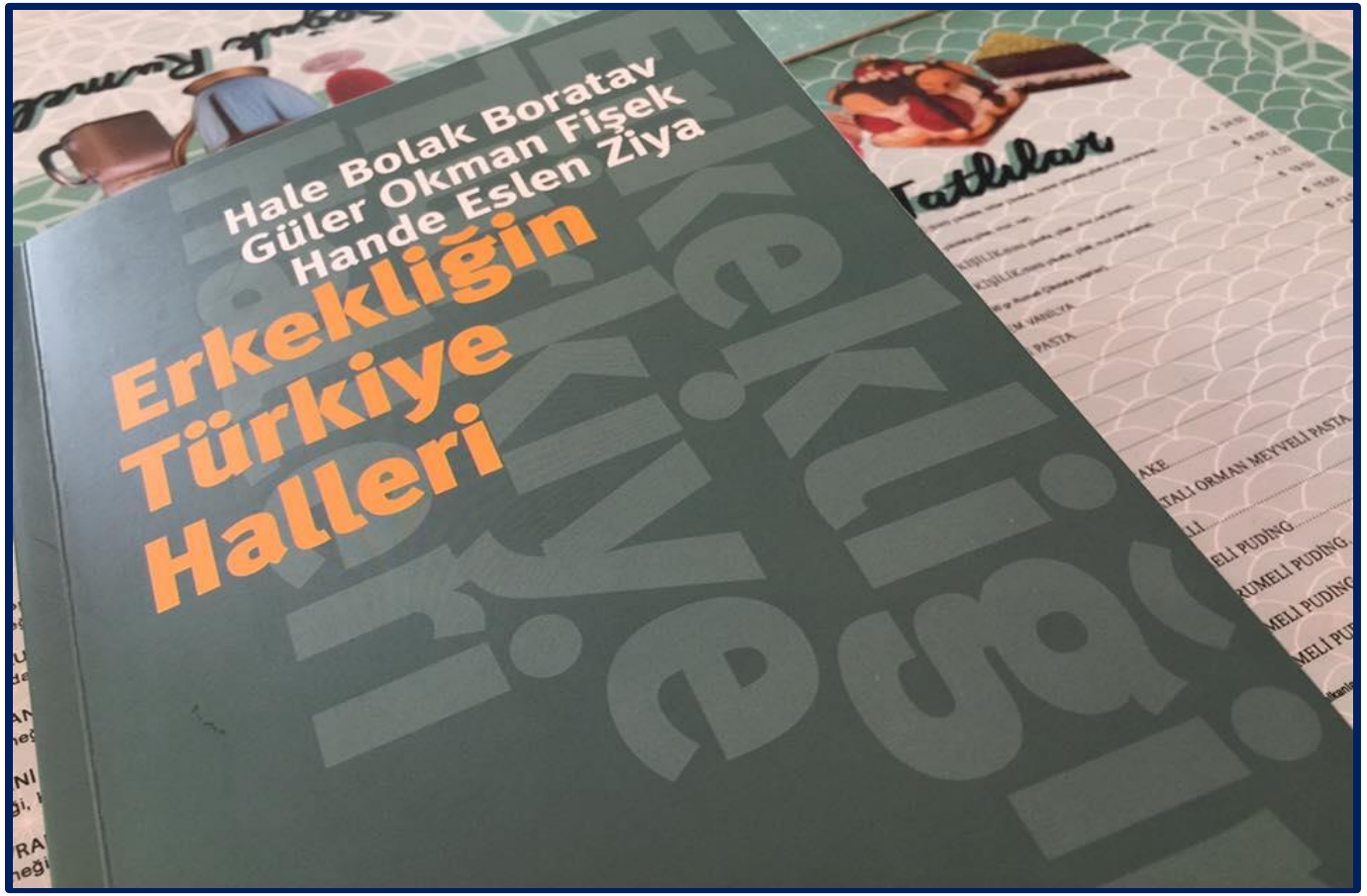
En belirleyici faktör

ANNE

GEBELİK
DOĞUM EYLEMİ
EMZİRME
BESLENME

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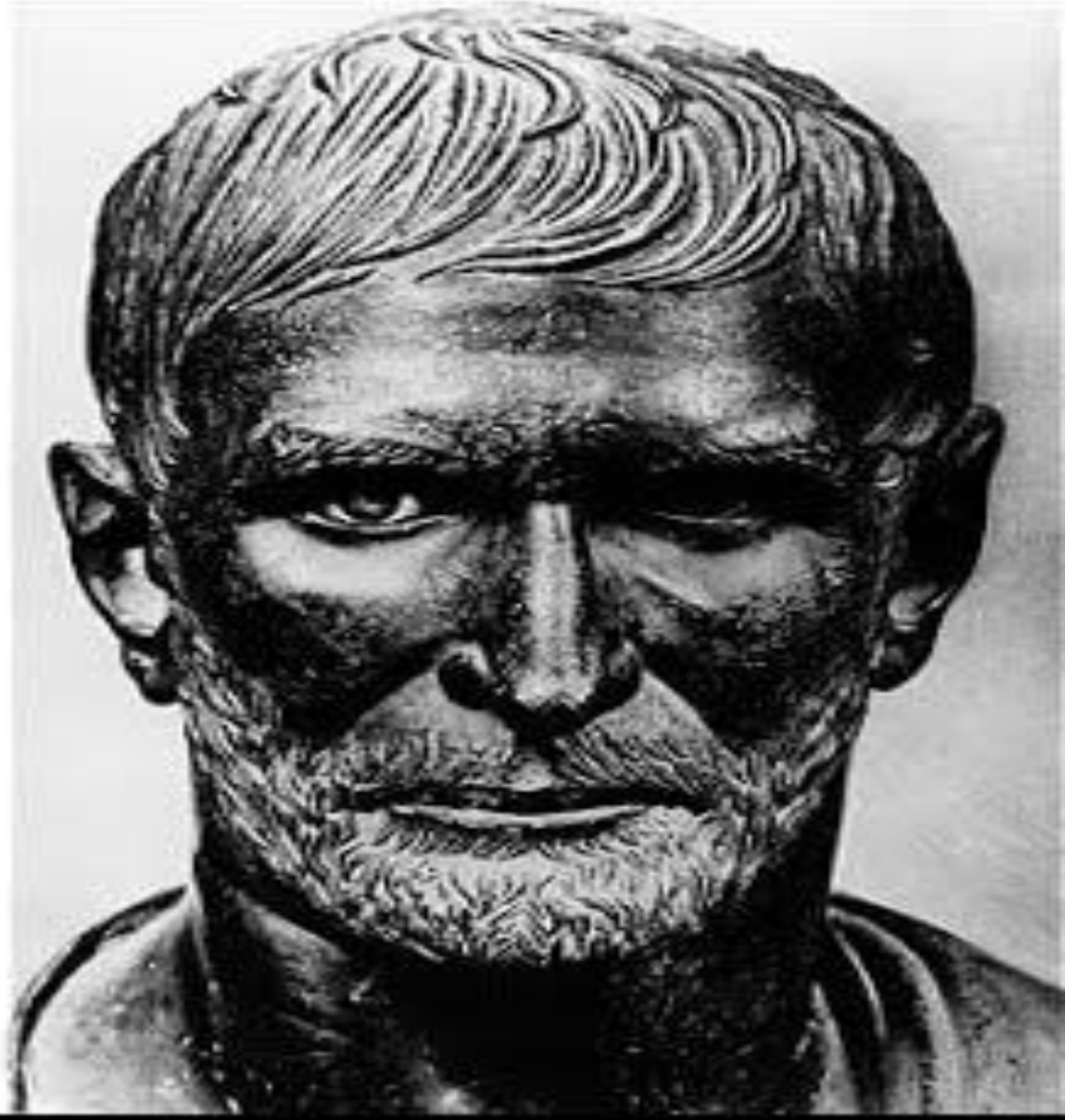
SENDE Mİ BRÜTÜS KİMDİR ??



SEZARYEN

MART 2019 YER: TÜRKİYE

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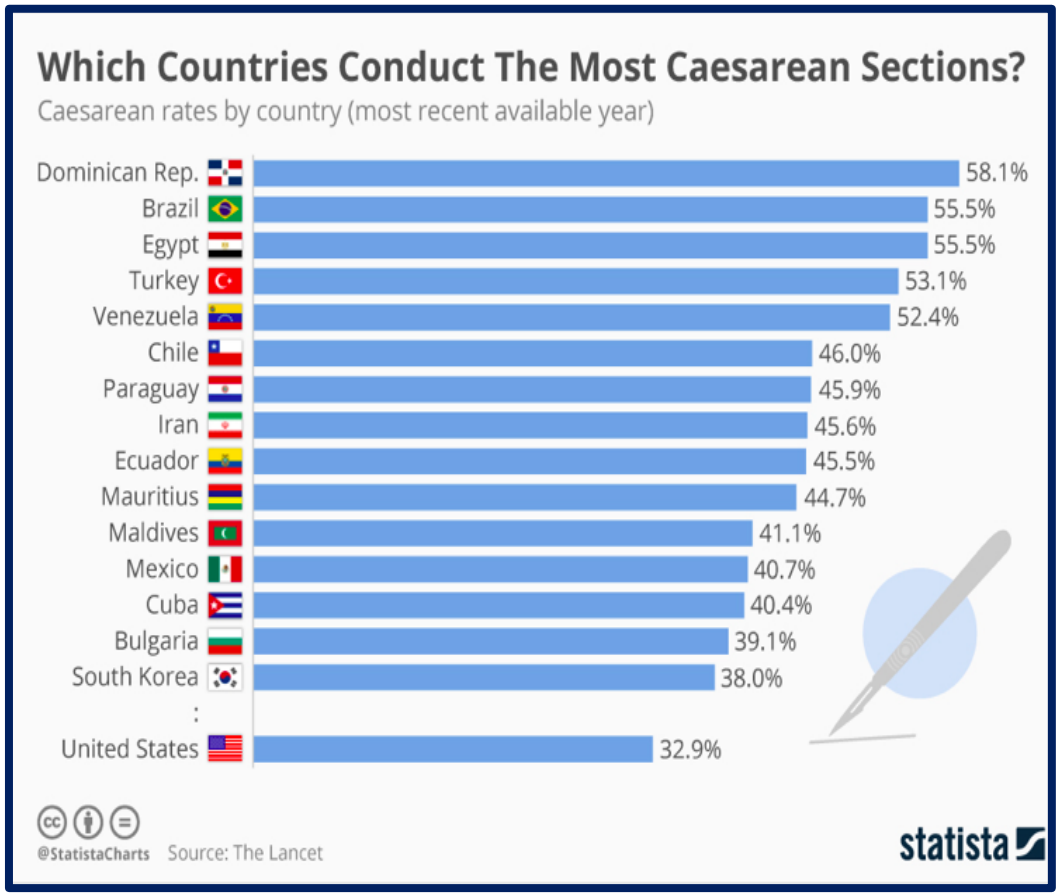
SEZARYEN



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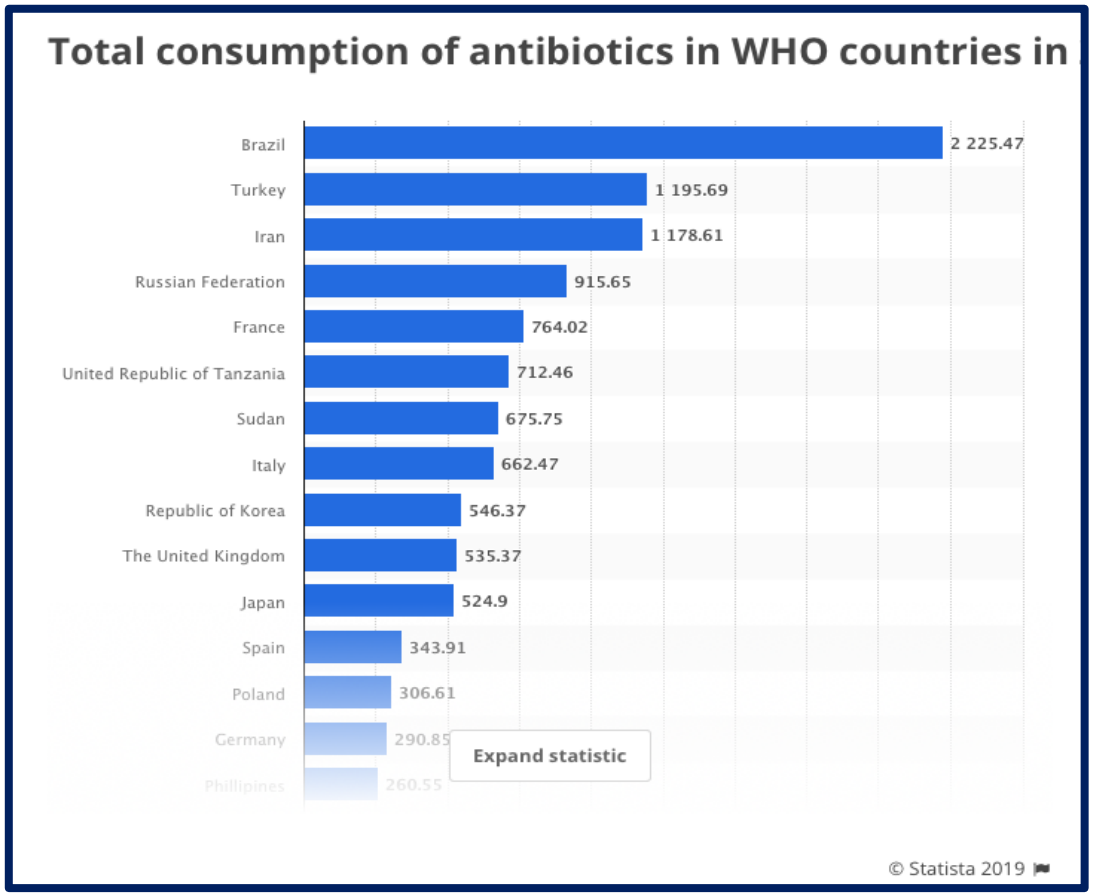
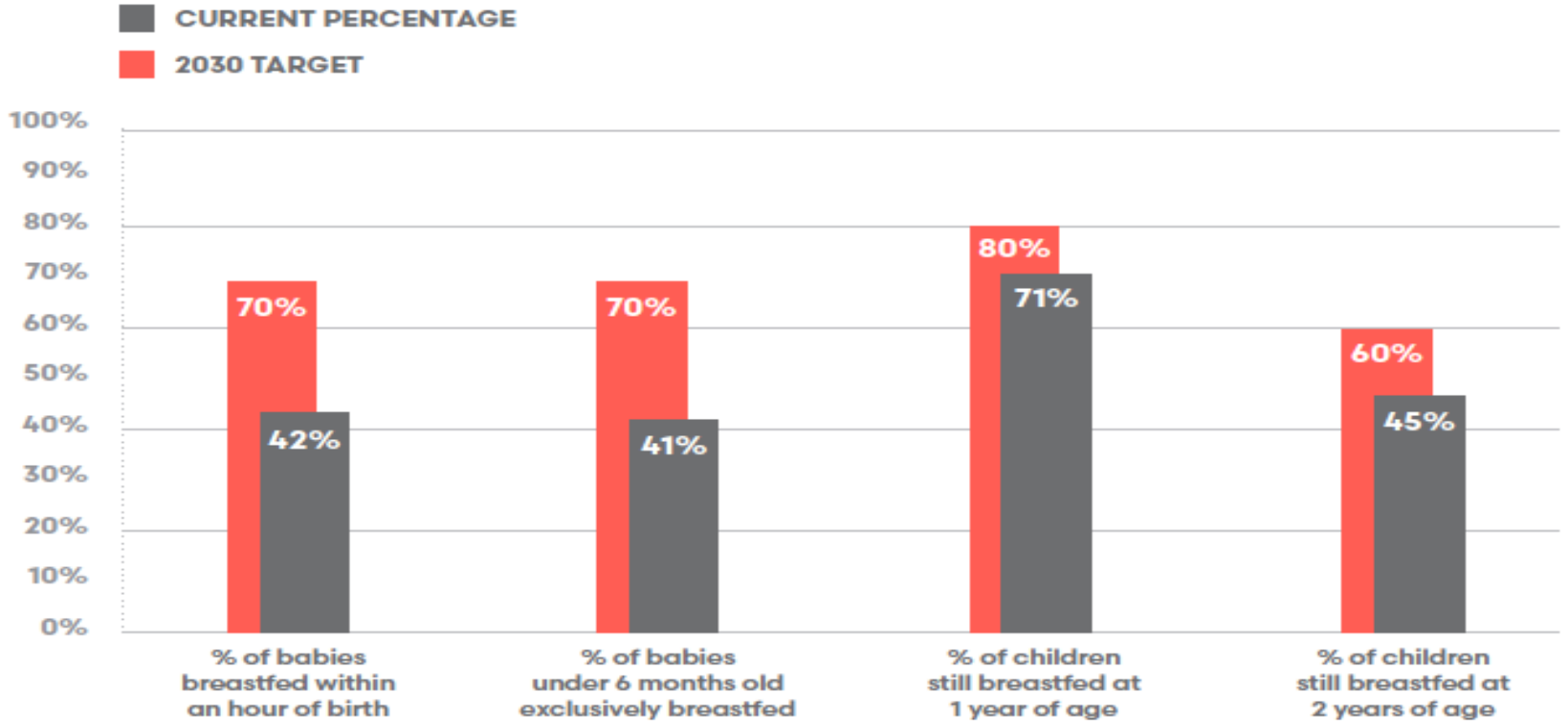


MART 2019
ANNE SÜTÜ

GLOBAL BREASTFEEDING SCORECARD, 2018

ENABLING WOMEN TO BREASTFEED THROUGH BETTER POLICIES AND PROGRAMMES

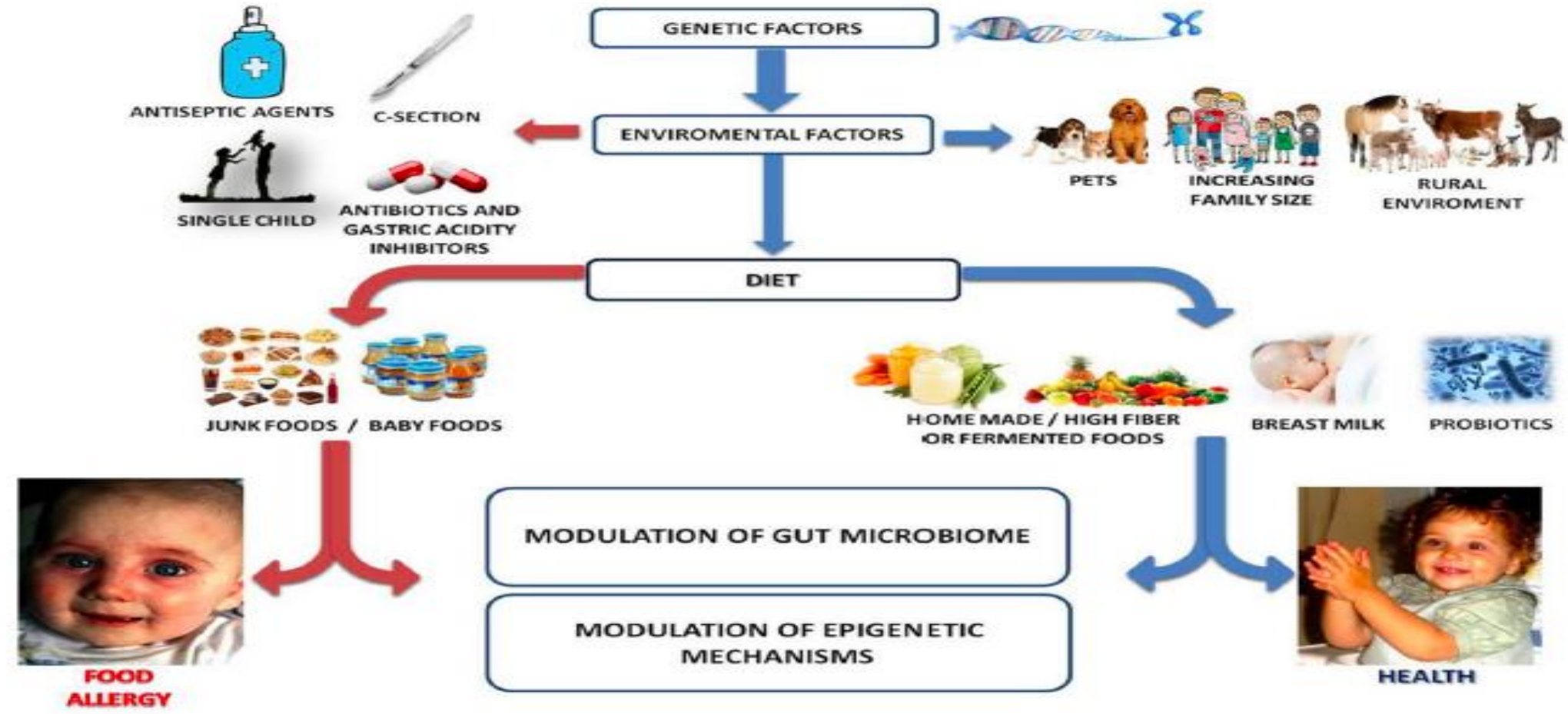
MART 2019
ANNE SÜTÜ



DOĞUM SONRASI İLK 1 SAAT ANNE SÜTÜ: %42

İLK 6 AY YALNIZ ANNE SÜTÜ: %41

MİKROBİYOTA
2019



Berni Canani et al. Front Immunology 2019

İLK 1000 GÜN MİKROBİYOTA
ETKİLİ FAKTÖRLER

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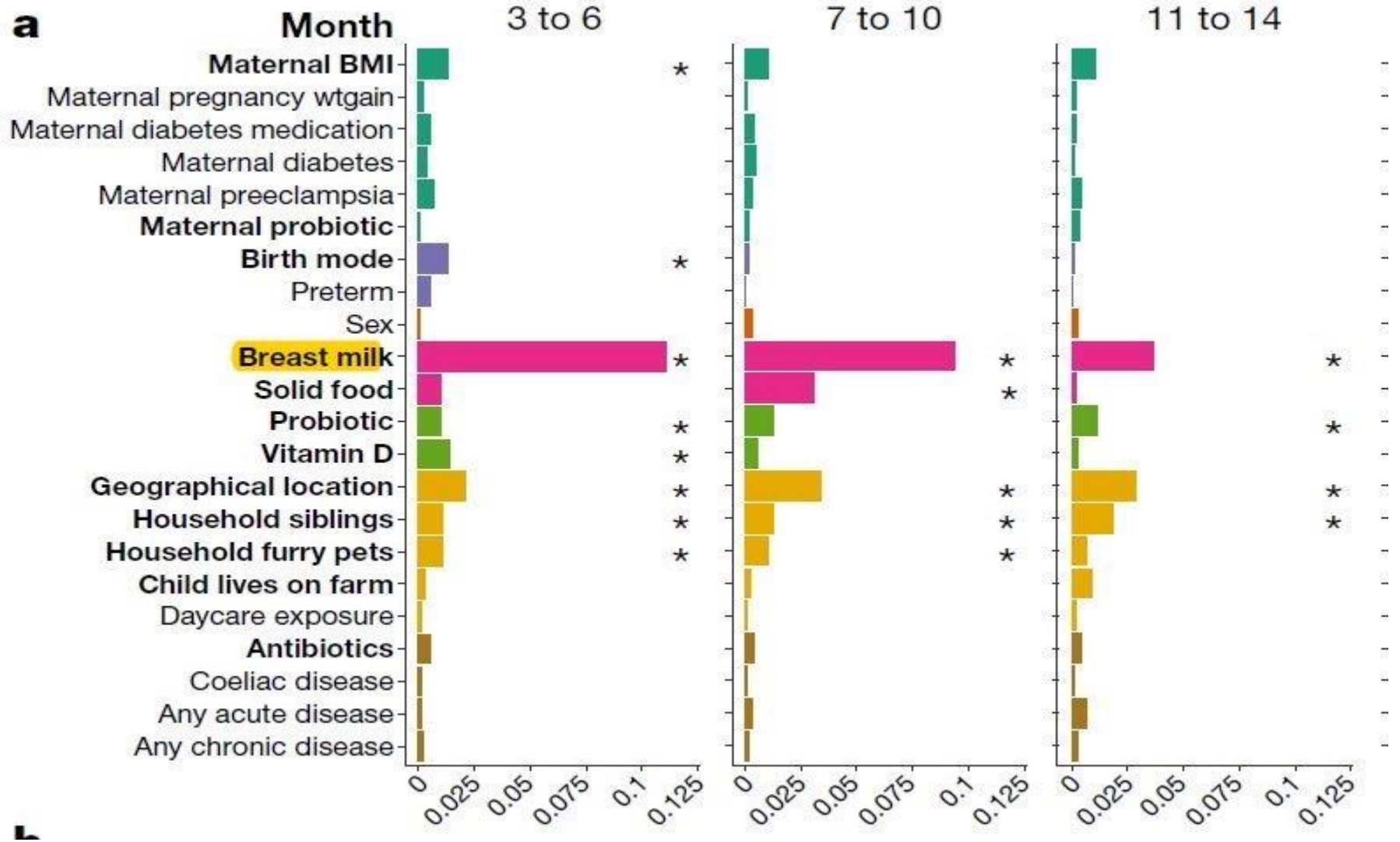

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ANNE SÜTÜ

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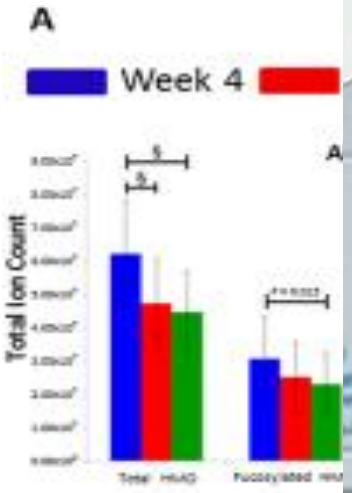

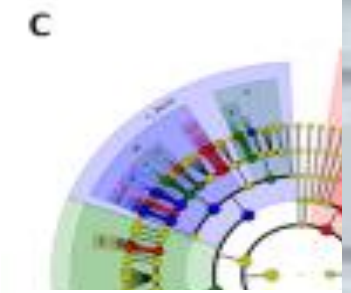

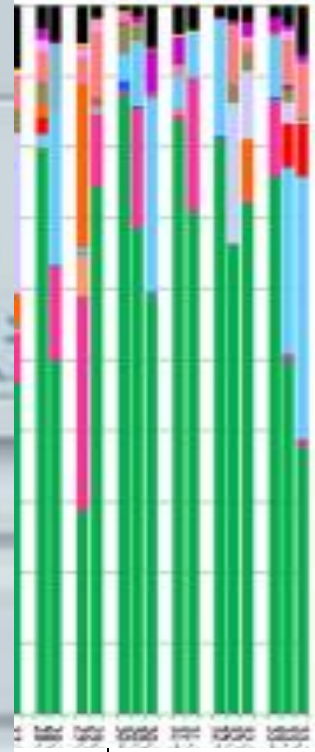

Bifidobacterial species	Unknown
Percent of total bifidobac	0.179

MİKROBİYOTA
2018

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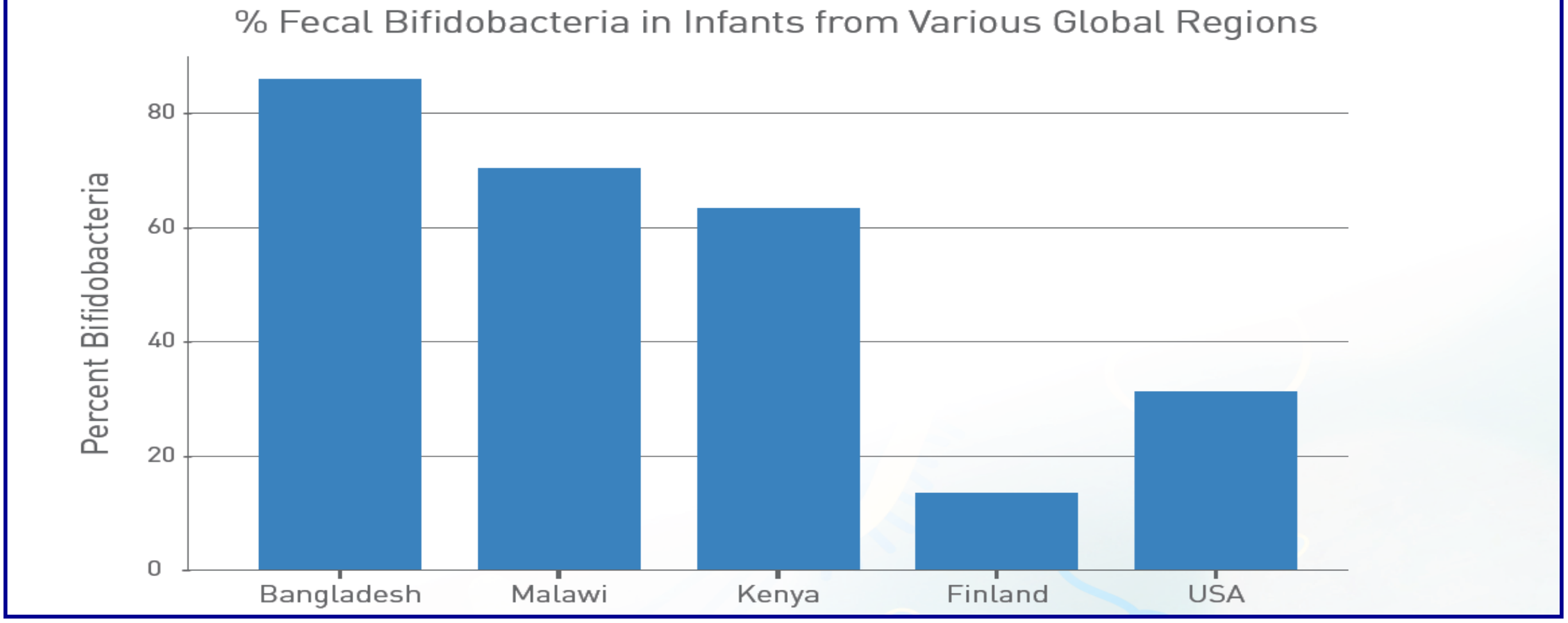


MİKROBİYOTA
2018

- Anne sütü ile beslenen bebeklerde intestinal mikrobiyota öncüsü
  - **BIFIDOBACTERIA**

  - Low-BIF anneler
  - Low-BIF bebekler

ANNE SÜT MİKROBİYOTA KOMPOZİSYONU

HUMAN MILK MICROBIOTA COMPOSITION:

RELATIONSHIP WITH GESTATIONAL AGE, DELIVERY MODE, BIRTH WEIGHT

Meltem Dinleyici [1, 2*], Vicente Perez Brocal [4*], Sertac Arslanoglu [5],

Ozge Aydemir [1,3] , Sibel Sevuk Ozumut[5], Neslihan Tekin [1, 3],

Yvan Vandenplas, Andres Moya [4**] and Ener Cagri Dinleyici [1**]

Dinleyici et al., submitted 2019

ANNE SÜT MİKROBİYOTA KOMPOZİSYONU

HUMAN MILK MICROBIOTA COMPOSITION:

RELATIONSHIP WITH GESTATIONAL AGE, DELIVERY MODE, BIRTH WEIGHT

(Day 7-15 and Day 45-90)

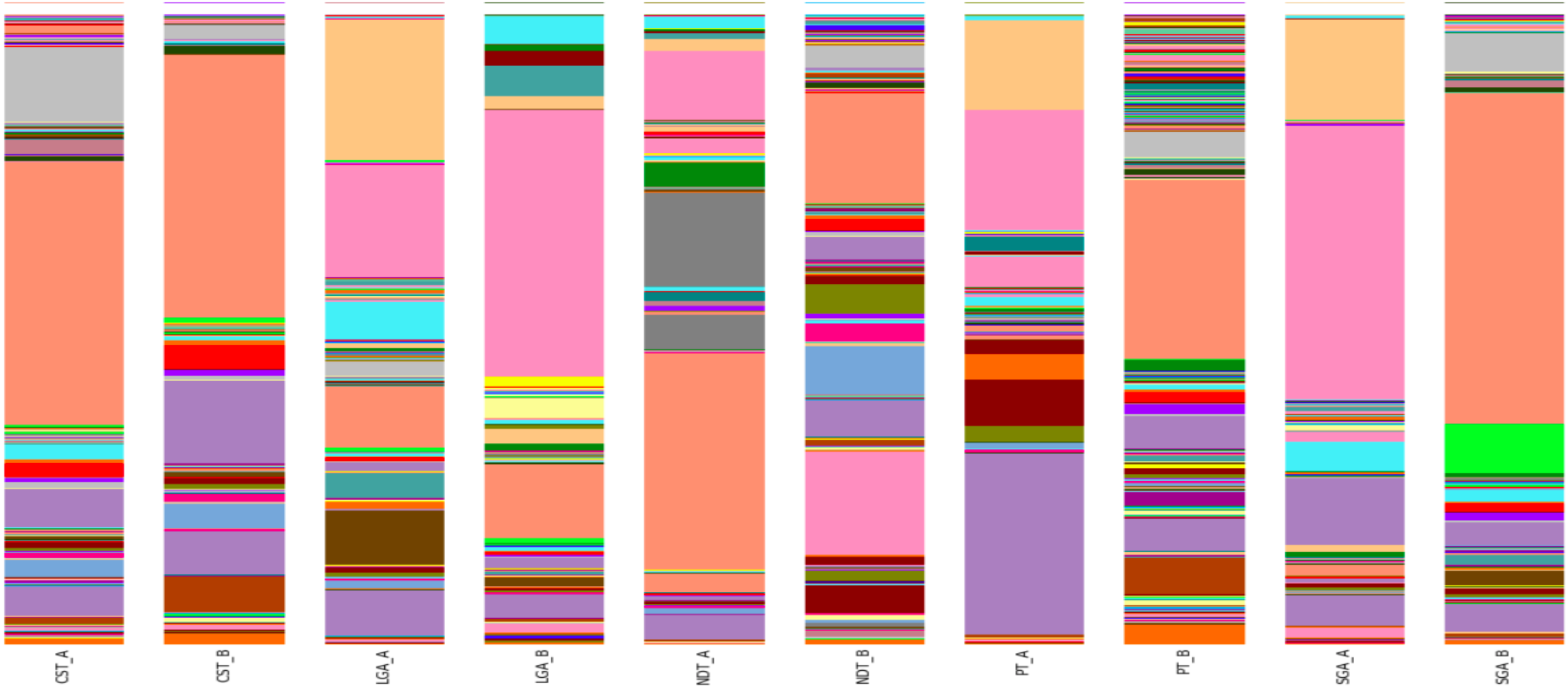
Study protocol includes 5 different groups

1. Normal spontaneous delivery- term newborn (NS-T)
2. Caesarean deliveries-term newborn (CS-T)
3. Premature group (Newborn babies with gestational age below 37 weeks) (PT)
4. Small for gestational age groups (SGA)
5. Large for gestational age groups (LGA)

Dinleyici et al., submitted 2019

ANNE SÜTÜ MİKROBİYOTA
2019

ener çağrı dinleyici



Dinleyici et al., submitted 2019

ANNE SÜTÜ MİKOBİYOTA 2019

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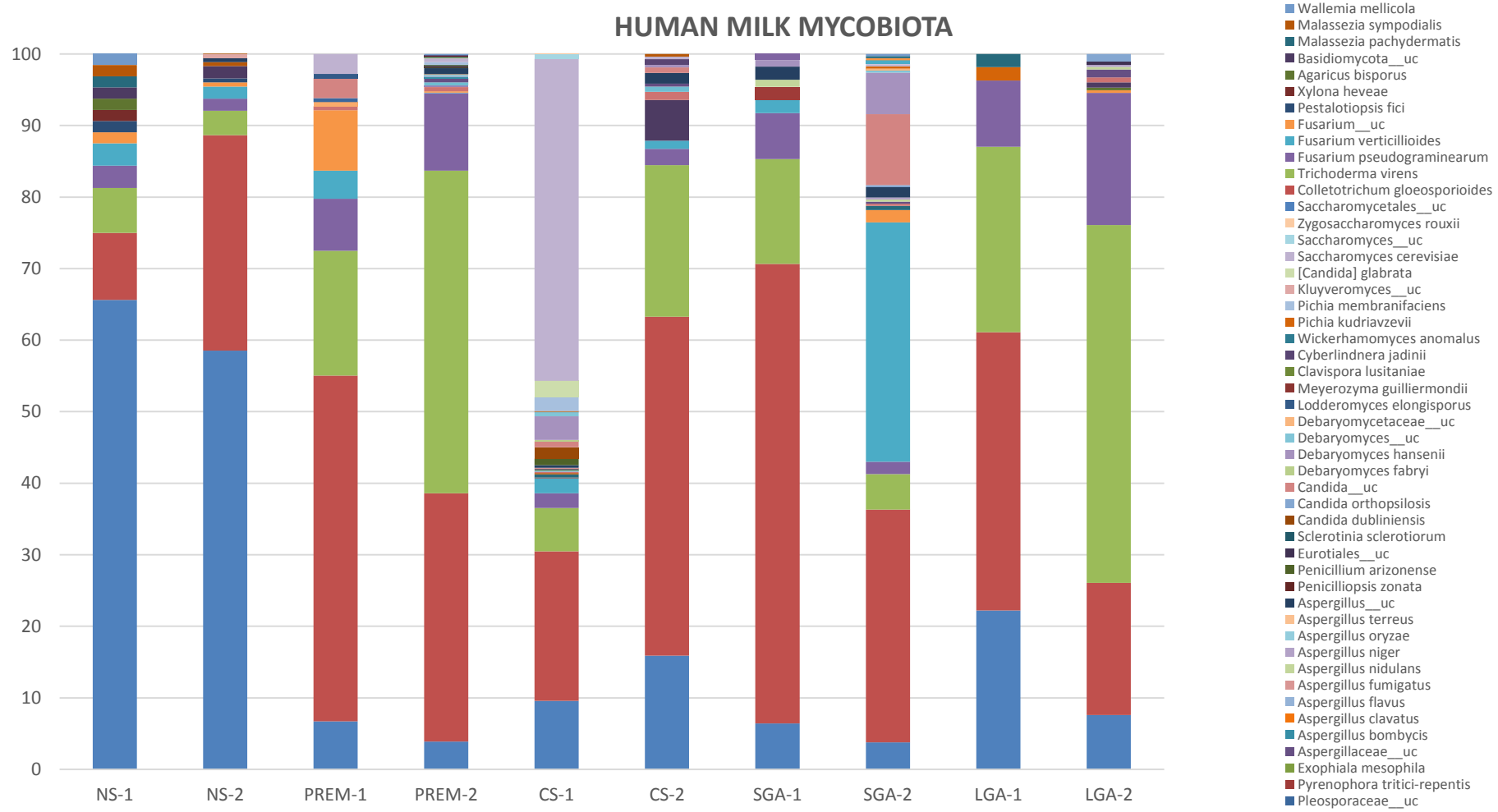

Dinleyici et al., submitted 2019

HUMAN MILK MICROBIOTA 2019

ener çağrı dinleyici

- CELLULAR PROCESSES AND SIGNALING
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- CELLULAR PROCESSES AND SIGNALING|INFORMATION STORAGE AND PROCESSING
- CELLULAR PROCESSES AND SIGNALING|METABOLISM
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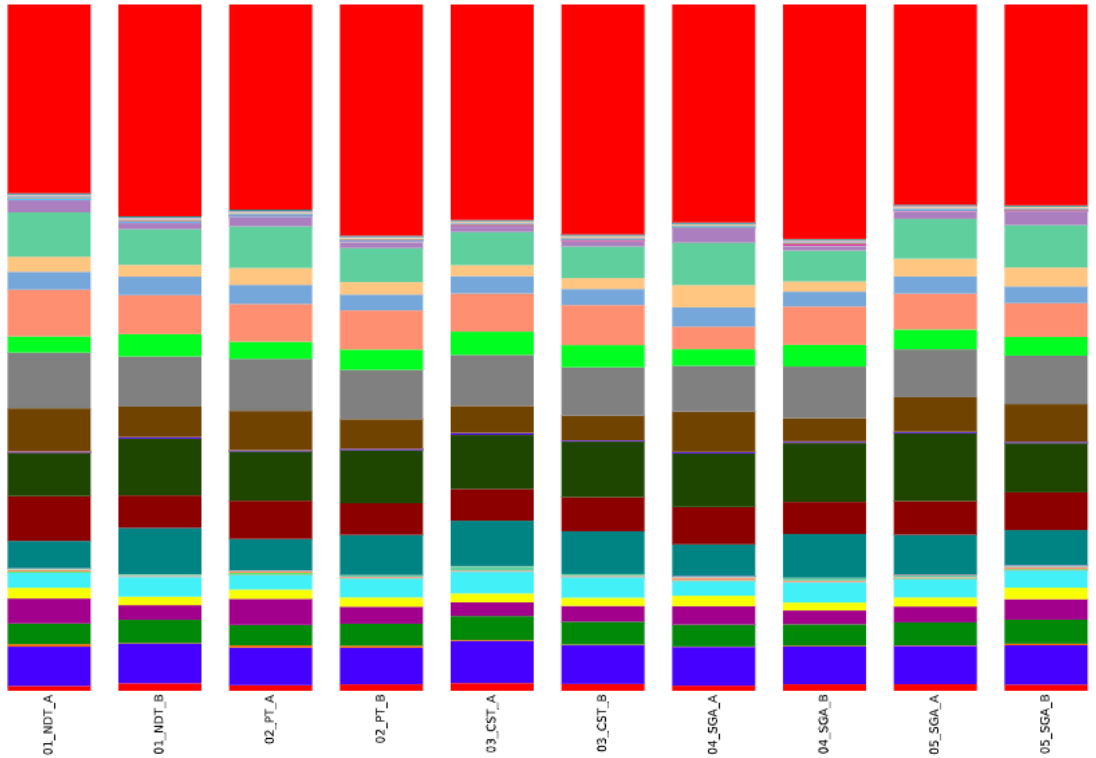
- METABOLISM|METABOLISM|METABOLISM
- POORLY CHARACTERIZED



Dinleyici et al., submitted 2019

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İLAÇLAR

ener çağrı dinleyici

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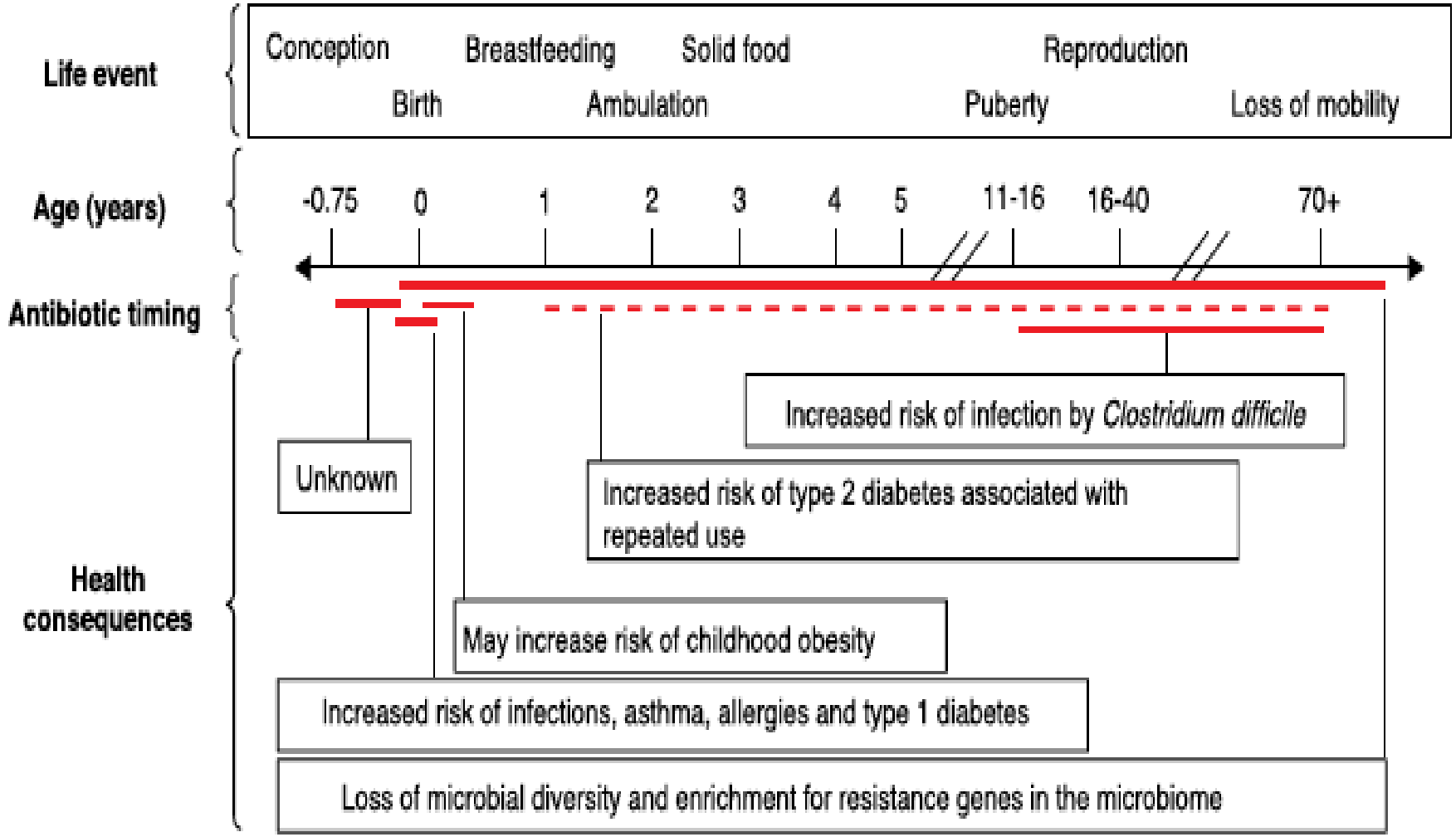
ANTİBİYOTİKLER



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ANTİBİYOTİKLER

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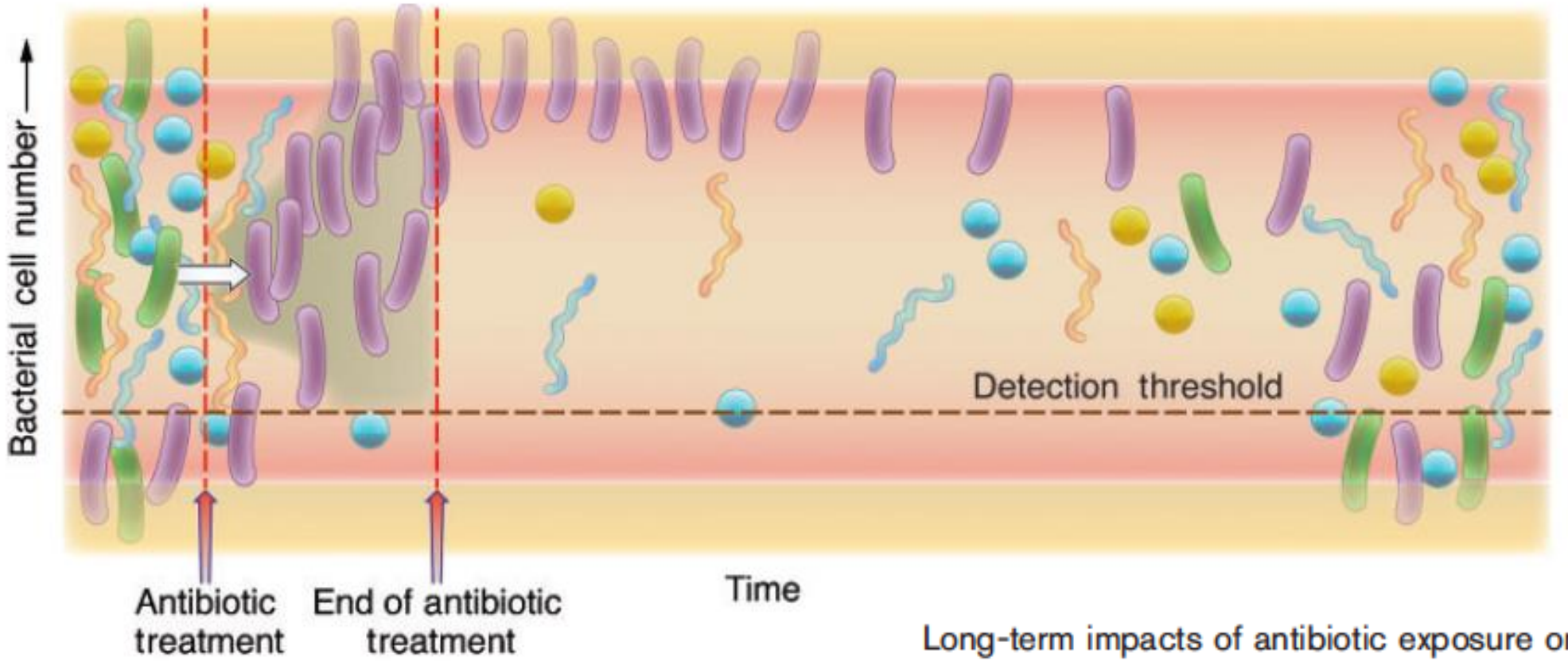

Long-term impacts of antibiotic exposure on the human intestinal microbiota

Cecilia Jernberg,[1] Sonja Löfmark,[2] Charlotta Edlund[3,4] and Janet K. Jansson[5,6]

Microbiology (2010), 156, 3216–3223

MİKROBİYOTA
ANTİBİYOTİKLER-hangileri

ener çağrı dinleyici

↓↓, Strong suppression; ↓, moderate suppression; ↑, increase in number; ↑↓, positive and negative effects seen in different studies. NC, No change detected; +, resistant strains detected. The table is adapted from the paper by Sullivan *et al.* (2001).

Antibiotic	Impact on:			Emergence of resistant strains in:	
	Anaerobes	Aerobic Gram positive cocci	Enterobacteria	Enterococci	Enterobacteria
Amoxicillin/clavulanic acid	NC	↑	↑	NC	NC
Ciprofloxacin (high conc. in faeces)	NC	NC	↓↓	NC	+
Clarithromycin/metronidazole	↓	↑	↓	+	+
Cephalosporins (high conc. in faeces)	NC	↑	↓↓	NC	+
Clindamycin	↓↓	↑	↑	+	+
Vancomycin	↓	↑↓	NC	+	+

Long-term impacts of antibiotic exposure on the human intestinal microbiota

Cecilia Jernberg,[1] Sonja Löfmark,[2] Charlotta Edlund[3,4] and Janet K. Jansson[5,6]

Microbiology (2010), 156, 3216–3223

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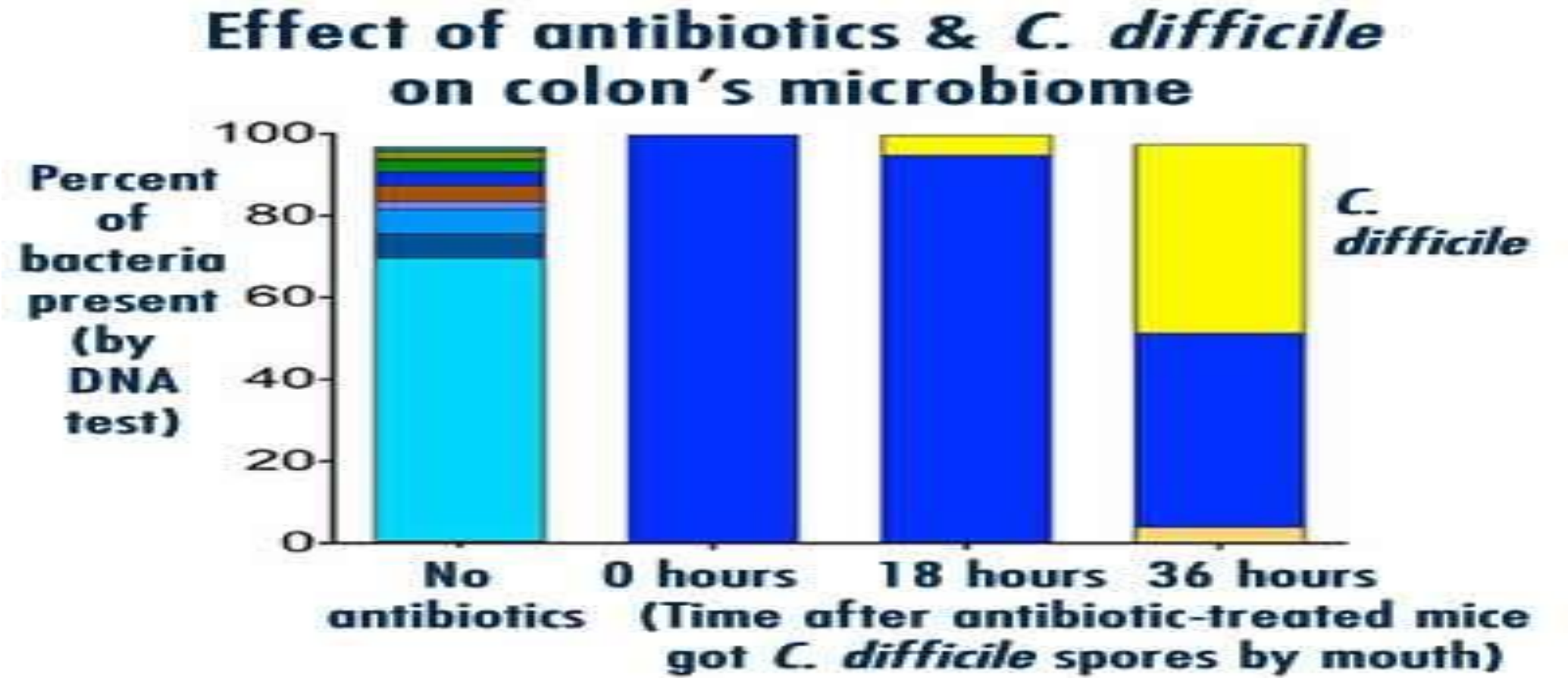
ANTİBİYOTİKLER

ener çağrı dinleyici



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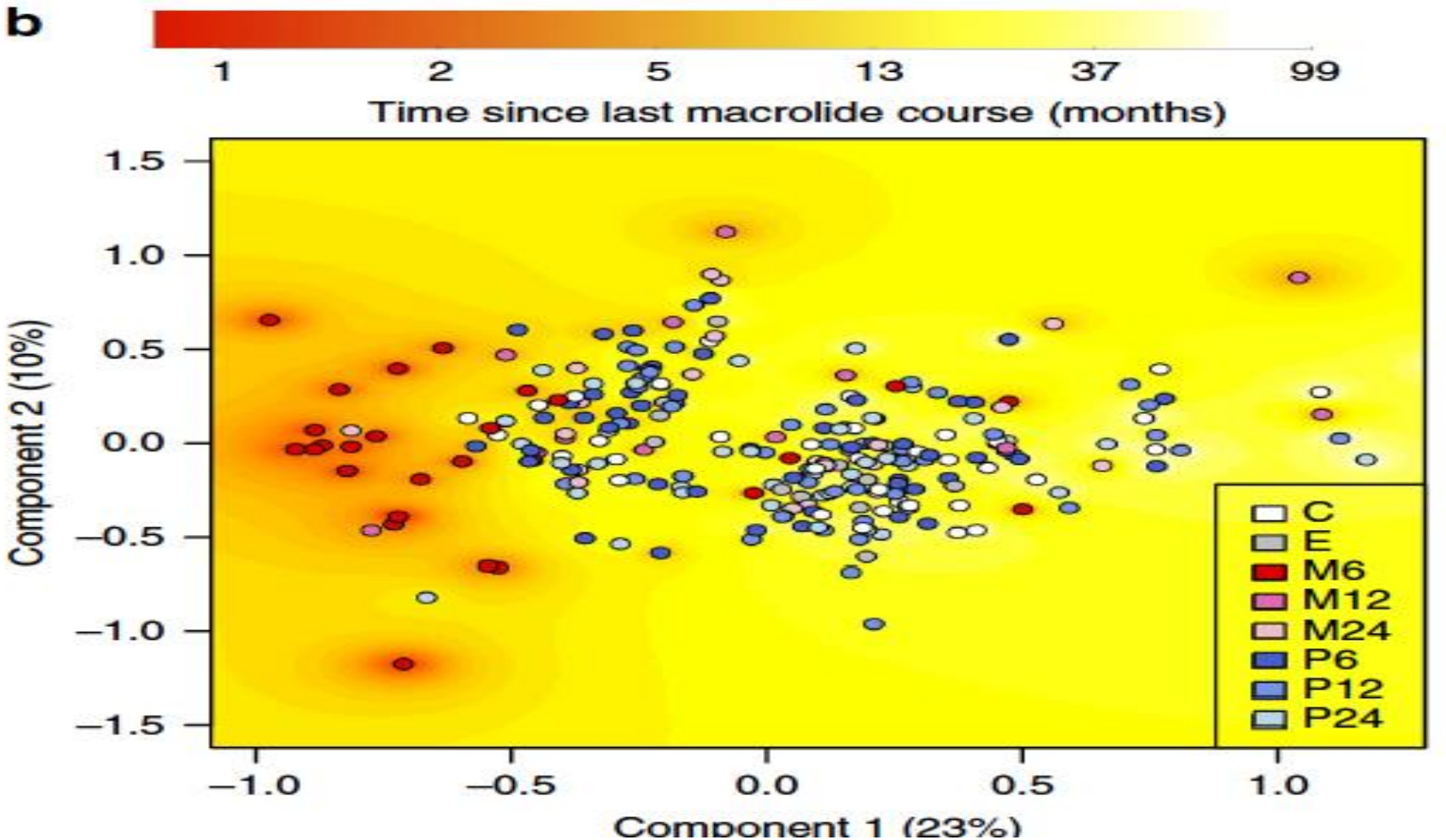
ANTİBİYOTİKLER

ener çağrı dinleyici

Actinobacteria
Firmicutes
Bacteroidetes
Proteobacteria
Verrucomicrobia



ANTİBİYOTİK İLİŞKİLİ İSHAL

ener çağrı dinleyici

World Journal of Gastroenterology

Submit a Manuscript: http://www.wjgnet.com/esps/
Help Desk: http://www.wjgnet.com/esps/helpdesk.aspx
DOI: 10.3748/wjg.v22.i11.3078

World J Gastroenterol 2016 March 21; 22(11): 3078-3104
ISSN 1007-9327 (print) ISSN 2219-2840 (online)

REVIEW

Comparison of pediatric and adult antibiotic-associated diarrhea and *Clostridium difficile* infections

Lynne Vernice McFarland, Metehan Ozen, Ener Cagri Dinleyici, Shan Goh

MİKROBİYOTA
ANTİBİYOTİK DIŞI İLAÇLAR

ener çağrı dinleyici

ARTICLE

doi:10.1038/nature25979

Extensive impact of non-antibiotic drugs on human gut bacteria

A few commonly used non-antibiotic drugs have recently been associated with changes in gut microbiome composition, but the extent of this phenomenon is unknown. Here, we screened more than 1,000 marketed drugs against 40 representative gut bacterial strains, and found that 24% of the drugs with human targets, including members of all therapeutic classes, inhibited the growth of at least one strain *in vitro*. Particular classes, such as the chemically diverse antipsychotics, were overrepresented in this group. The effects of human-targeted drugs on gut bacteria are reflected on their antibiotic-like side effects in humans and are concordant with existing human cohort studies. Susceptibility to antibiotics and human-targeted drugs correlates across bacterial species, suggesting common resistance mechanisms, which we verified for some drugs. The potential risk of non-antibiotics promoting antibiotic resistance warrants further exploration. Our results provide a resource for future research on drug–microbiome interactions, opening new paths for side effect control and drug repurposing, and broadening our view of antibiotic resistance.

ANNE SÜTÜ
ANTİBİYOTİK KALINTI

ener çağrı dinleyici

European Review for Medical and Pharmacological Sciences 2018; 22: 6560-6566

Human milk antibiotic residue levels and their relationship with delivery mode, maternal antibiotic use and maternal dietary habits

M. DINLEYICI[1], G.K. YILDIRIM[2], O. AYDEMIR[3], T.B. KAYA[4], Y. BILDIRICI[4], K.B. CARMAN[5]

ANNE SÜTÜ
ANTİBİYOTİK KALINTI

ener çağrı dinleyici

Results: 83 mothers aged between 17 to 41 years (mean age 29.7 ± 6.2 years), have been enrolled. 56.6% of pregnant women have been C-section, 31 mothers have been received one dose antibiotic prophylaxis (first generation cephalosporin) and 18 mothers have received antibiotic treatment, maximum 7 days after delivery. 71 out of 83 human milk samples (85.5%) were positive for beta-lactams and 12 positive samples for quinolones (14.5%). Two positive samples for amphenicol, 2 positive for basitrasin, 5 positive samples for cefuroxime, 4 positive samples for polymyxine, one sample for sulfonamide, two positive samples for tobramycine have been noted. There are no differences between the positive antibiotic residues (for beta-lactams and quinolones) between mother received or not received antibiotics during labor and after. The presence of beta lactams or quinolones in human milk was not associated with the maternal dietary habits.

Human milk antibiotic residue levels and their relationship with delivery mode, maternal antibiotic use and maternal dietary habits

M. DINLEYICI[1], G.K. YILDIRIM[2], O. AYDEMIR[3], T.B. KAYA[4], Y. BILDIRICI[4], K.B. CARMAN[5]

MİKROBİYOTA
BESLENME

ener çağrı dinleyici

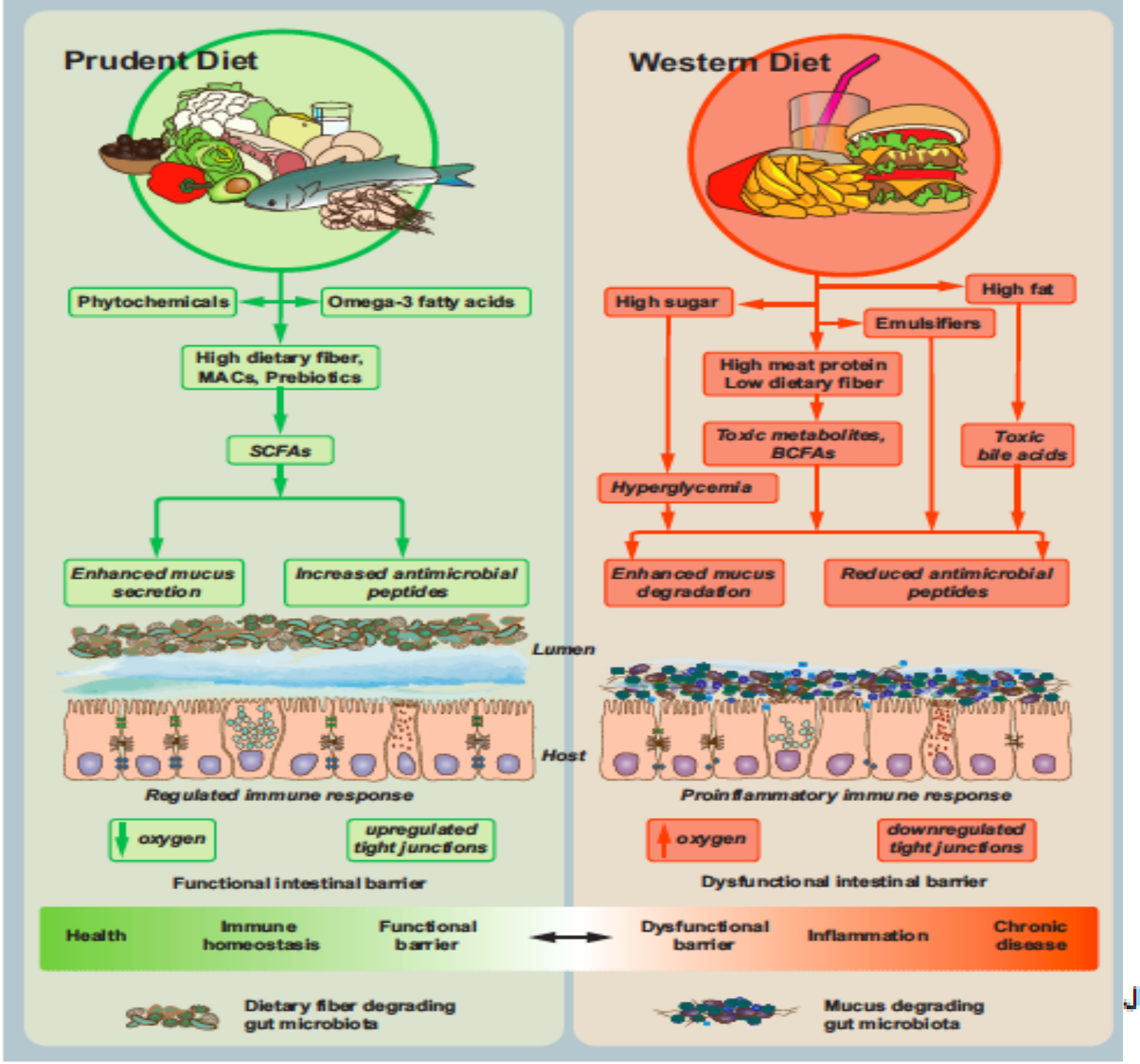
ener çağrı dinleyici

Cell Host & Microbe

Review

The Impact (Microbiota i

Kassem Makki,[1] Edward C.



CellPress

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BESLENME

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DİSBİYOZİS

ener çağrı dinleyici

MİKROBİYOTA
DİSBİYOZİS

ener çağrı dinleyici

Health + Diversity and function - **Disease**

Dysbiosis

Facultative anaerobes:
enterobacteria
enterococci
lactobacilli

Inter-individual variations

Ageing

Anaerobes:
Bifidobacterium
Clostridium
Bacteroides

Core genome?

Enterotypes?
i) *Bacteroides*
ii) *Prevotella*
iii) *Ruminococcus*

Intestinal

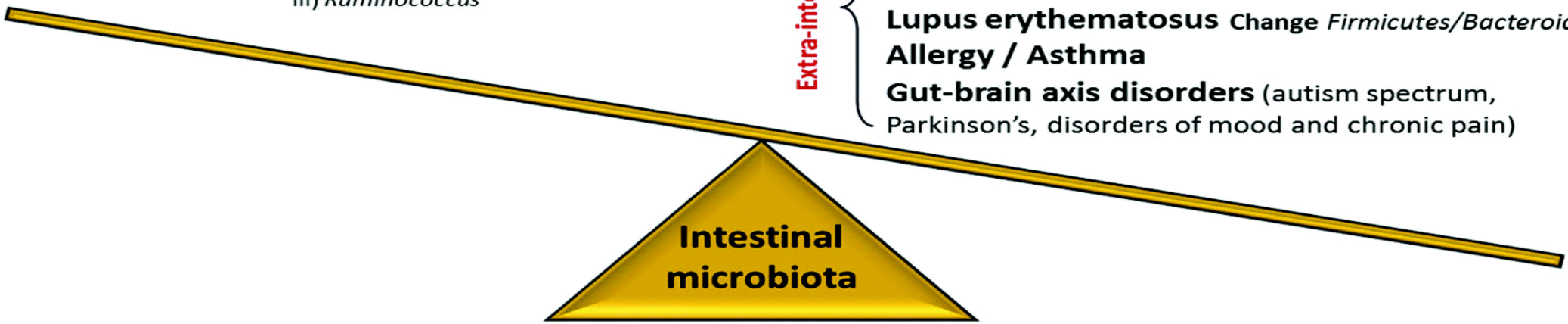
- **IBD** (inflammatory bowel disease)
  - Crohn´s disease (CD)
  - Ulcerative colitis (UC)

  Change *Firmicutes/Bacteroidetes*
  ↓ *F. prausnitzii*
  ↑ *Enterobacteriaceae*
- **IBS** (irritable bowel syndrome)
- **Coeliac disease**
- **CRC** (colorectal cancer)
- **CDI** (*C. difficile* infection)

Extra-intestinal

- **Obesity**
- **Type II diabetes**
- **Metabolic syndrome**

  Changes in *Firmicutes/Bacteroidetes* ratio
  ↓ butyrate-producers
  ↑ Opportunistic pathogens
  ↑ Oxidative stress
- **Lupus erythematosus** **Change** *Firmicutes/Bacteroidetes*
- **Allergy / Asthma**
- **Gut-brain axis disorders** (autism spectrum, Parkinson's, disorders of mood and chronic pain)



MİKROBİYOTA
ENFEKSİYON HASTALIKLARI

ener çağrı dinleyici

nature microbiology

REVIEW ARTICLE

https://doi.org/10.1038/s41564-018-0278-4

The role of the microbiota in infectious diseases

Josie Libertucci[1] and Vincent B. Young[1,2*]

NATURE MICROBIOLOGY | VOL 4 | JANUARY 2019 | 35–45 | www.nature.com/naturemicrobiology

MİKROBİYOTA
ENFEKSİYON HASTALIKLARI

ener çağrı dinleyici

Table 1 | Examples of microbiota associated with altered mucosal immunity and increased infectious disease susceptibility

Site	Infectious disease/condition	Community structure	Immune component	References
Gastrointestinal tract	*Entamoeba histolytica*, *Giardia*, *Cryptosporidium*, *Blastocystis hominis*	↑ Prevotellaceae ↑ *Prevotella copri* ↑ Proteobacteria ↓ Firmicutes	Augmented T_h17-mediated response ↑ IL-23, IL-1, IL-6, IL-8	150-155
	Simian immunodeficiency virus	↑ Pasteurellaceae, *Aggregatibacter*, *Actinobacillus*, *Mycoplasma*	↓ Expression of TLR4, TLR8	
	HIV	↑ Proteobacteria, *Prevotella* ↓ Firmicutes	↑ Activated T cells and myeloid dendritic cells	
Respiratory tract	Fungal or viral pneumonia	↑ *Prevotella*, *Veillonella*	↑ T_h17 cells, IL-1α, IL-1β, IL-7	114, 156-157
Female reproductive tract	Bacterial vaginosis (clinical condition associated with susceptibility to infection)	↑ Diversity ↓ *Lactobacillus* ↑ *Gardnerella vaginalis*, *A. vaginae*,	↑ IL-1β, IL-12p70 ↓ IP-10, elafin	158-160
	HIV	↑ Diversity ↓ *Lactobacillus* ↑ *Gardnerella vaginalis*, *A. vaginae*, *Prevotella bivia*	↑ Activated $CD4^+$ T cells, IL-23, IL-1β, IL-17	

MİKROBİYOTA-AKUT İSHAL
FACID STUDY

ener çağrı dinleyici

frontiers

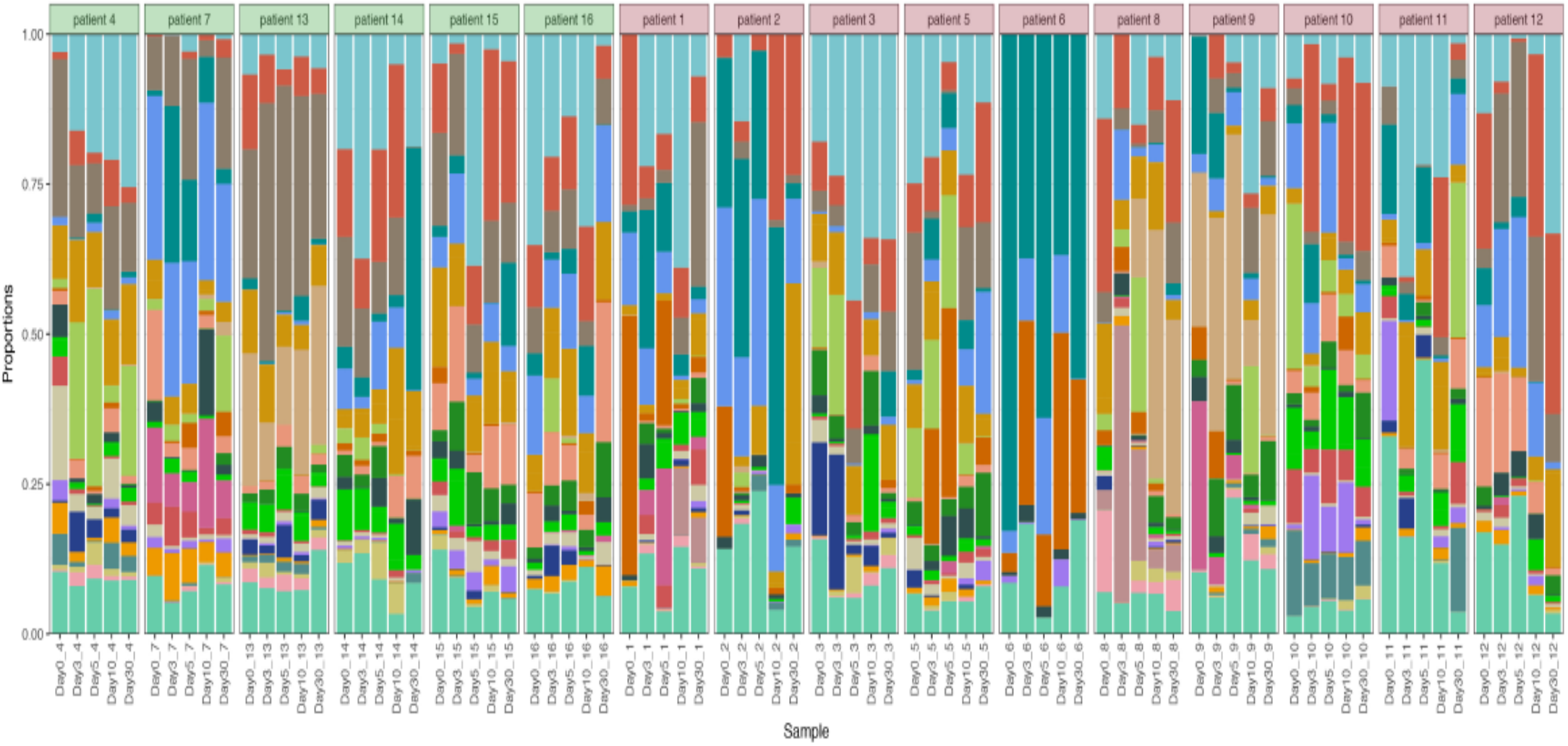
Time series analysis of the microbiota of children suffering from acute infectious diarrhea and their recovery after probiotic treatment

Ener Cagri Dinleyici [1,†], Daniel Martínez-Martínez [2,†], Ates Kara [3], Adem Karbuz [4], Nazan Dalgic [5], Ozge Metin [6], Ahmet Sami Yazar [7], Sirin Guven [7], Zafer Kurugol [8], Ozden Turel [9], Mehmet Kucukkoc [9], Olcay Yasa [10], Makbule Eren [1], Metehan Ozen [11], Jose Manuel Martí,[2], Carlos P. Garay,[2], Yvan Vandenplas [12], and Andrés Moya [2,13,14,*]

Dinleyici EC et al. Frontiers Microbiology 2018.

AKUT İSHAL
FACID STUDY

ener çağrı dinleyici



Dinleyici EC et al. s to Frontiers Microbiology 2018.

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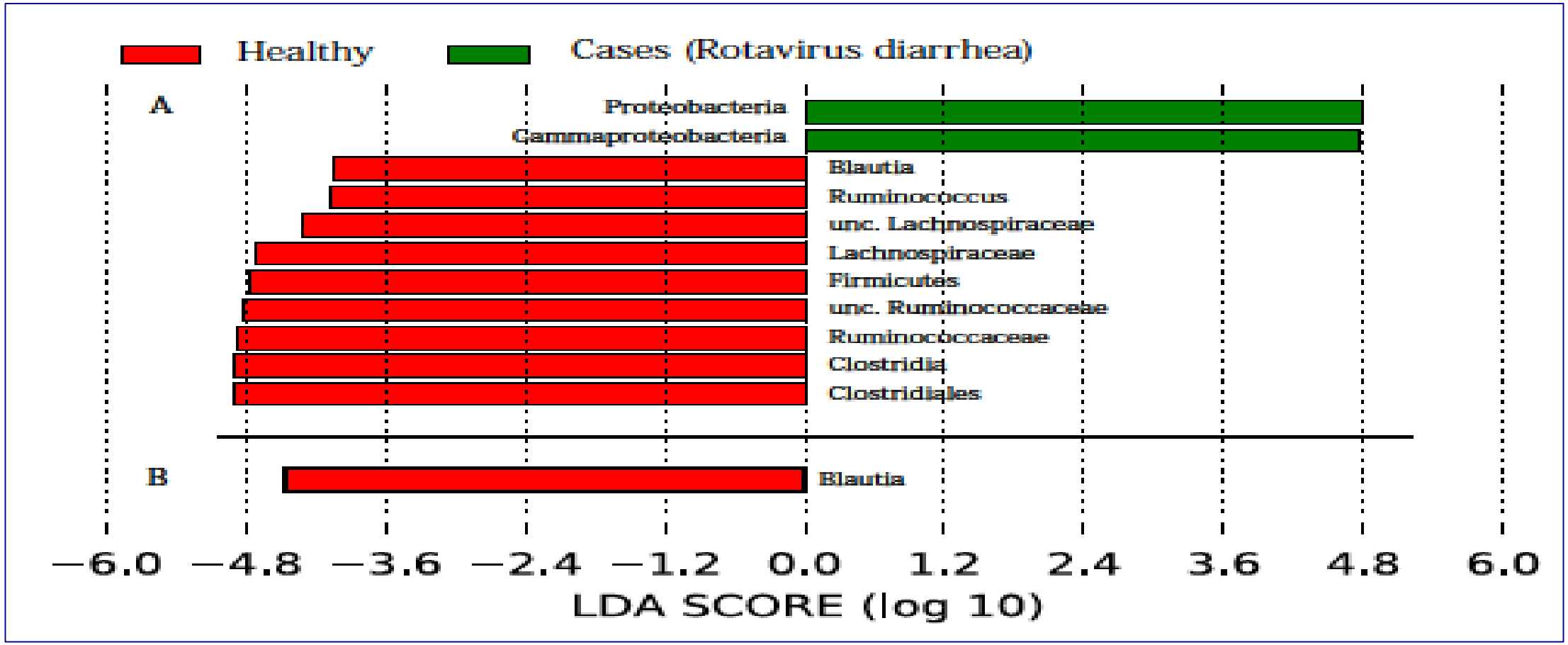
FACID STUDY



Dinleyici EC et al. Frontiers Microbiology 2018.

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FACID STUDY

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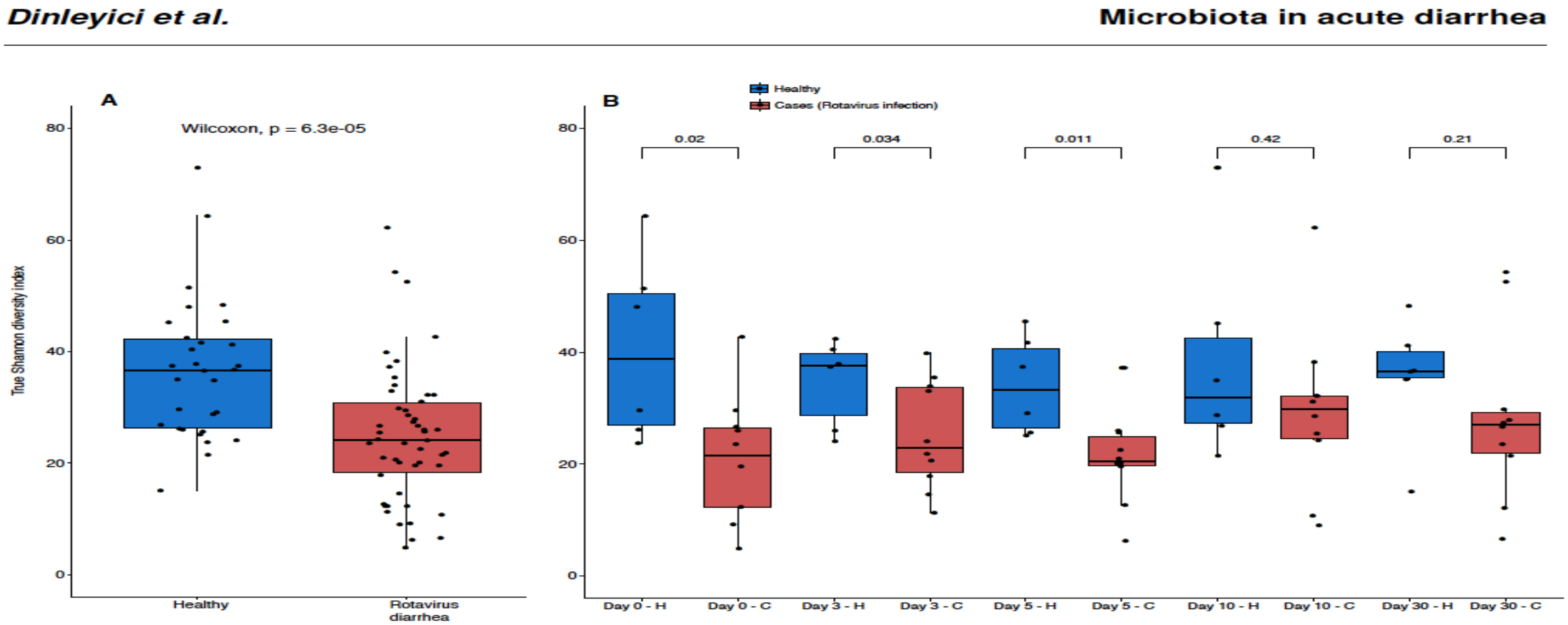

Dinleyici EC et al. Frontiers Microbiology 2018.

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FACID STUDY

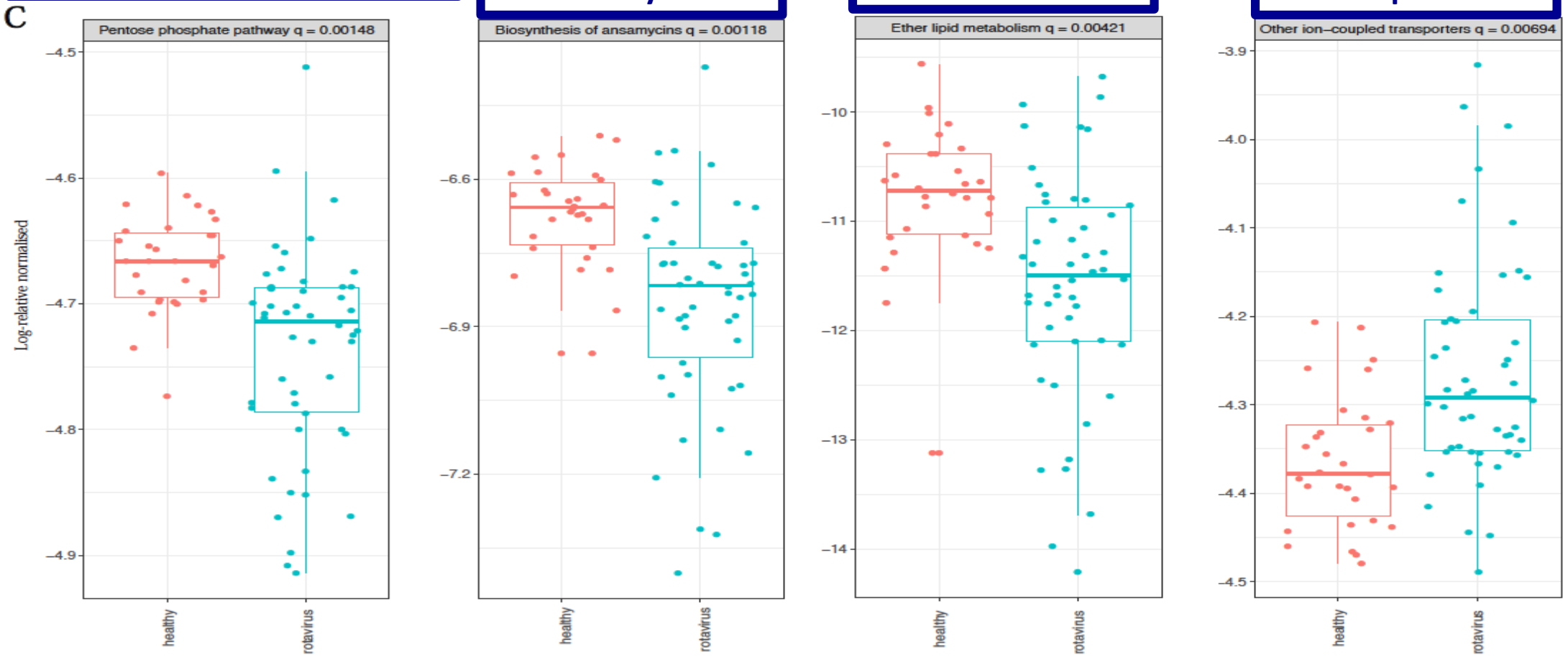
ener çağrı dinleyici

Pentose phosphate pathway

Biosynthesis of ansamycins

Either lipid metabolism

Other ion coupled trasnporters



Dinleyici EC et al. Frontiers Microbiology 2018.

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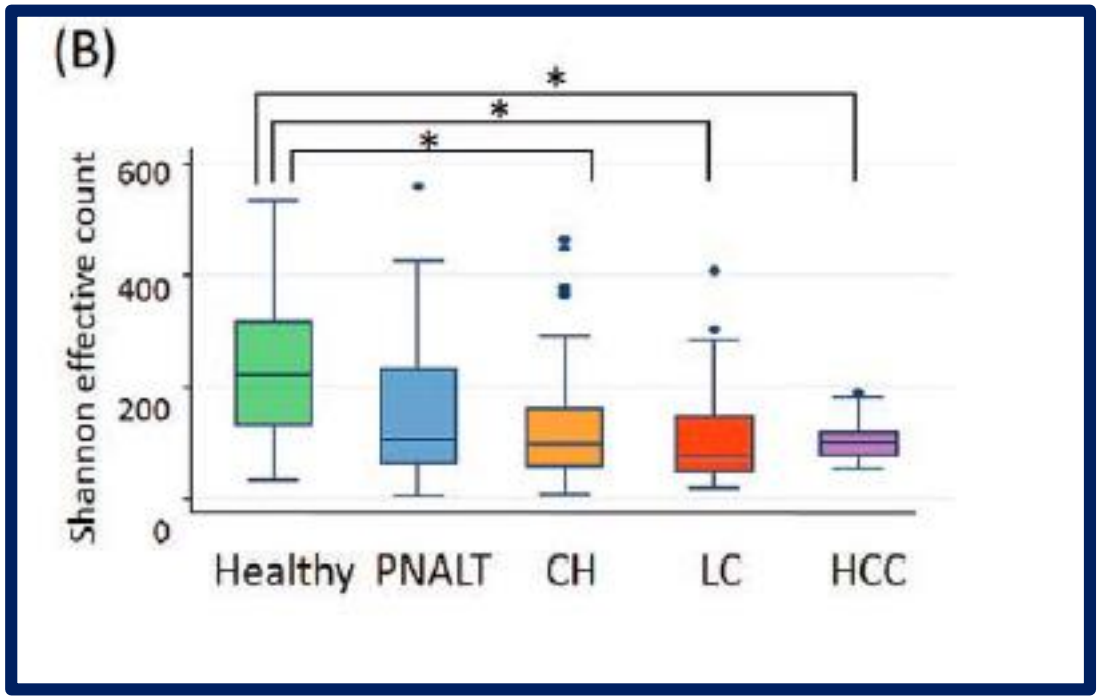
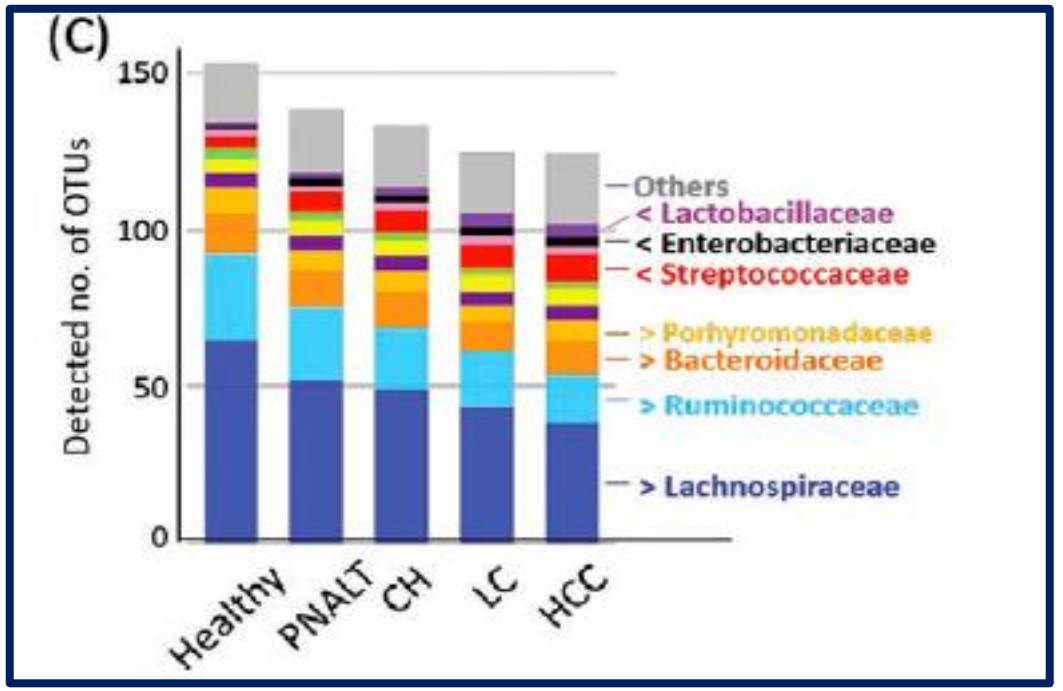
HEPATİT C

ener çağrı dinleyici





Clinical Infectious Diseases

MAJOR ARTICLE

IDSA Infectious Diseases Society of America
hivma hiv medicine association
OXFORD

Gut Dysbiosis Associated With Hepatitis C Virus Infection

Takako Inoue,[1] Jiro Nakayama,[2] Kei Moriya,[3] Hideto Kawaratani,[3] Rie Momoda,[2] Kiyoaki Ito,[4] Etsuko Iio,[5] Shunsuke Nojiri,[5] Kei Fujiwara,[5] Masashi Yoneda,[4] Hitoshi Yoshiji,[3] and Yasuhito Tanaka[1,6]

MİKROBİYOTA
HEPATİT C

ener çağrı dinleyici

Received: 9 August 2018 | First decision: 27 August 2018 | Accepted: 7 September 2018

DOI: 10.1111/apt.15004

Check for updates

WILEY AP&T Alimentary Pharmacology & Therapeutics

Influence of hepatitis C virus eradication with direct-acting antivirals on the gut microbiota in patients with cirrhosis

Francesca Romana Ponziani[1] | Lorenza Putignani[2,3] | Francesco Paroni Sterbini[4] | Valentina Petito[1] | Anna Picca[5] | Federica Del Chierico[2] | Sofia Reddel[2] | Riccardo Calvani[5] | Emanuele Marzetti[5] | Maurizio Sanguinetti[4] | Antonio Gasbarrini[1] | Maurizio Pompili[1]

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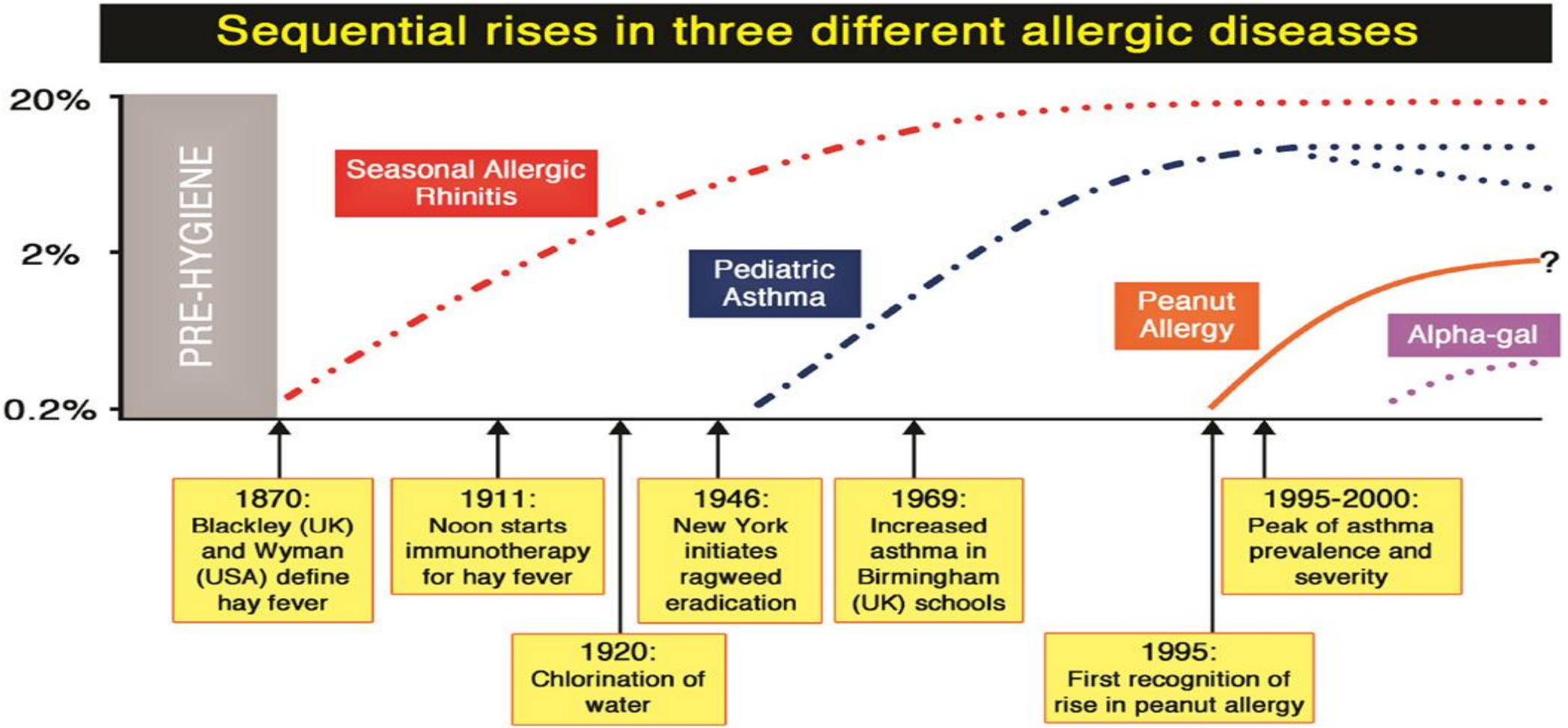
ALERJİK HASTALIKLAR



Thomas Platt-Mills. J Allerg Clin Immunol 2015

MART 2019
ALERJİK HASTALIKLAR

Figure 5. The circle of causality. From the megatrend of urbanization to increase of non-communicable (inflammatory) diseases. Or the other way around, from symptoms to background factors.

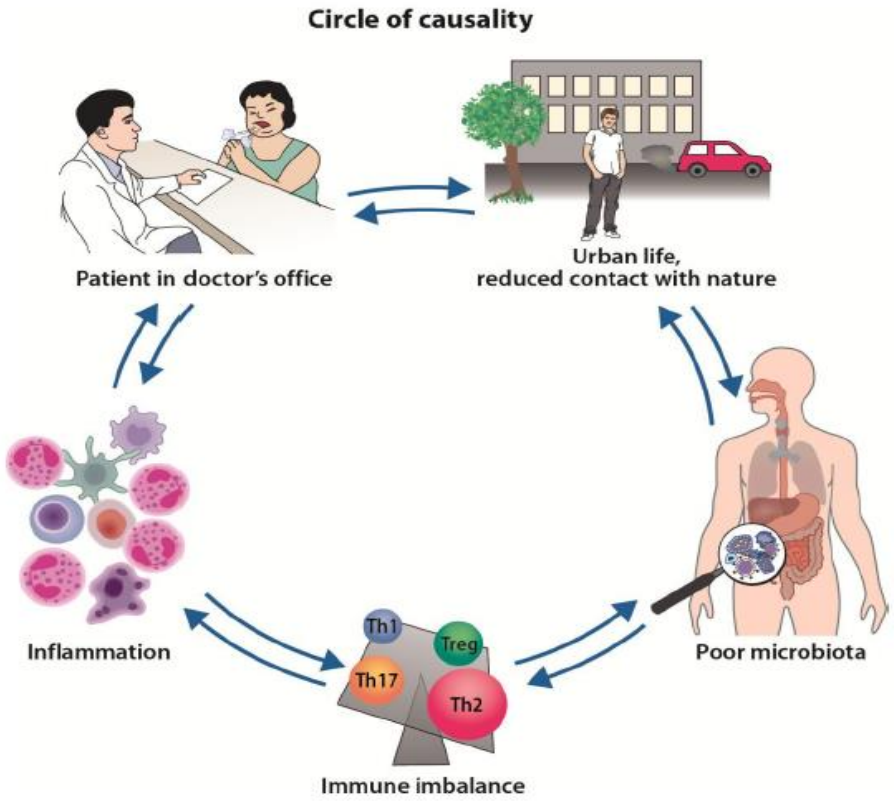
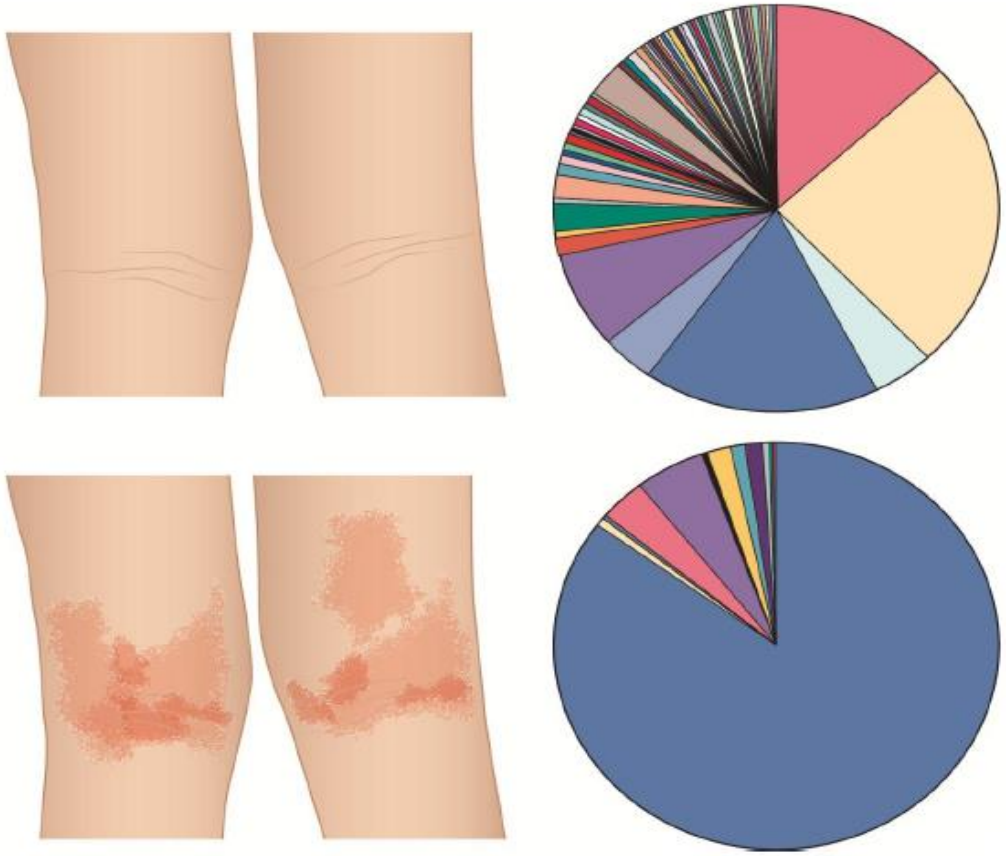


Figure 2. Microbiota on healthy and inflamed skin, where microbial diversity and balance is lost (8, modified).



Haahtela T. Biodiversity hypothesis. Allergy 5 Mart 2019

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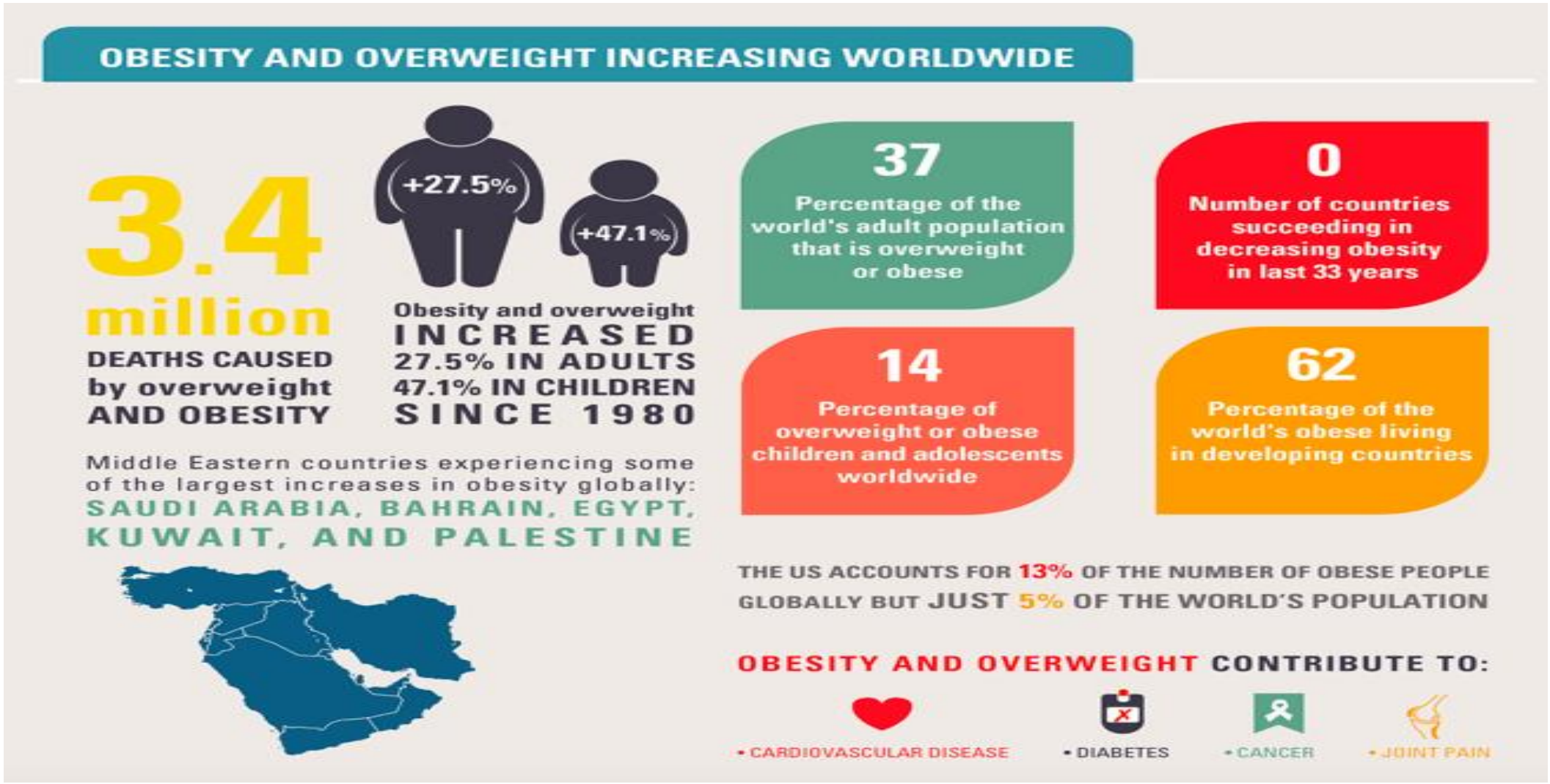
OBESİTE



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2019

ener çağrı dinleyici

Endocrine (2018) 61:357–371
https://doi.org/10.1007/s12020-018-1605-5

REVIEW

CrossMark

Microbiota and metabolic diseases

Alessia Pascale[1] · Nicoletta Marchesi[1] · Cristina Marelli[1] · Adriana Coppola[2] · Livio Luzi[3,4] · Stefano Govoni[1] · Andrea Giustina[5] · Carmine Gazzaruso[2]

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2019

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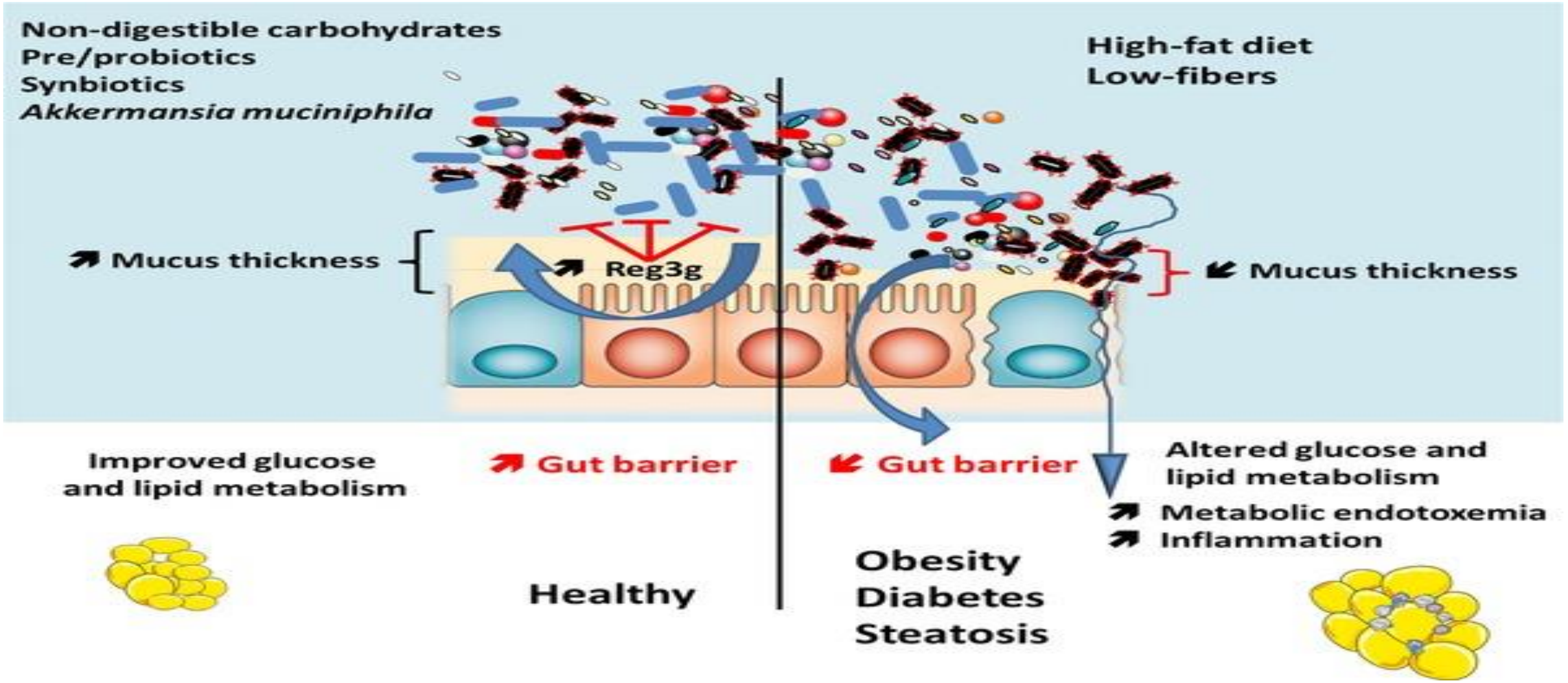
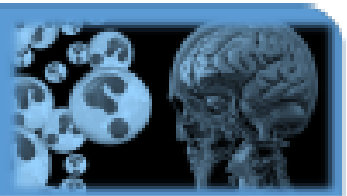


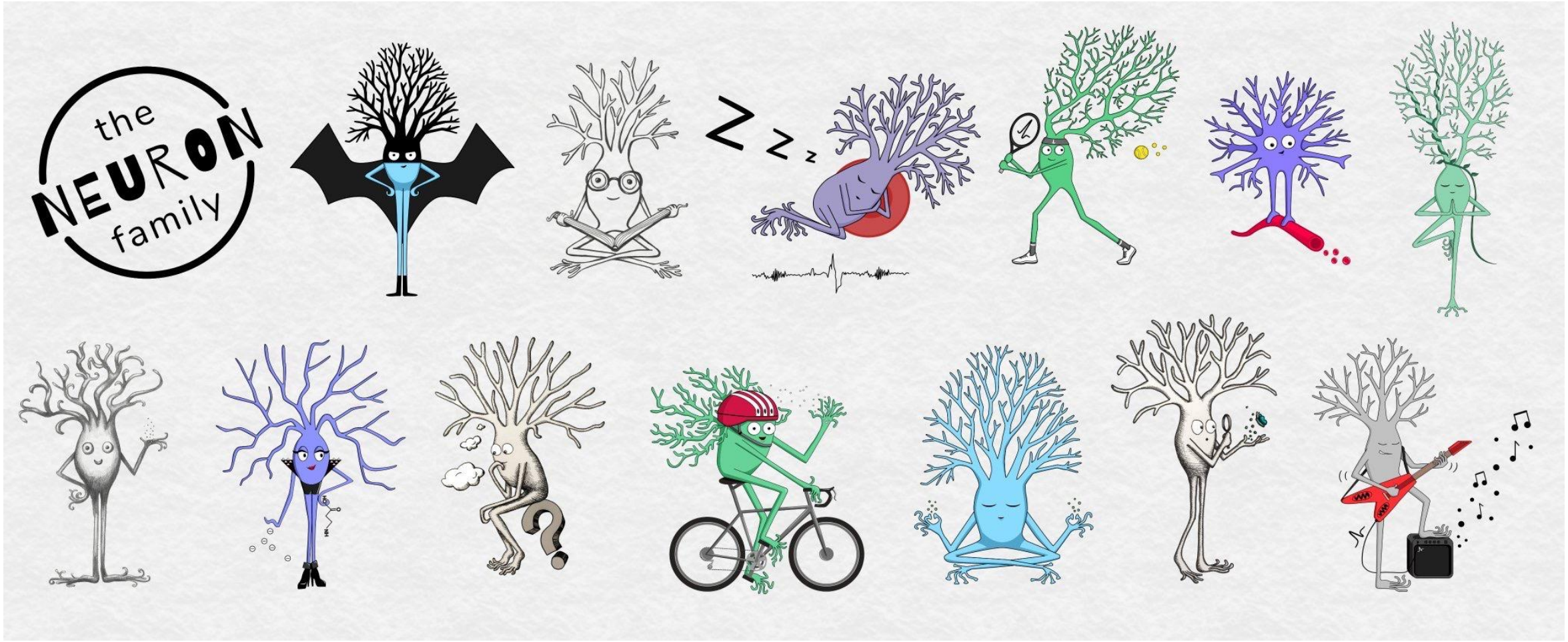
AKKERMANSIA MUCINIPHILIA

ener çağrı dinleyici

					
	Obesity	**Non treated Type 2 diabetic**	**Treated Type 2 diabetic**	**Gastric Bypass**	**Multiple sclerosis Parkinson disease**
***A.muciniphila* levels**	↘↘	↘↘	↗(↗)	↗↗↗	↗
Major confounding factors	Low level of fibers ingested High fat diet : saturated and low polyunsaturated omega-3 Decreased mucus layer thickness / production ?		Metformin is an energy source for *A.muciniphila* Metformin increases goblet cells number and changes the gut microbiota	High flux of undigested nutrients as energy source for *A.muciniphila*	Increased intestinal transit time and constipation Drug treatments Caloric restriction period or altered food intake (i.e., lower energy)
Proof of concept of a direct link between the presence of A.muciniphila and the disease	☑	☑	☑	☑	☒

MİKROBİYOTA
BAĞIRSAK-BEYİN AKSI

ener çağrı dinleyici



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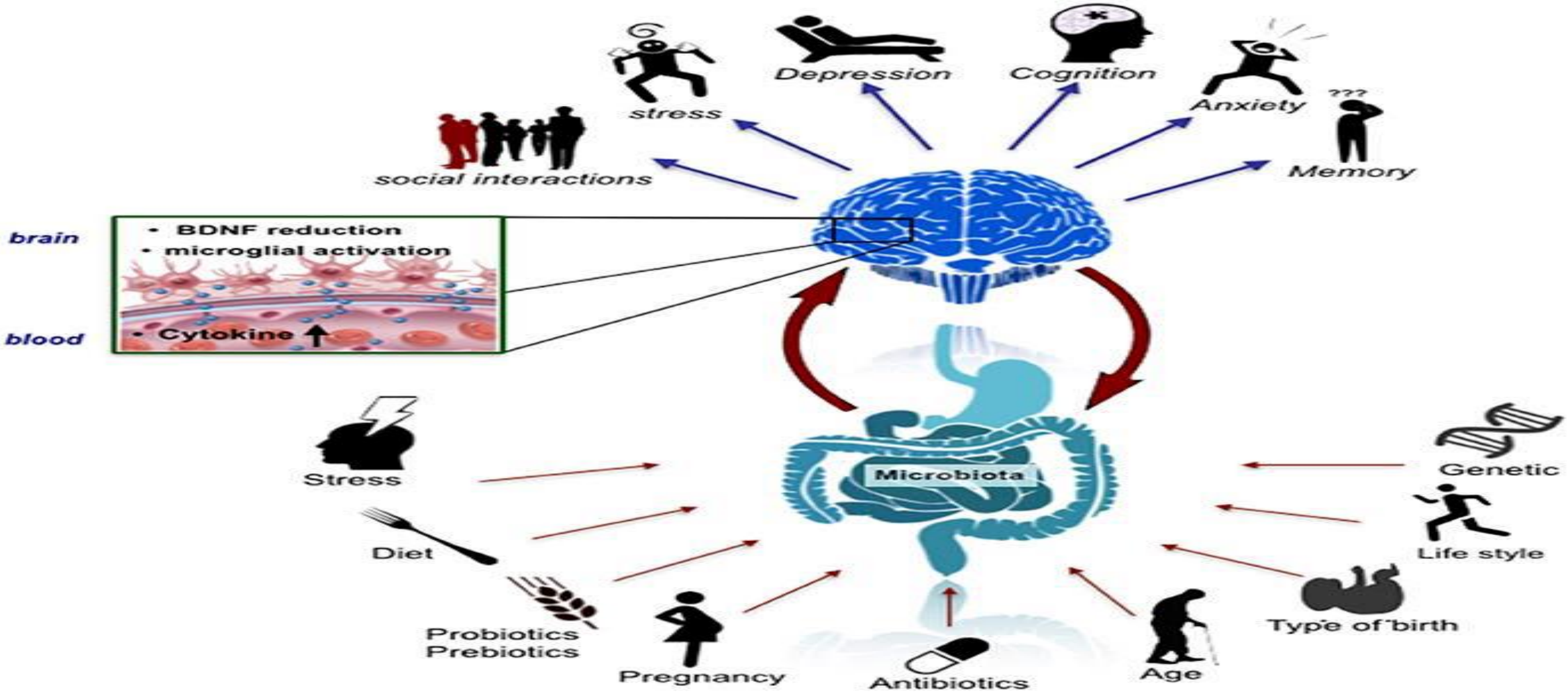
BAĞIRSAK-BEYİN AKSI

ener çağrı dinleyici



ANTİBİYOTİKLER
NÖROPSİKİYATRİK HASTALIKLAR

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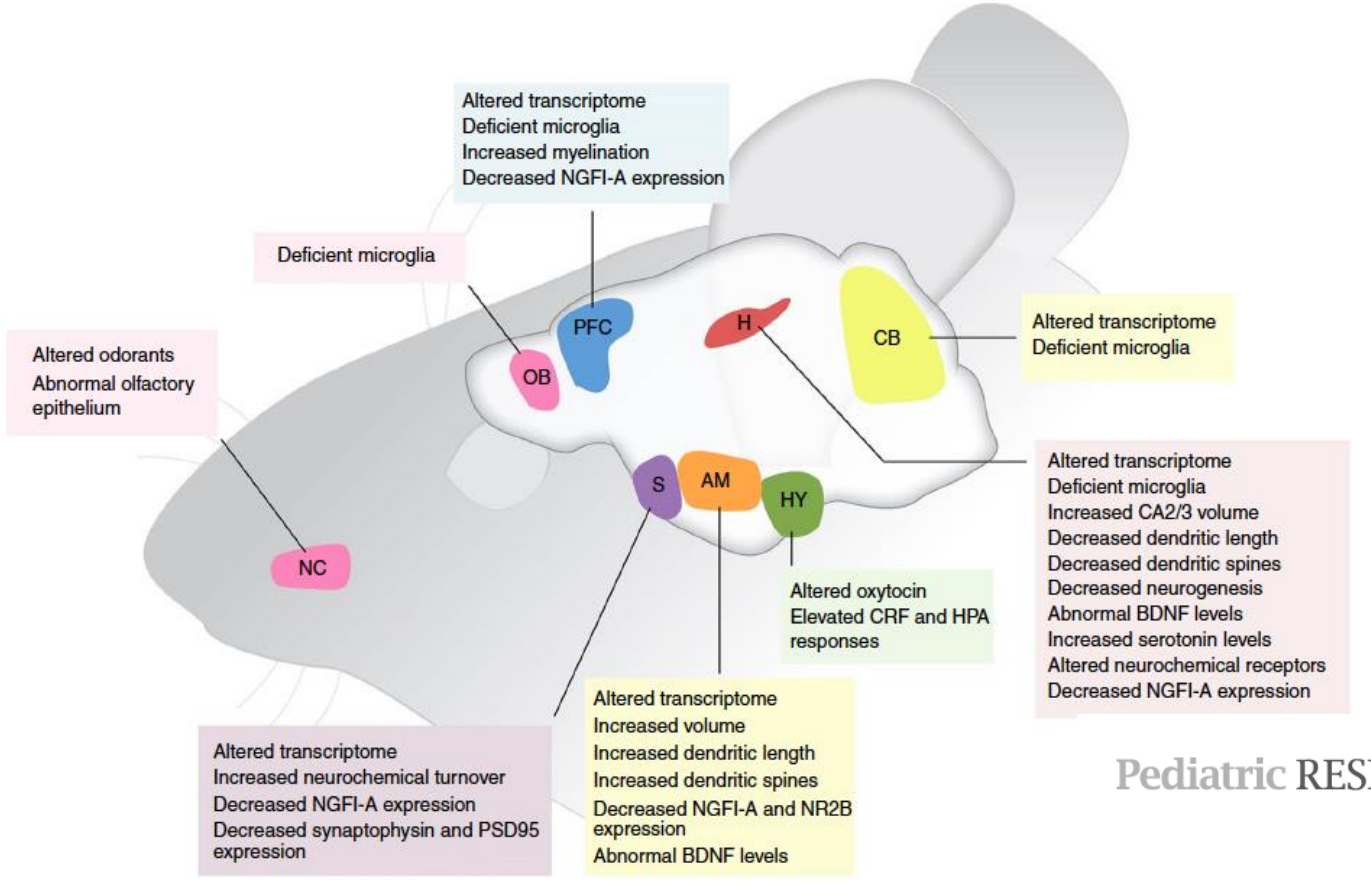
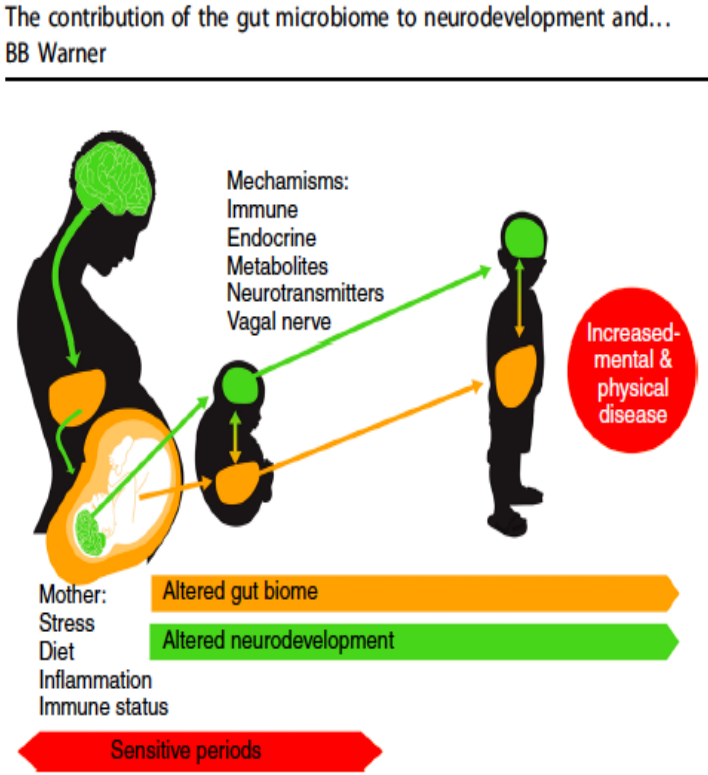




Pediatric RESEARCH

Fig. 2 Developmental windows for gut microbial impact on neurodevelopment, impacted by prenatal exposures and potential mechanism involved

REVIEW ARTICLE

The contribution of the gut microbiome to neurodevelopment and neuropsychiatric disorders

Barbara B. Warner[1]

MİKROBİYOTA
ENDOMETRİOSİS

ener çağrı dinleyici

www.nature.com/scientificreports

SCIENTIFIC REPORTS

OPEN

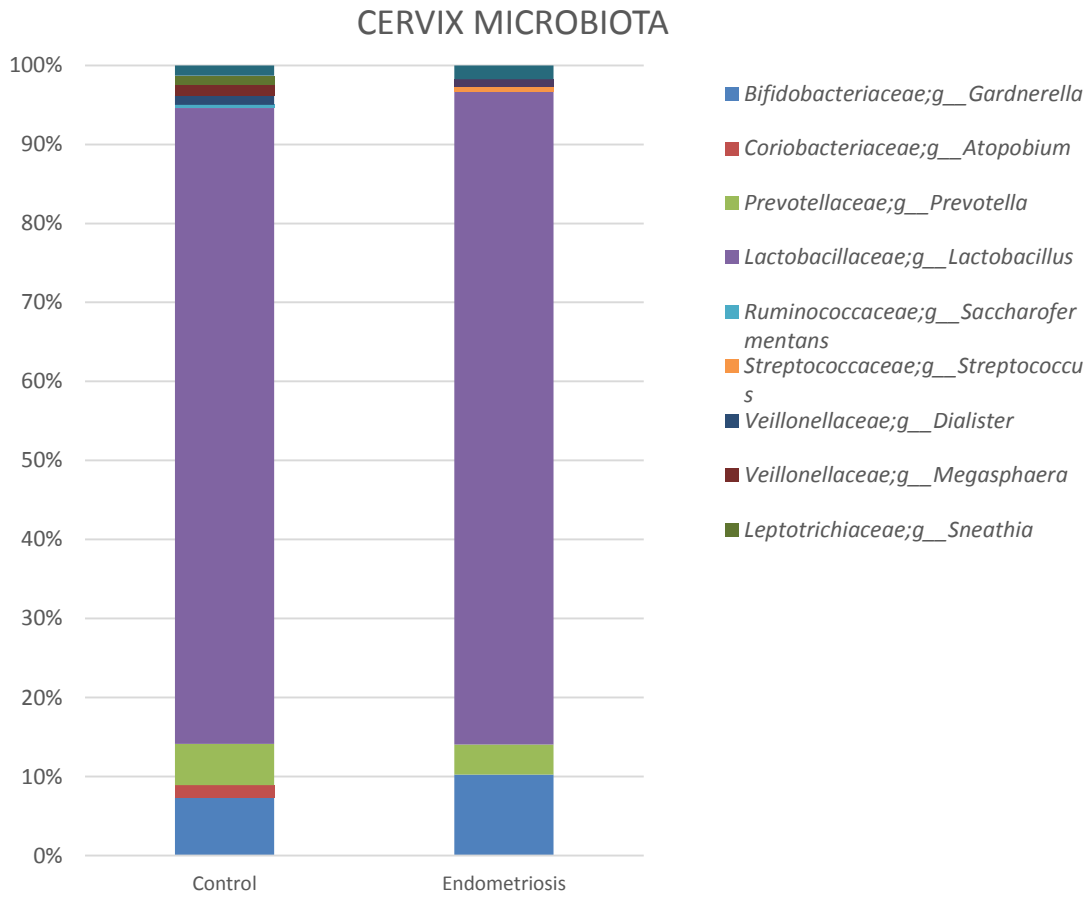
The Endobiota Study: Comparison of Vaginal, Cervical and Gut Microbiota Between Women with Stage 3/4 Endometriosis and Healthy Controls

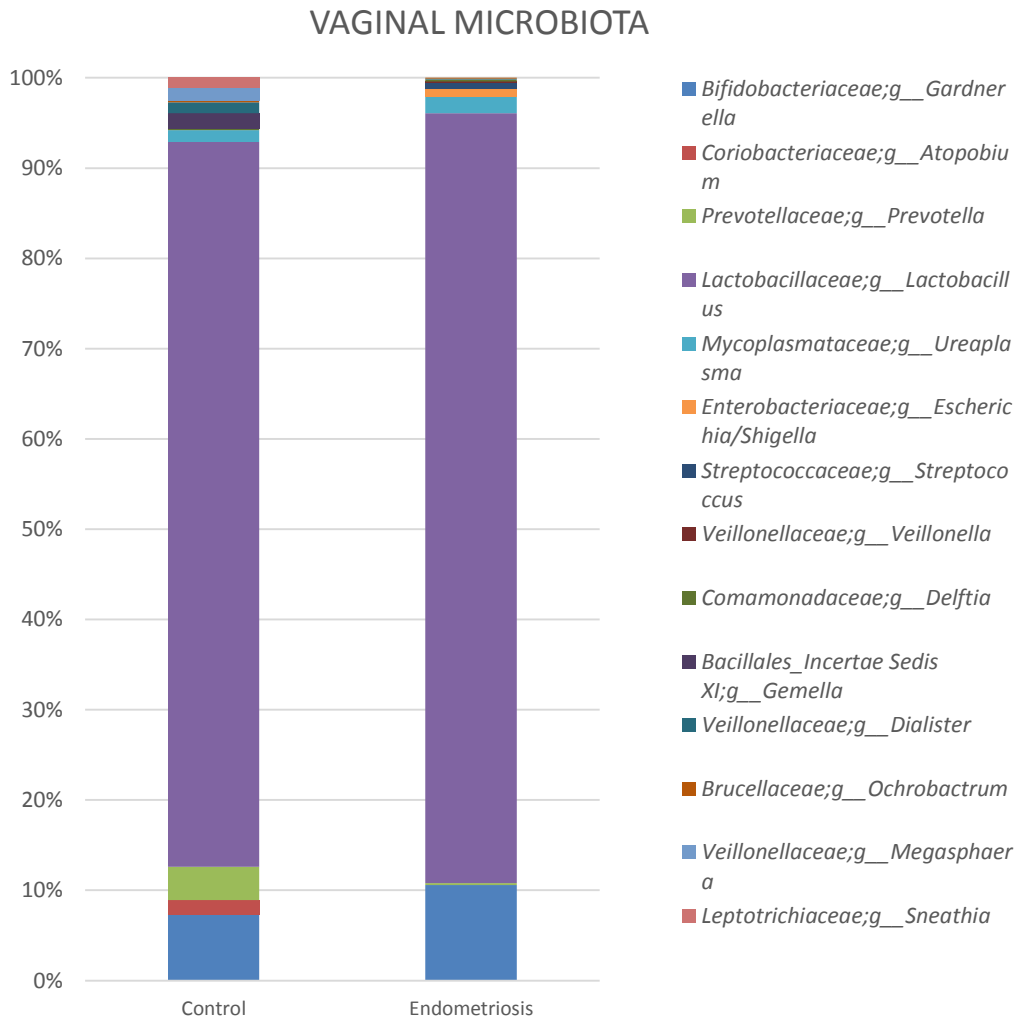
Received: 10 August 2018
Accepted: 30 January 2019
Published online: 18 February 2019

Baris Ata[1], Sule Yildiz[2], Engin Turkgeldi[2], Vicente Pérez Brocal[3], Ener Cagri Dinleyici[4], Andrés Moya[3,5,6] & Bulent Urman[1]

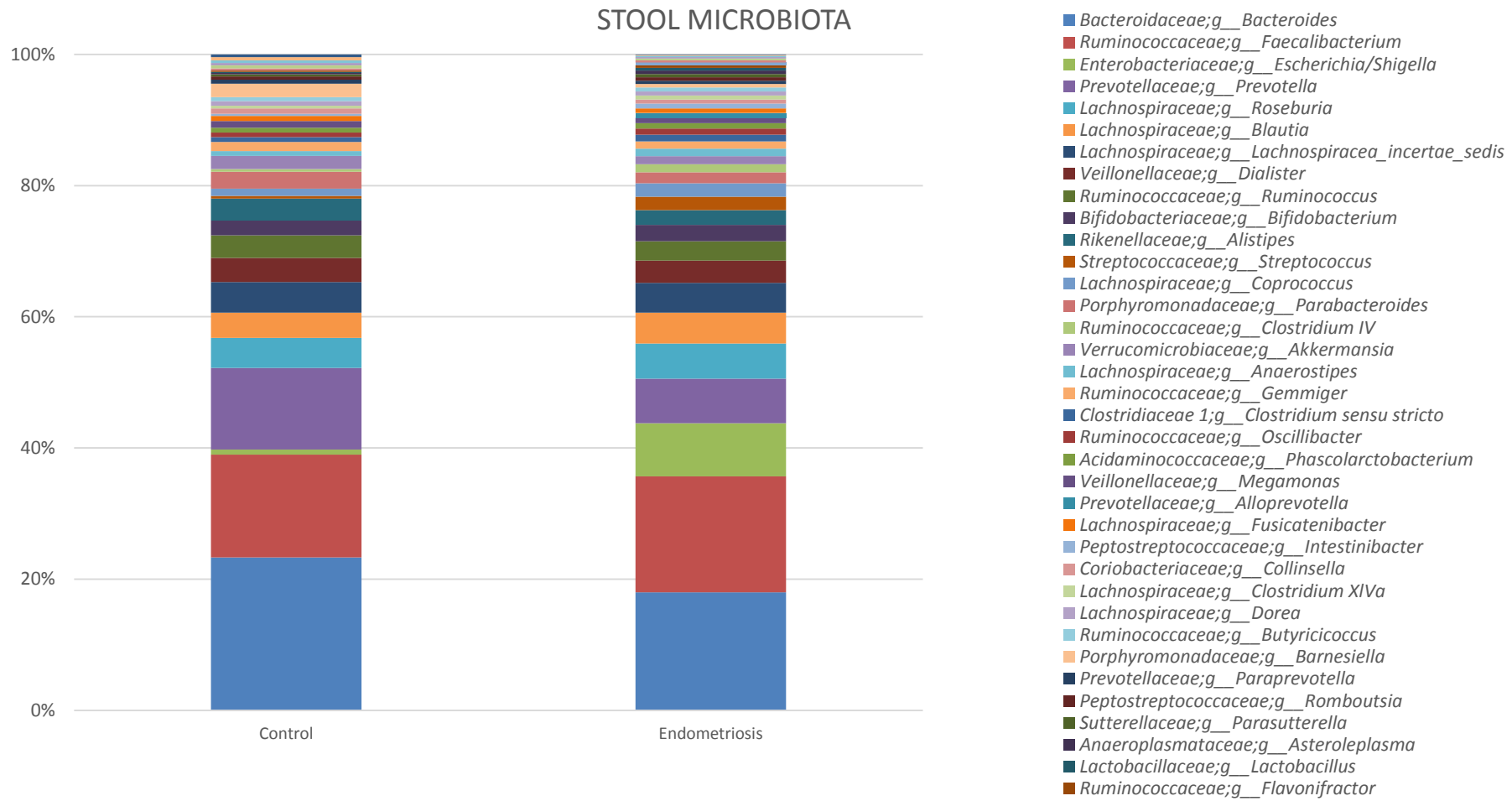
ENDOBIOTA STUDY

ener çağrı dinleyici





ENDOBIOTA STUDY



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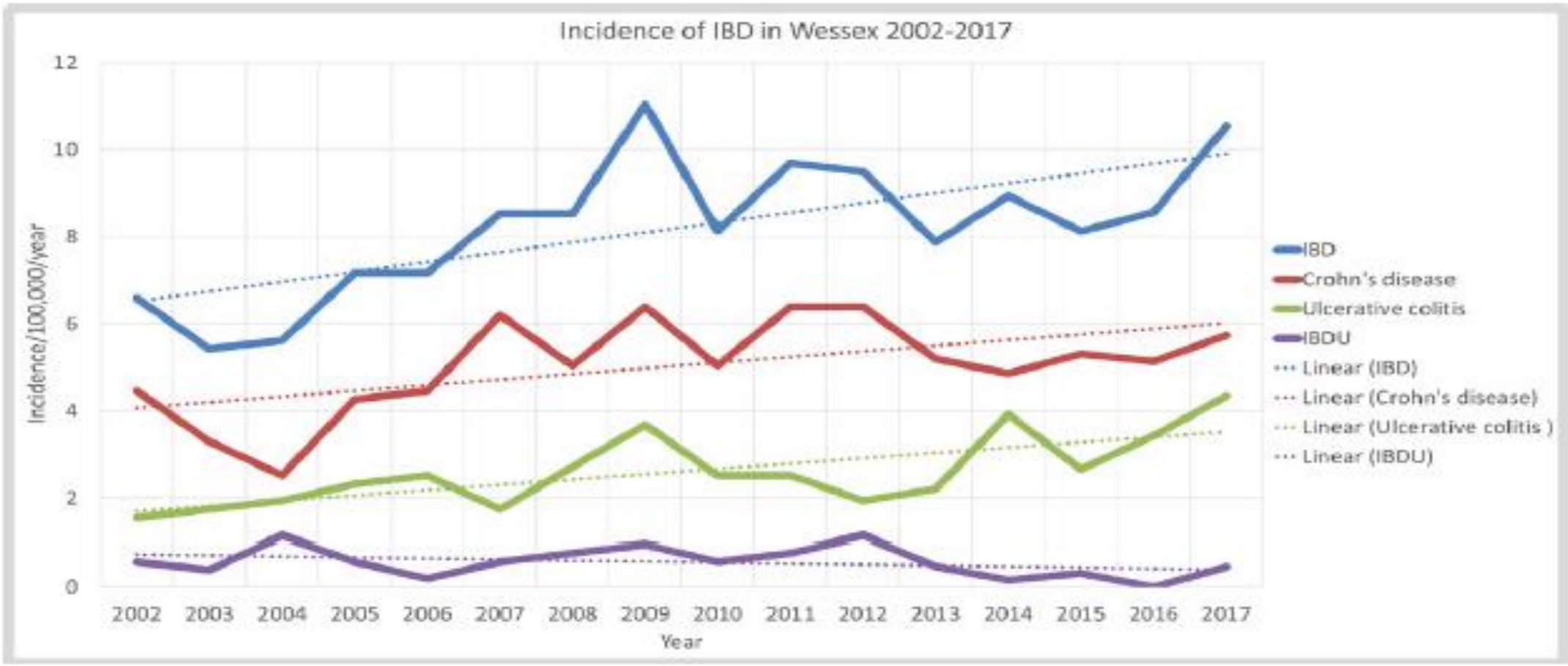

Ashton et al. Arch Dis Child 2018

MİKROBİYOTA
KANSER

ener çağrı dinleyici

nature medicine

FOCUS | REVIEW ARTICLE

https://doi.org/10.1038/s41591-019-0377-7

The microbiome, cancer, and cancer therapy

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KANSERDE TEDAVİ YANITI?

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Gut microbiome modulates response to anti–PD-1 immunotherapy in melanoma patients

Science. 2018 Jan 5;359(6371):104-108. doi: 10.1126/science.aao3290.

The commensal microbiome is associated with anti-PD-1 efficacy in metastatic melanoma patients.

Matson V[1], Fessler J[1], Bao R[2,3], Chongsuwat T[4], Zha Y[4], Alegre ML[4], Luke JJ[4], Gajewski TF[1,4].

Science
AAAS

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Soldati *et al. J Transl Med* (2018) 16:75
https://doi.org/10.1186/s12967-018-1448-0

Journal of Translational Medicine

REVIEW Open Access

The influence of diet on anti-cancer immune responsiveness

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Abstract

Immunotherapy has matured into standard treatment for several cancers, but much remains to be done to extend the reach of its effectiveness particularly to cancers that are resistant within each indication. This review proposes that nutrition can affect and potentially enhance the immune response against cancer. The general mechanisms that link nutritional principles to immune function and may influence the effectiveness of anticancer immunotherapy are examined. This represents also the premise for a research project aimed at identifying the best diet for immunotherapy enhancement against tumours (D.I.E.T project). Particular attention is turned to the gut microbiota and the impact of its composition on the immune system. Also, the dietary patterns effecting immune function are discussed including the value of adhering to a healthy diets such as the Mediterranean, Veg, Japanese, or a Microbiota-regulating diet, the very low ketogenic diet, which have been demonstrated to lower the risk of developing several cancers and reduce the mortality associated with them. Finally, supplements, as omega-3 and polyphenols, are discussed as potential approaches that could benefit healthy dietary and lifestyle habits in the context of immunotherapy.

Keywords: Immunotherapy, Healthy diet, Cancer, Microbiome, Functional supplements

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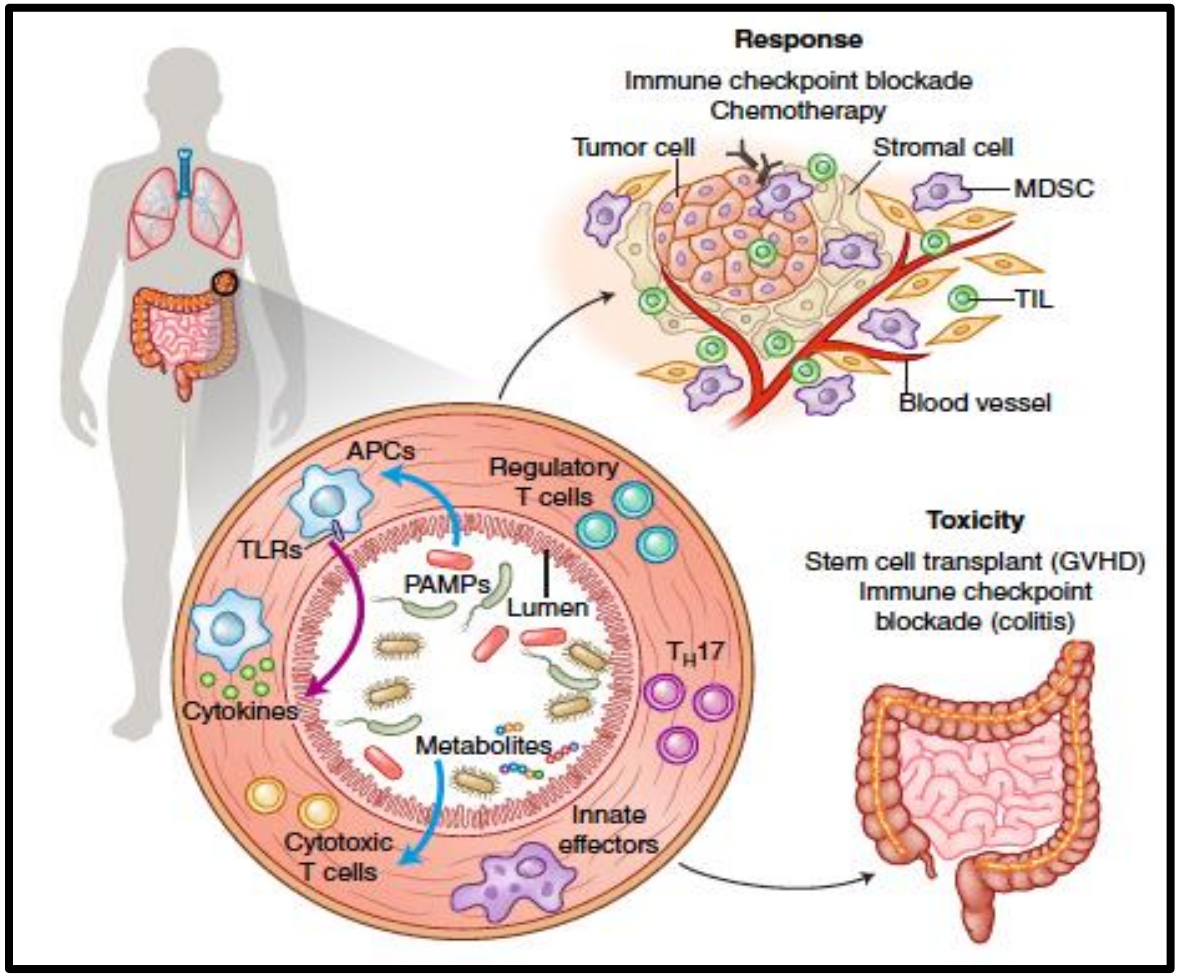
Liver/biliary tract
- Exposure to bacteria and/or metabolites via portal venous system
- Production of secondary bile acids may alter immune function (NKT cells) influencing tumor growth (primary and metastatic)
- DNA damage and hepatotoxicity induced by secondary bile acids and other mechanisms
- Induction of nonalcoholic steatohepatitis and other conditions that predispose to cirrhosis and subsequent cancer formation

Stomach
- Induction of a chronic inflammatory state
- Direct genotoxic effects on gastric mucosa

Breast
- Affects levels of circulating estrogens
- Alters balances in energy metabolism

Colon
- Chronic inflammatory state induced by toxins or alterations in signaling pathways
- Potentiation of inflammatory state by breakdown of normal mucosal barrier
- Production of toxins that are directly genotoxic
- Increases local production of reactive oxygen species
- Induction of oncogenic transcriptional activity potentially via β-catenin–Wnt signaling pathways
- Impairment of antitumor immune function



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HEDEF SAĞLIKLI MİKROBİYOTA

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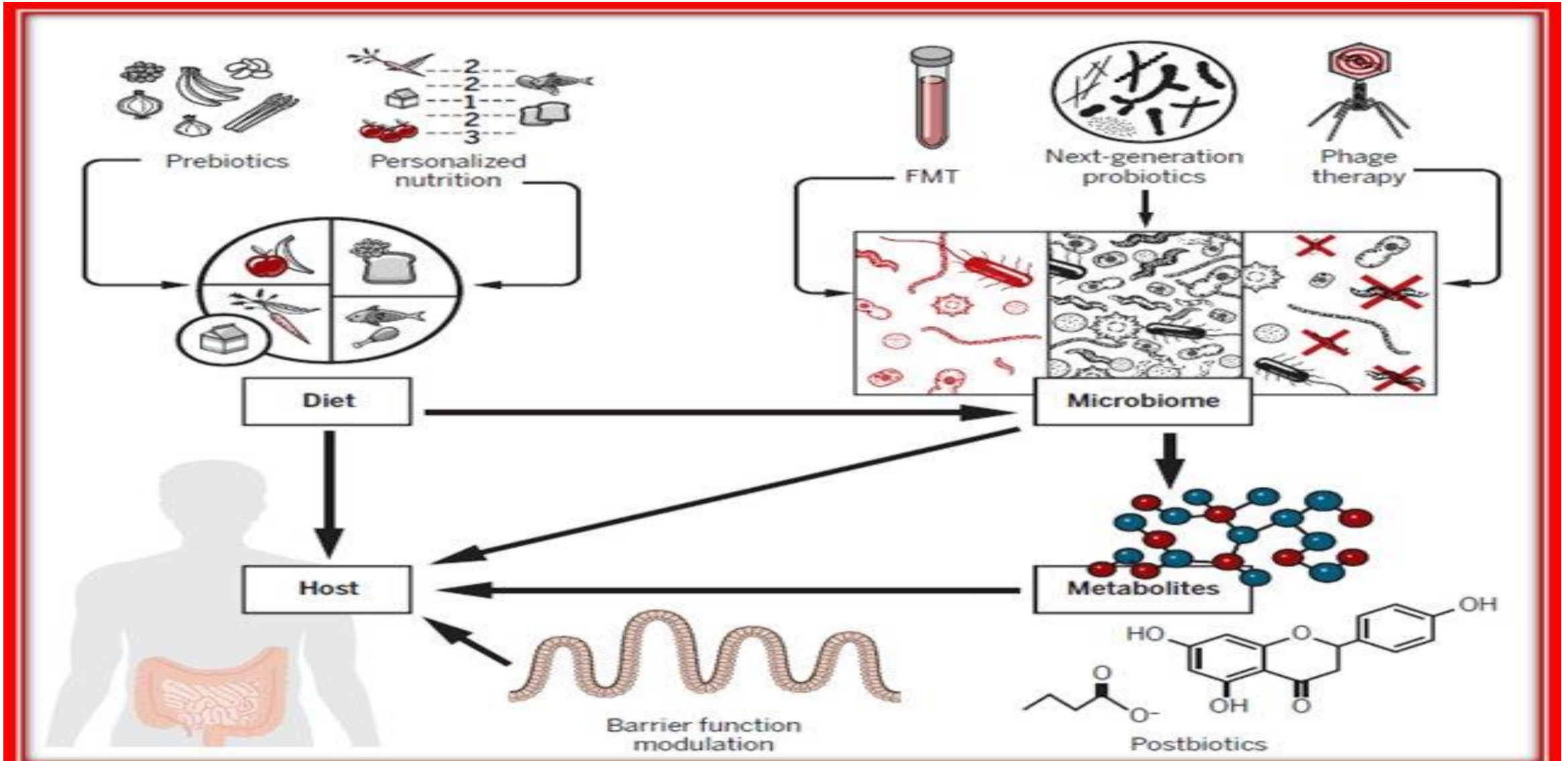

FEKAL TRANSPLANTASYON??

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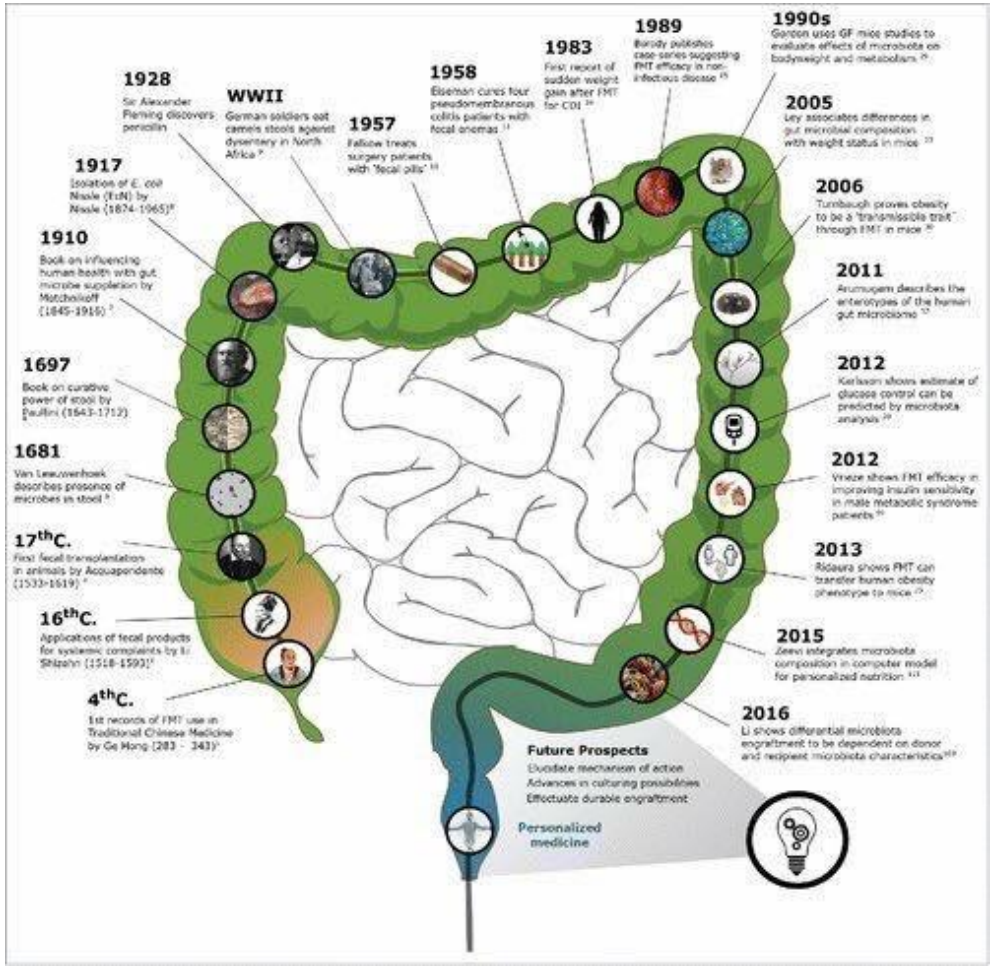

MICROBIOLOGY

Microbiome conservancy stores global fecal samples

Research could help prevent or treat diseases of the gut

Science 2 NOVEMBER 2018 • VOL 362 ISSUE 6414

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Review Article

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Influence of Altered Gut Microbiota Composition on Aging and Aging-Related Diseases

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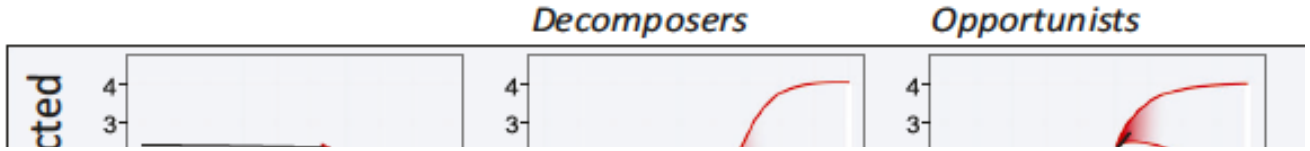
Obligately host-associated

Non-obligately host-associated



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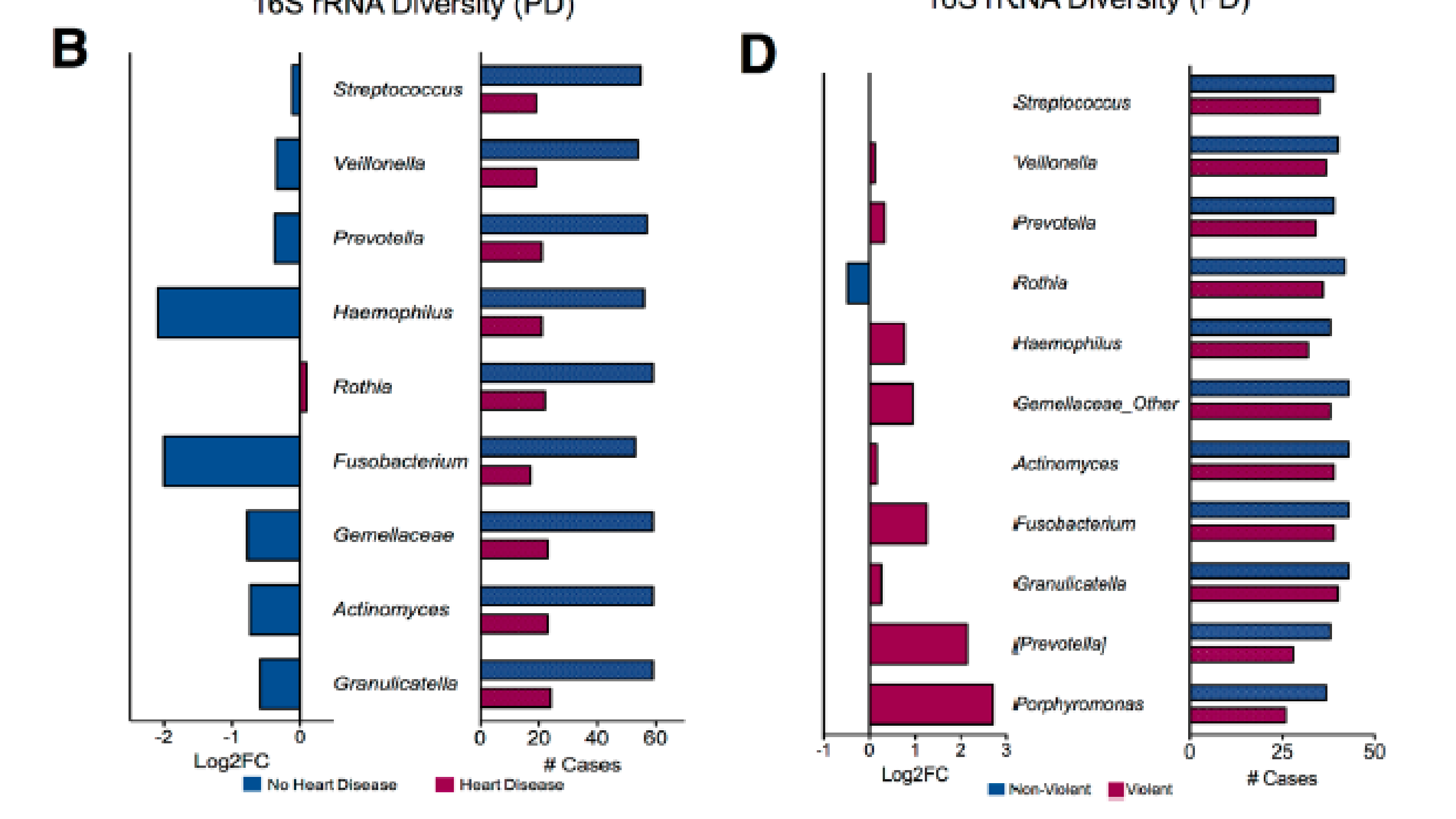
	Class	Order	Family	Genus	Assigned Group
OTU 12	*Saprospirae*	[Saprospirales]	NA	NA	Food associated
OTU 9		[Saprospirales]	*Saprospiraceae*	NA	Obl. host-associated
OTU 17	*Flavobacteriia*	Flavobacteriales	*Flavobacteriaceae*	*Flavobacterium*	Food associated
OTU 2	*Cytophagia*	Cytophagales	*Cytophagaceae*	*Emticicia*	Other
OTU 16	*Actinobacteria*	Actinomycetales	*Microbacteriaceae*	NA	Medium associated
OTU 15		Actinomycetales	*Microbacteriaceae*	*Clavibacter*	Medium associated
OTU 6	*Alphaproteobacteria*	Rhodobacterales	*Rhodobacteraceae*	*Rhodobacter*	Opportunists
OTU 18	*Gammaproteobacteria*	Pseudomonadales	*Moraxellaceae*	*Acinetobacter*	Other
OTU 10		Alteromonadales	*[Chromatiaceae]*[1]	*Rheinheimera*	Decomposer
OTU 4		Alteromonadales	*[Chromatiaceae]*[1]	*Rheinheimera*	Other
OTU 5		Pseudomonadales	*Pseudomonadaceae*	*Pseudomonas*	Opportunists
OTU 8		Pseudomonadales	*Pseudomonadaceae*	NA	Other
OTU 1	*Betaproteobacteria*	Burkholderiales	*Comamonadaceae*	*Rubrivivax*	Obl. host-associated
OTU 7		Burkholderiales	*Comamonadaceae*	NA	Decomposer
OTU 11		Burkholderiales	*Comamonadaceae*	NA	Opportunists
OTU 13		Burkholderiales	*Comamonadaceae*	*Methylibium*	Medium associated
OTU 3		Burkholderiales	*Comamonadaceae*	*Limnohabitans*	Obl. host-associated
OTU 425		Burkholderiales	*Comamonadaceae*	*Limnohabitans*	Obl. host-associated
OTU 14	*Deltaproteobacteria*	Myxococcales	NA	NA	Opportunists


16S rRNA Diversity (PD)
B
Streptococcus
Veillonella
Prevotella
Haemophilus
Rothia
Fusobacterium
Gemellaceae
Actinomyces
Granulicatella
-2
-1
0
Log2FC
0
20
40
60
Cases
No Heart Disease
Heart Disease
16S rRNA Diversity (PD)
D
Streptococcus
Veillonella
Prevotella
Rothia
Haemophilus
Gemellaceae_Other
Actinomyces
Fusobacterium
Granulicatella
[Prevotella]
Porphyromonas
-1
0
1
2
3
Log2FC
0
25
50
Cases
Non-Violent
Violent

DEVAM EDEN ÇALIŞMALAR

- BEHÇET HASTALIĞI ORAL AFT VE İNTESTİNAL MİKROBİYOTA
- FİBROMİYALJİ VE MİKROBİYOTA
- FMF HASTALIĞINDA MİKROBİYOTA
- TALASEMİ NEDENİL İLE KİT YAPILAN HASTALARDA MİKROBİYOTA KOMPOZİSYONU
- ANNE SÜTÜ VİROME ANALİZİ
- ANNE SÜTÜ ANTİBİYOTİK İÇERİĞİ VE MİKROBİYOYA KOMPOZİSYONU
- PEDİATRİK SEPSİS OLGULARINDA NAZOFARİNGEAL VE İNTESTİNAL MİKROBİYOTA ANALİZİ
- İNVAZİV MENİNGOKOK ENFEKSİYONU OLGULARINDA MİKROBİYOTA
- OBEZ ERGENLERDE MİKROBİYOTA KOMPOZİSYONU VE PROBİYOTİKLERİN ETKİSİ

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BELÇİKA

YVAN VANDENPLAS

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Excellence is a road, not a destination

Cont'd, 2019. Ener Cagri Dinleyici