Mikrobiotanın Önemi ve Rolü

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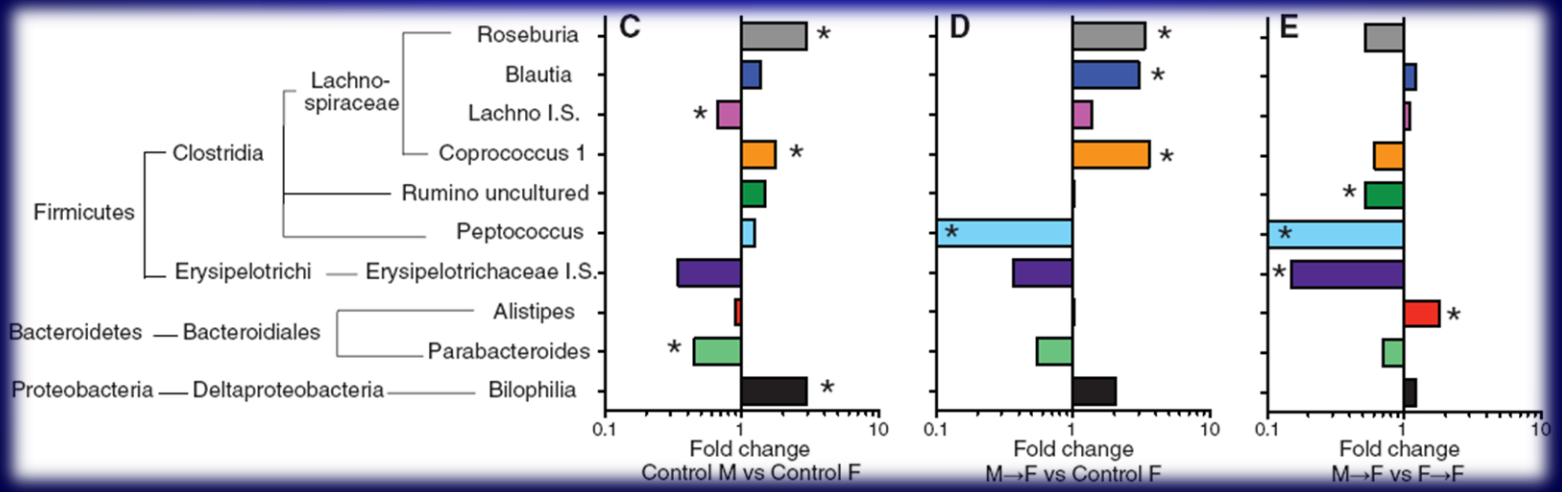
Çocuk Sağlığı ve Hastalıkları Anabilim Dalı
Enfeksiyon Hastalıkları Ünitesi

Sex Differences in the Gut Microbiome Drive Hormone-Dependent Regulation of Autoimmunity

Janet G. M. Markle,[1,2] Daniel N. Frank,[3] Steven Mortin-Toth,[1] Charles E. Robertson,[4] Leah M. Feazel,[3] Ulrike Rolle-Kampczyk,[5] Martin von Bergen,[5,6,7] Kathy D. McCoy,[8] Andrew J. Macpherson,[8] Jayne S. Danska[1,2,9]*

- Otoimmün hastalıklara yatkınlıkta mikrobiotanın rolü var
- Komensal bakteriler seks hormonlarının düzeyini değiştiriyor
- Cinsiyete bağlı tip 1 DM duyarlığının kaynağı mikrobiyota
- Erişkin erkek farelerden, olgunlaşmamış dişi farelere mikrobiota aktarımı testosteron artışına ve otoimmün hastalıklara dirence yol açıyor



Science 2013;339: 1084

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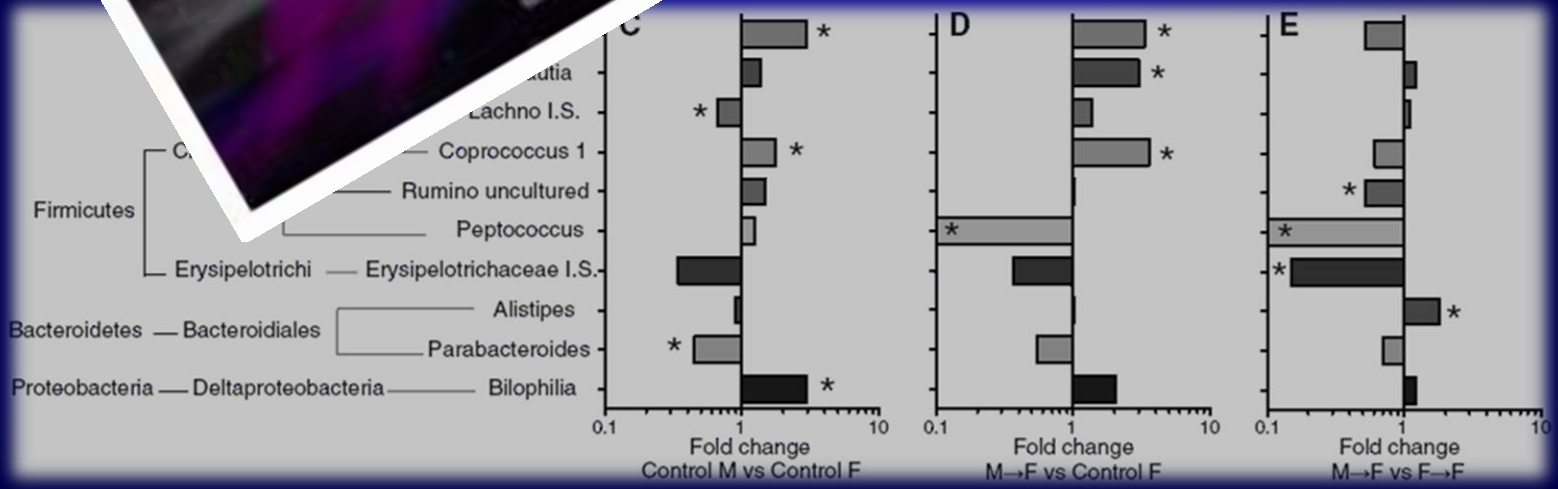
- …lıkta mikrobiotanın rolü var
- …nlarının düzeyini değiştiriyor
- …n kaynağı mikrobiyota
- …mış dişi farelere mikrobiota aktarımı tes… …astalıklara dirence yol açıyor



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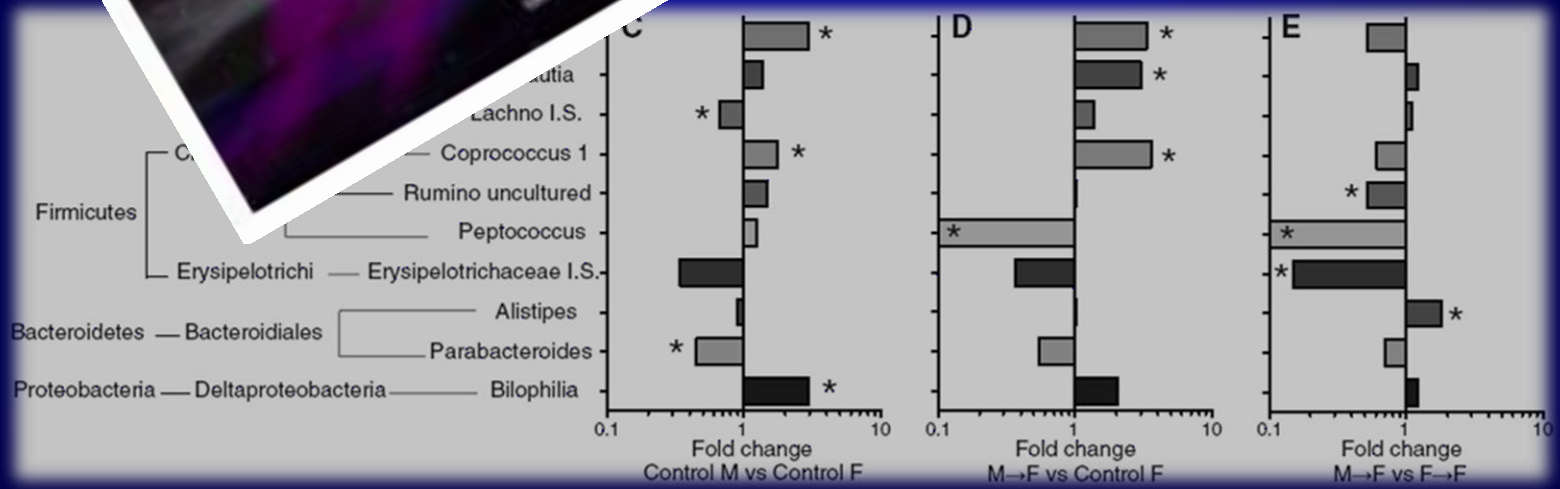
…lıkta mikrobiotanın rolü var

…nlarının düzeyini değiştiriyor

The top 100 papers

- …aktarımı

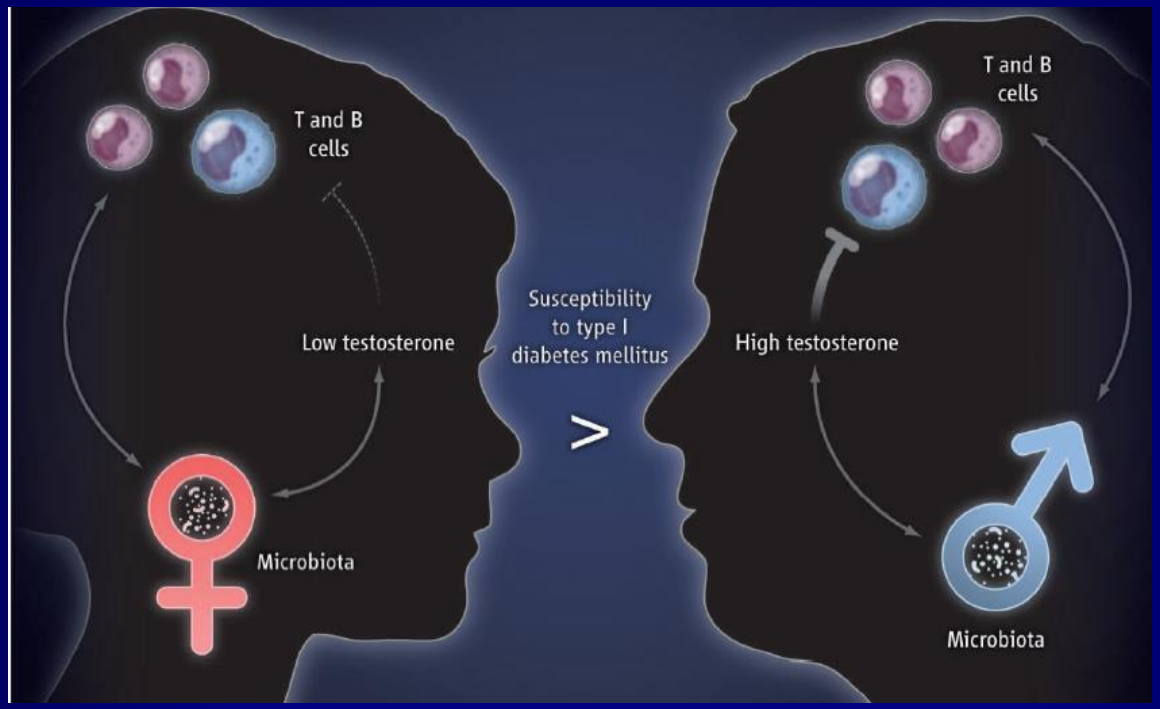
tes… …astalıklara dirence yol açıyor



Science 2013;339: 1084

Welcome to the Microgenderome

Magdalena B. Flak, Joana F. Neves, Richard S. Blumberg

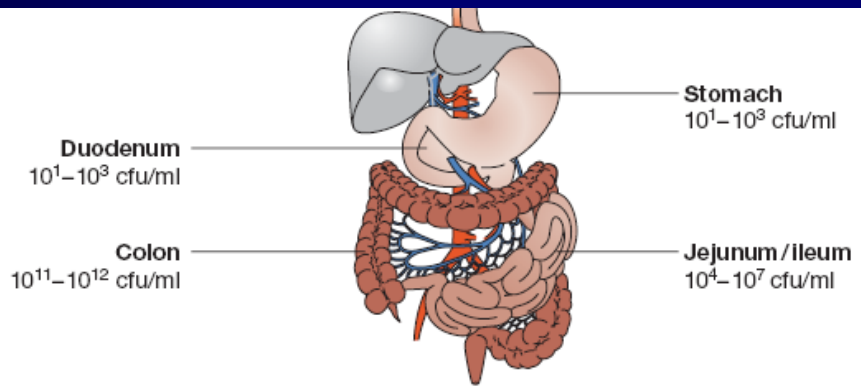


- Erkeklerde püberte döneminde barsak MİKROBİYOTASI değişiyor
- Testosteron üretimi artıyor
- Bu durum B ve T hücre fonksiyonlarını güçlendiriyor

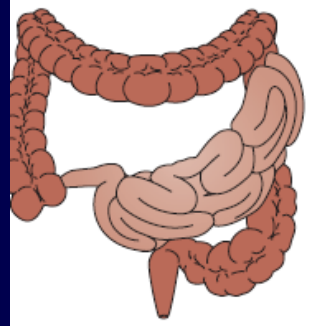
Science 2013;339: 1044

The gut flora as a forgotten organ

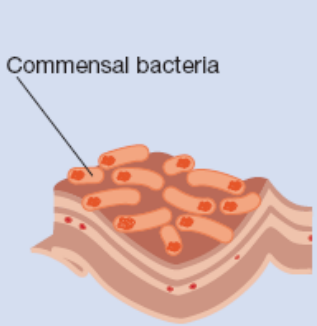
Ann M. O'Hara[1] & Fergus Shanahan[1,2+]

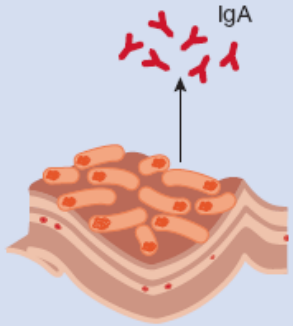


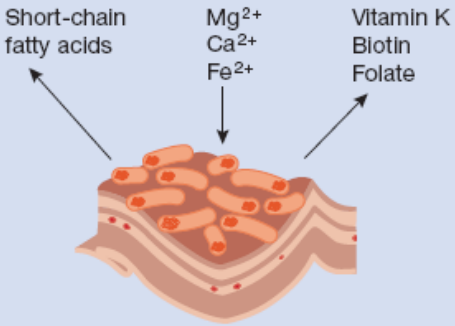
Anaerobic genera	Aerobic genera
Bifidobacterium	*Escherichia*
Clostridium	*Enterococcus*
Bacteroides	*Streptococcus*
Eubacterium	*Klebsiella*



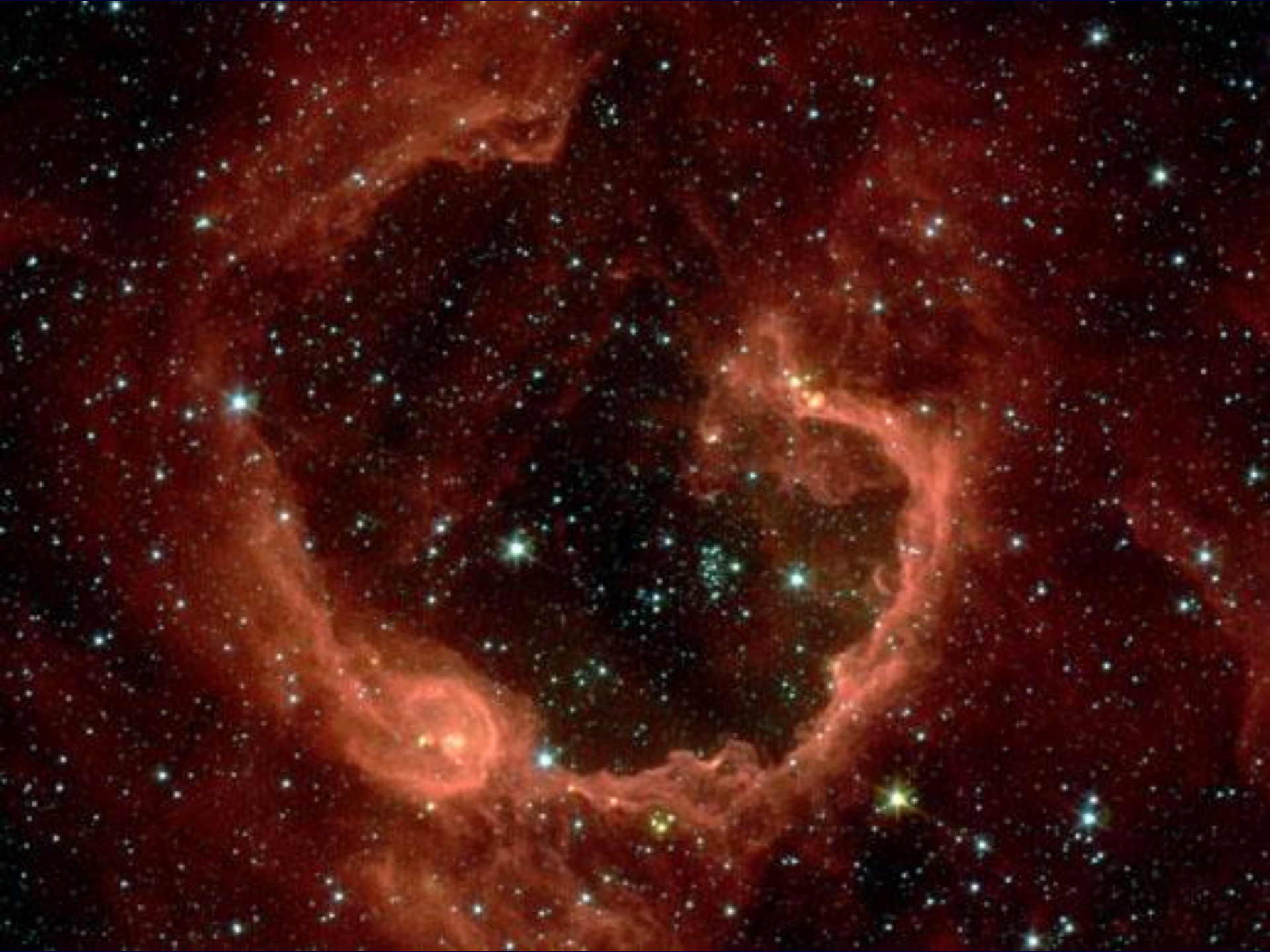
Protective functions	Structural functions	Metabolic functions	
Pathogen displacement	Barrier fortification	Control IEC differentiation and proliferation	Ferment non-digestible dietary residue and endogenous epithelial-derived mucus
Nutrient competition	Induction of IgA	Metabolize dietary carcinogens	Ion absorption
Receptor competition	Apical tightening of tight junctions	Synthesize vitamins e.g., biotin, folate	Salvage of energy
Production of anti-microbial factors e.g., bacteriocins, lactic acids	Immune system development		







EMBO 2006;7: 688



Bakteri:
3.5 milyar yıl

İnsan:
195.000 yıl

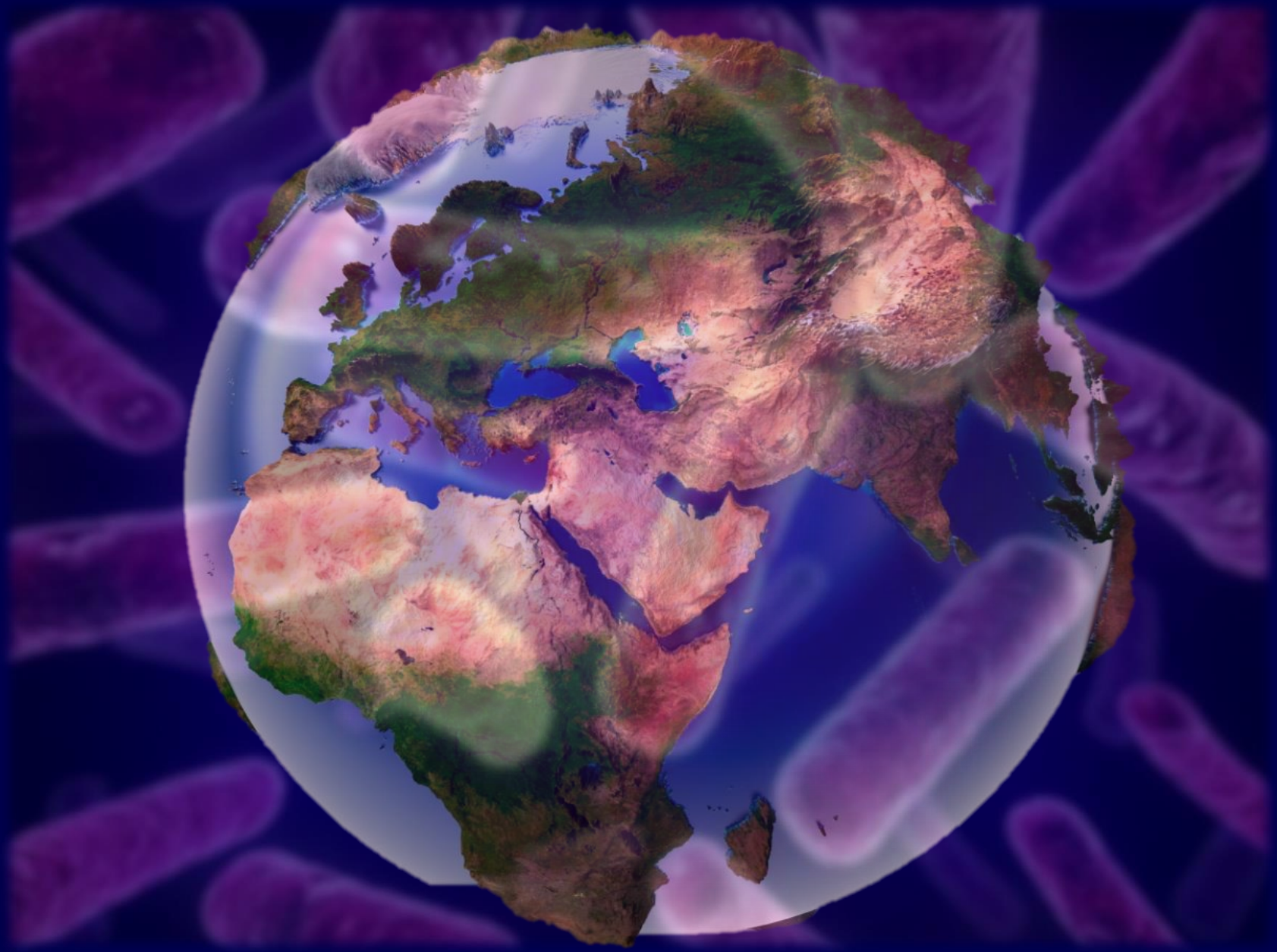
4.5 Milyar yıl

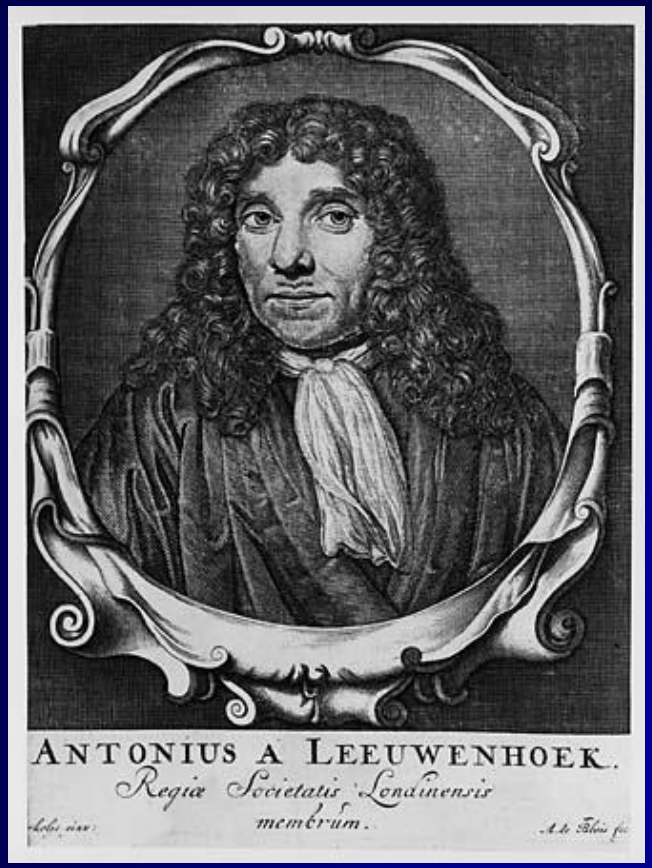
24 saat üzerinden değerlendirildiğinde bakteriler 1 gündür, biz bugün saat 12 ise,11.59.58'den itibaren varız

3.5 milyar yıl

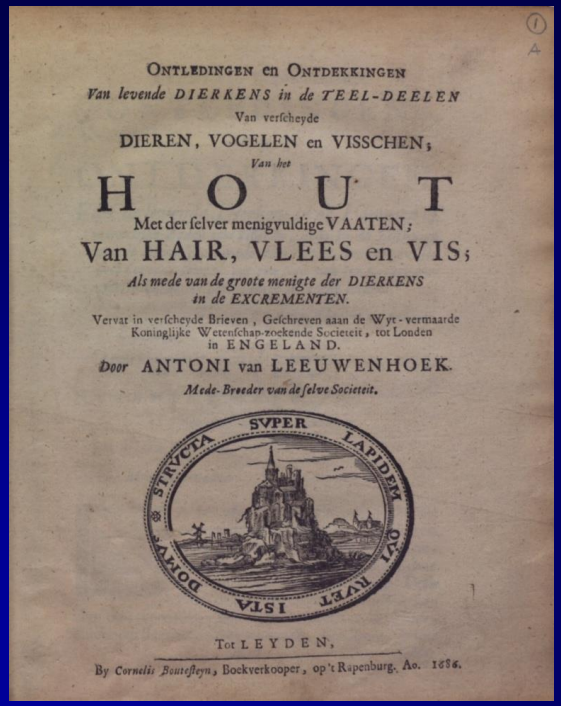
İnsan:
195.000 yıl

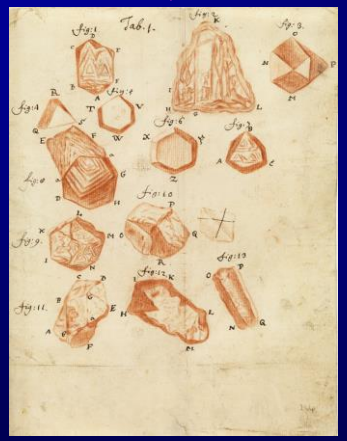
4.5 Milyar yıl





Antonie van Leeuwenhoek
(1632-1723)


ONTLEDINGEN en ONTDEKKINGEN
Van levende DIERKENS in de TEEL-DEELEN
Van verscheyde
DIEREN, VOGELEN en VISSCHEN;
Van het
H O U T
Met der selver menigvuldige VAATEN;
Van HAIR, VLEES en VIS;
Als mede van de groote menigte der DIERKENS in de EXCREMENTEN.
Vervat in verscheyde Brieven, Geschreven aaan de Wyt-vermaarde Koninglijke Wetenschan-zoekende Societeit, tot Londen in ENGELAND.
Door ANTONI van LEEUWENHOEK.
Mede-Broeder van de selve Societeit.
SVPER LAPIDEM ISTA
Tot LEYDEN,
By *Cornelis Boutesteyn*, Boekverkooper, op 't Rapenburg, Ao. 1684.



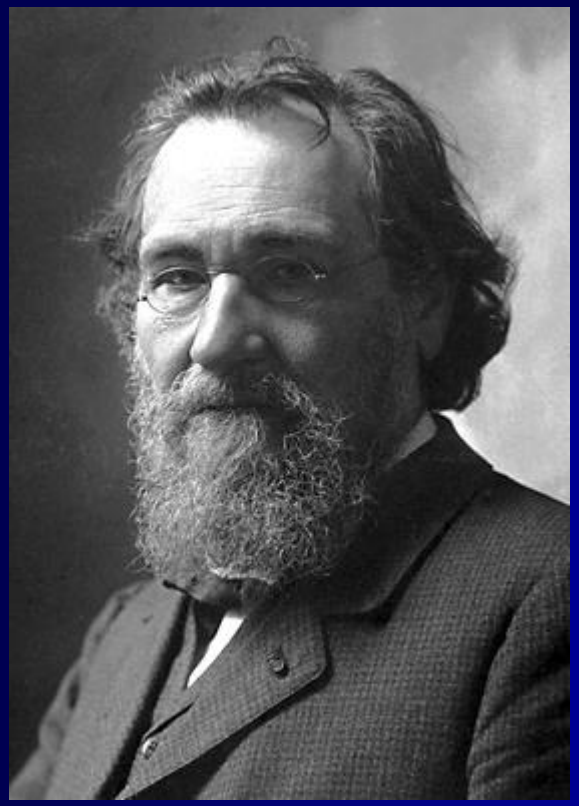
Animalcules

Benzer olmayan organizmaların birlikte yaşamı

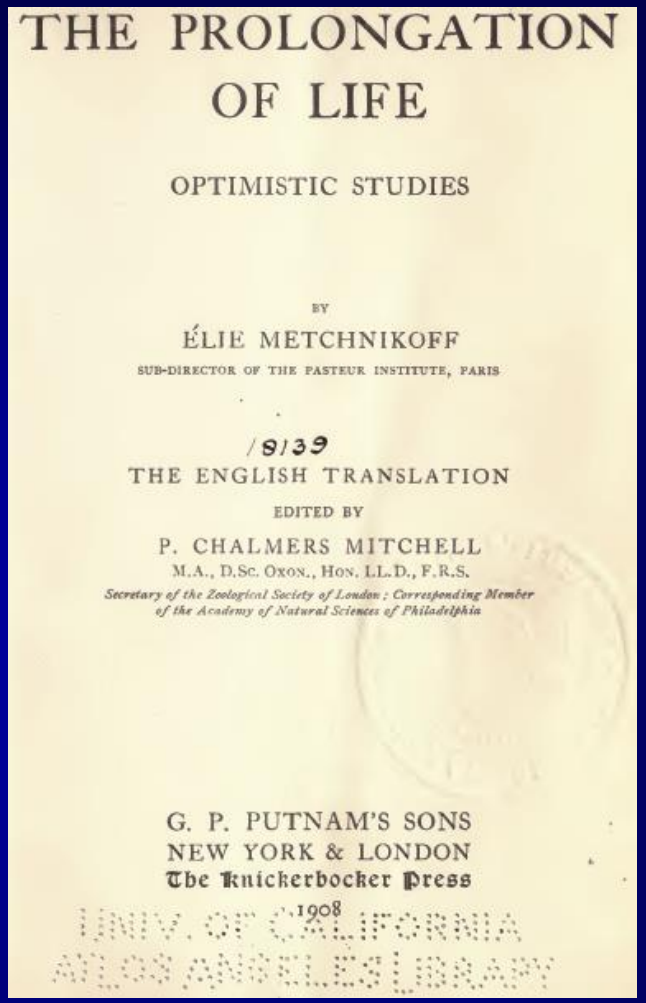
- Sembiyoz çeşitleri: *mutualizm, komensalizm, parazitizm*
- Mikroorganizamalarla aramızda hem yarış, hem işbirliği var
- SAVAŞ ve BARIŞ değil, ortak yaşam…

Benzer olmayan organizmaların birlikte yaşamı

- Sem izm
- Mik ği var
- SA



Elie Metchnikoff
(1845-1916)



THE PROLONGATION OF LIFE

OPTIMISTIC STUDIES

BY

ÉLIE METCHNIKOFF

SUB-DIRECTOR OF THE PASTEUR INSTITUTE, PARIS

/8139

THE ENGLISH TRANSLATION

EDITED BY

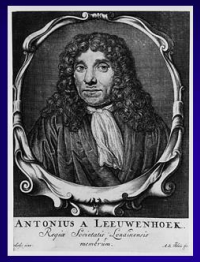
P. CHALMERS MITCHELL

M.A., D.Sc. Oxon., Hon. LL.D., F.R.S.

Secretary of the Zoological Society of London; Corresponding Member of the Academy of Natural Sciences of Philadelphia

G. P. PUTNAM'S SONS
NEW YORK & LONDON
The Knickerbocker Press
1908

- Disbiozis (*Disbacteriosis*): sembiozisin karşıtı
- Barsak mikrobiotasında kalitatif / kantitatif değişim
- Disbiozis bir dizi hastalığa yol açar: diyare, IBH, obezite, DM, alerji vb….
- Çoğunda barsak bakterilerine karşı immün yanıtta değişim söz konusu



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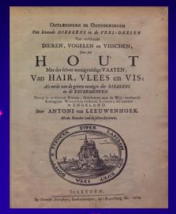
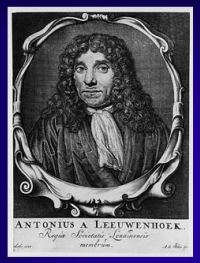


«Animalcules»



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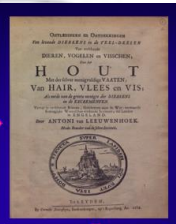
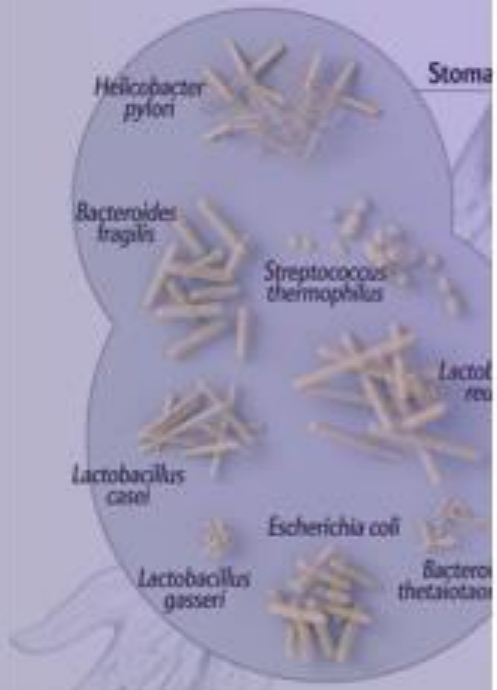


«Animalcules»

Ağız içinde bulunan mikroorganizma çeşidi 600'ün üzerinde



JOURNAL OF BACTERIOLOGY, Oct. 2010, p. 5002–5017 Vol. 192, No. 19
0021-9193/10/$12.00 doi:10.1128/JB.00542-10

The Human Oral Microbiome▽†‖

Floyd E. Dewhirst,[1,2]* Tuste Chen,[1] Jacques Izard,[1,2] Bruce J. Paster,[1,2] Anne C. R. Tanner,[1,2] Wen-Han Yu,[1] Abirami Lakshmanan,[1] and William G. Wade[1,3]

Department of Molecular Genetics, The Forsyth Institute, Cambridge, Massachusetts 02142[1]; Department of Oral Medicine, Infection and Immunity, Harvard School of Dental Medicine, Boston, Massachusetts 02115[2]; and King's College London Dental Institute at Guy's, King's College and St. Thomas' Hospitals, Infection Research Group, Guy's Campus, London SE1 9RT, United Kingdom[3]

Received 11 May 2010/Accepted 10 July 2010

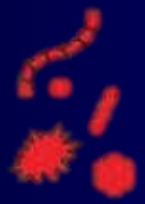
The human oral cavity contains a number of different habitats, including the teeth, gingival sulcus, tongue, cheeks, hard and soft palates, and tonsils, which are colonized by bacteria. The oral microbiome is comprised of over 600 prevalent taxa at the species level, with distinct subsets predominating at different habitats. The oral microbiome has been extensively characterized by cultivation and culture-independent molecular methods such as 16S rRNA cloning. Unfortunately, the vast majority of unnamed oral taxa are referenced by clone numbers or 16S rRNA GenBank accession numbers, often without taxonomic anchors. The first aim of this research was to collect 16S rRNA gene sequences into a curated phylogeny-based database, the Human Oral Microbiome Database (HOMD), and make it web accessible (www.homd.org). The HOMD includes 619 taxa in 13 phyla, as follows: *Actinobacteria*, *Bacteroidetes*, *Chlamydiae*, *Chloroflexi*, *Euryarchaeota*, *Firmicutes*, *Fusobacteria*, *Proteobacteria*, *Spirochaetes*, SR1, *Synergistetes*, *Tenericutes*, and TM7. The second aim was to analyze 36,043 16S rRNA gene clones isolated from studies of the oral microbiota to determine the relative abundance of taxa and identify novel candidate taxa. The analysis identified 1,179 taxa, of which 24% were named, 8% were cultivated but unnamed, and 68% were uncultivated phylotypes. Upon validation, 434 novel, nonsingleton taxa will be added to the HOMD. The number of taxa needed to account for 90%, 95%, or 99% of the clones examined is 259, 413, and 875, respectively. The HOMD is the first curated description of a human-associated microbiome and provides tools for use in understanding the role of the microbiome in health and disease.

Süperorganizma = Konak + Mikrobiotası

(100 trilyon mikrobiota + 10 trilyon «self» + 1 trilyon immün hücre)

İnsan vücudunda hücre sayısı

$\sim 10^{12}$ cells → $\sim 10^{4}$ genes → The mammalian metabolome



$\sim 10^{14}$ Bacteria
+ Archea
+ Fungi
+ Viruses

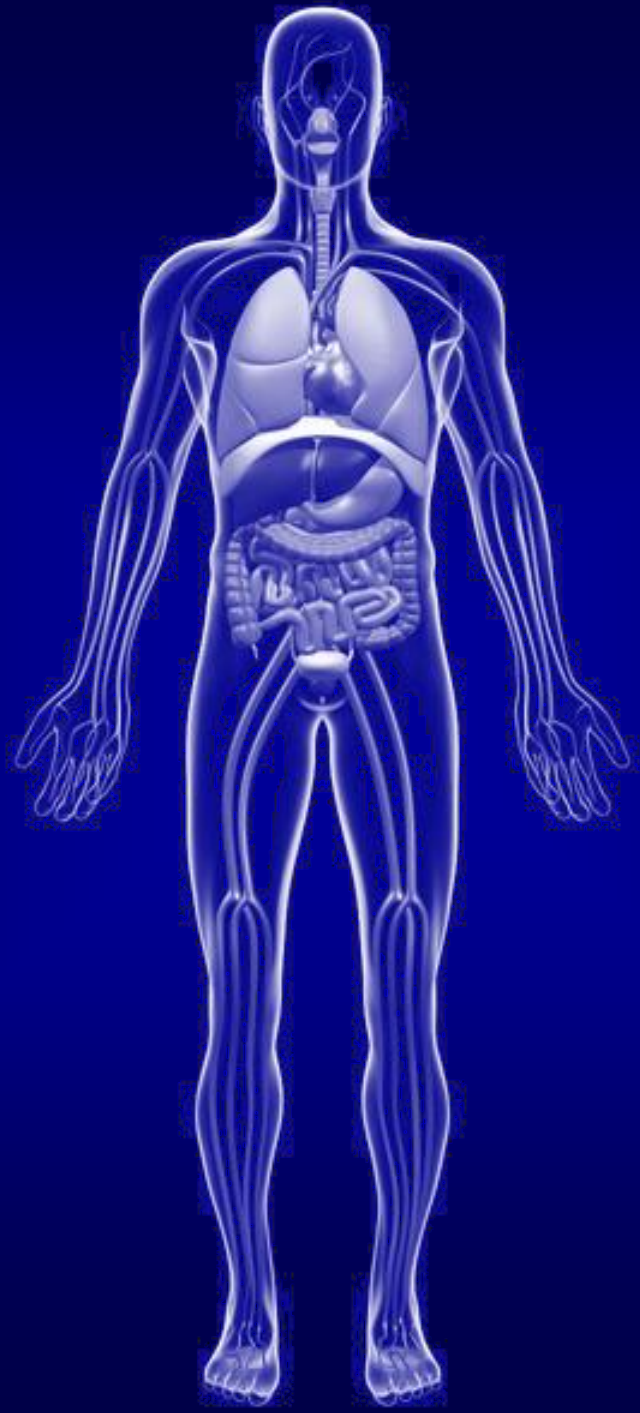
→ $> 10^{6}$ genes → The microbial metabolome

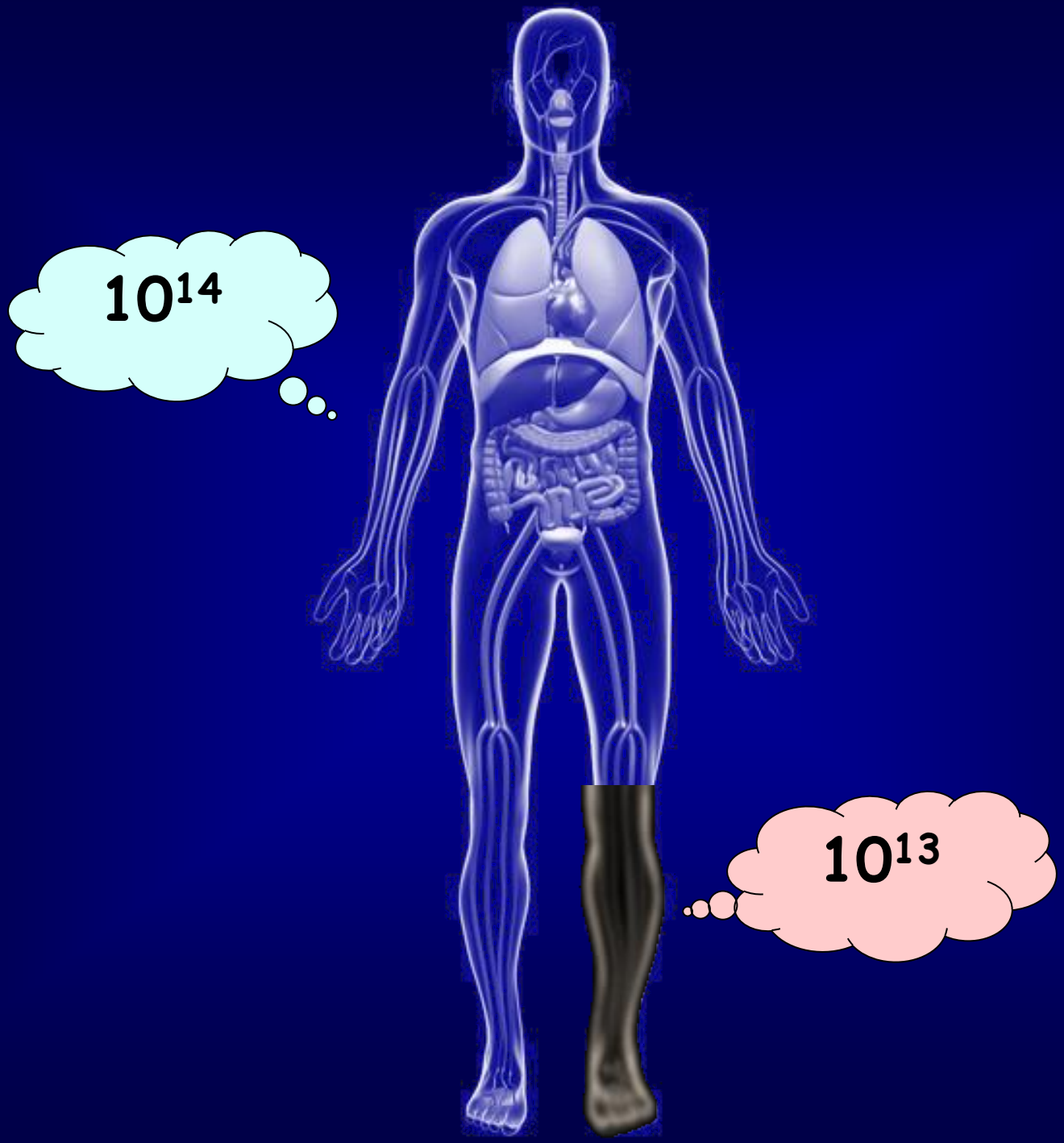
İnsan barsağında mikroorganizma sayısı (> 1000 tür)

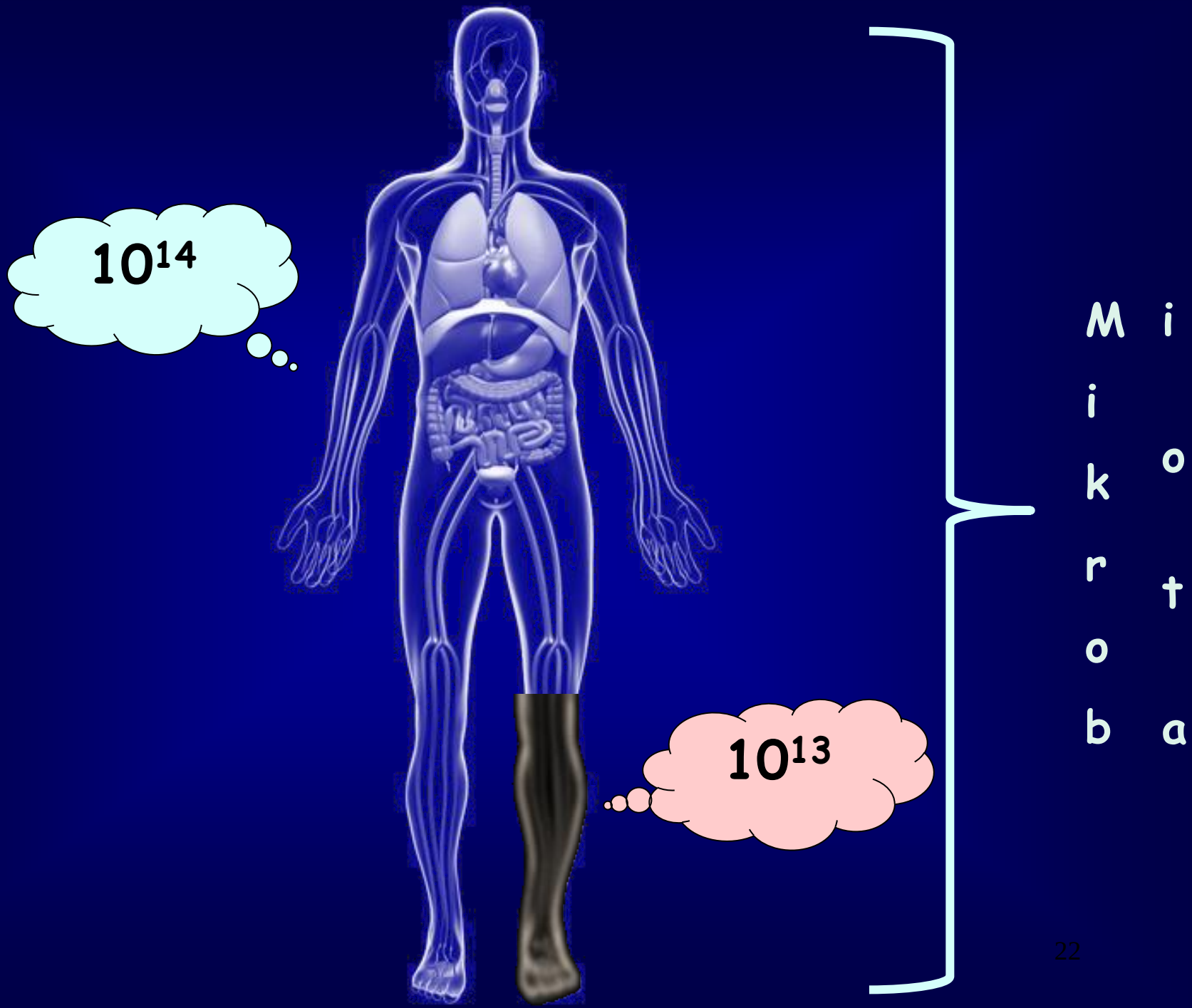
The mammalian metabolome +
- Processing of nutrients
- Degradation of xenobiotics
- Protection from new microbes
- Regulation of epithelial homeostasis

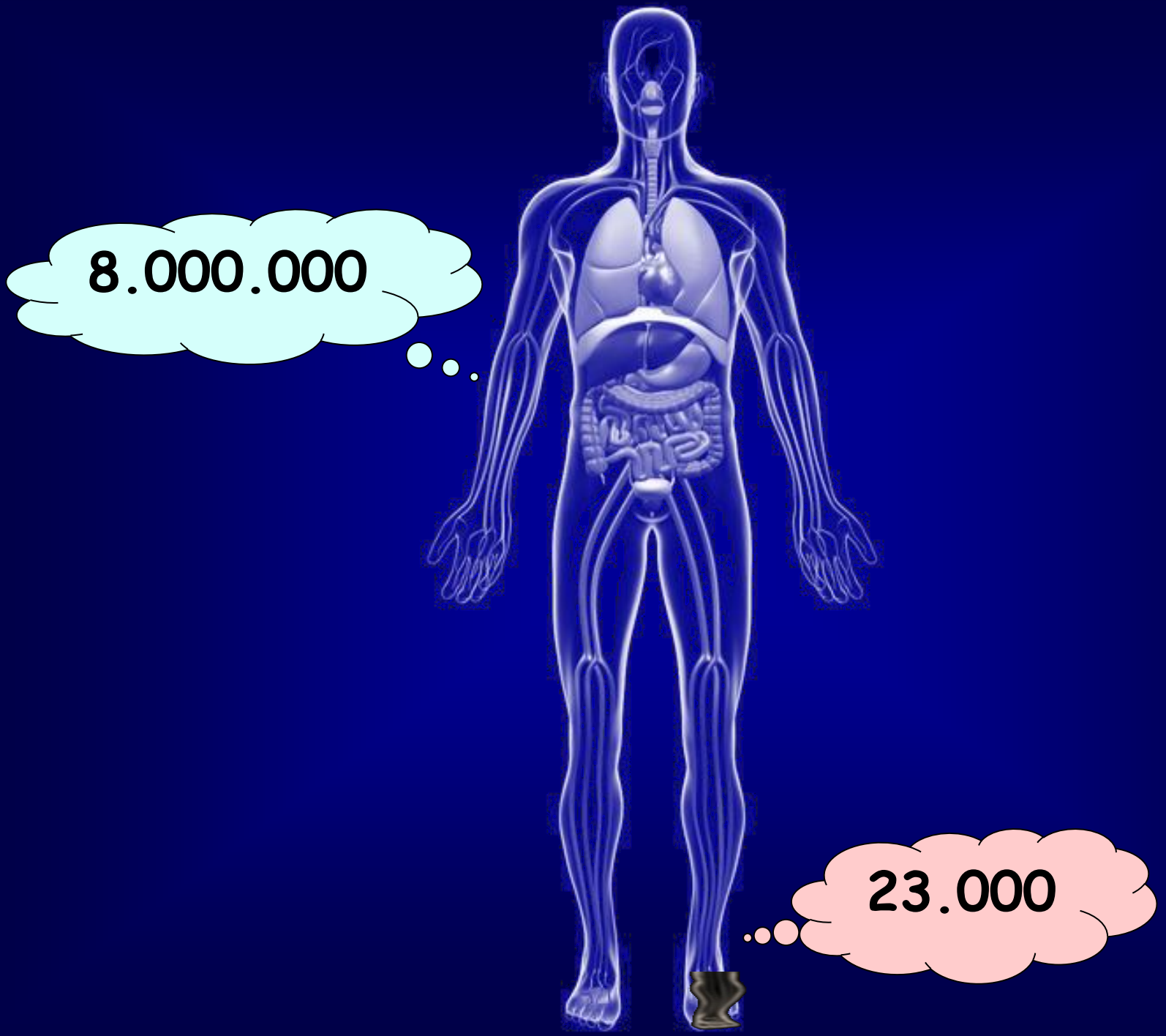
Optimal fitness

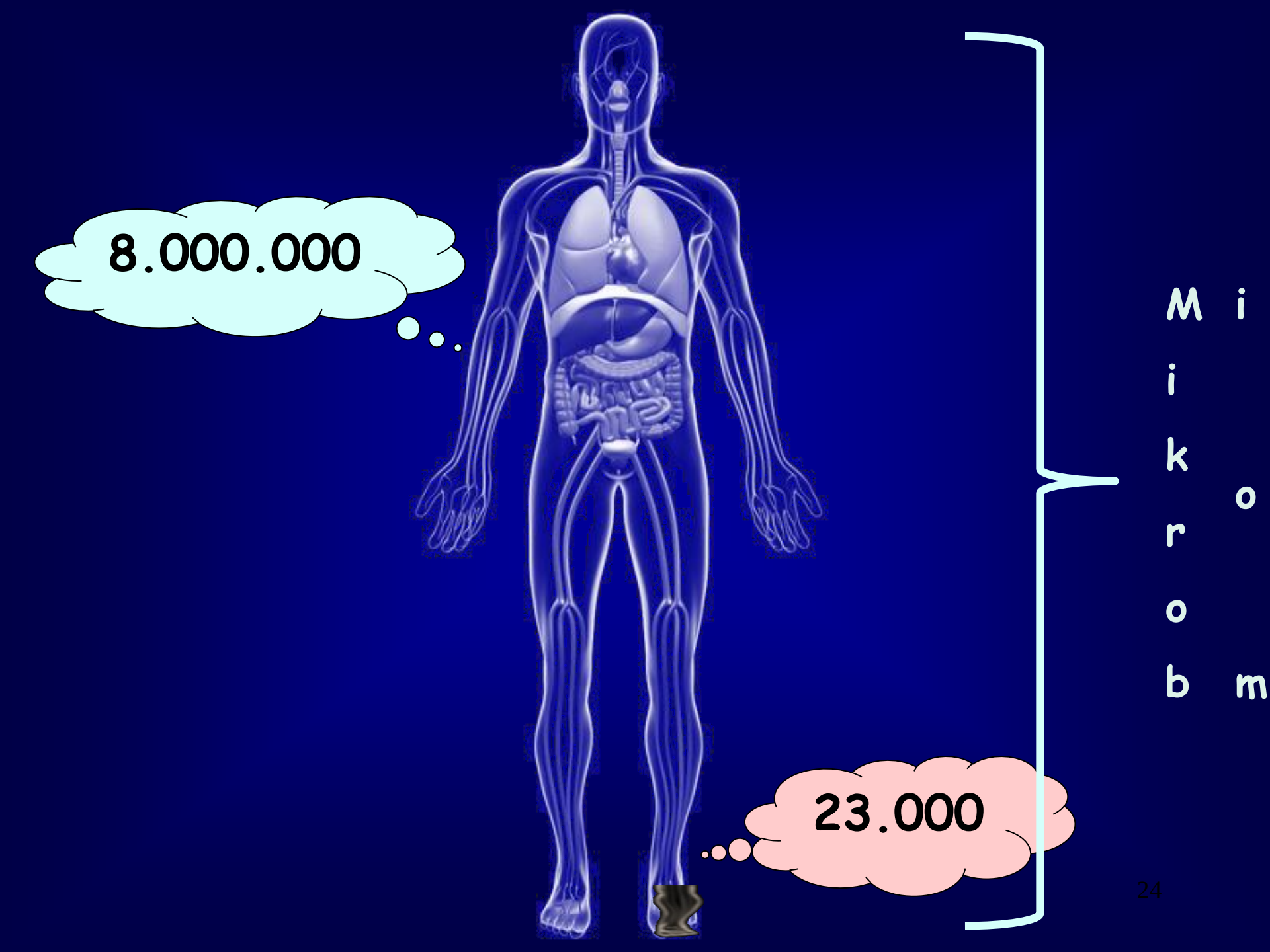
Mucosal Immunol 2010;3: 450




10^{14}
10^{13}


10^{14}
10^{13}
Mikroba


8.000.000
23.000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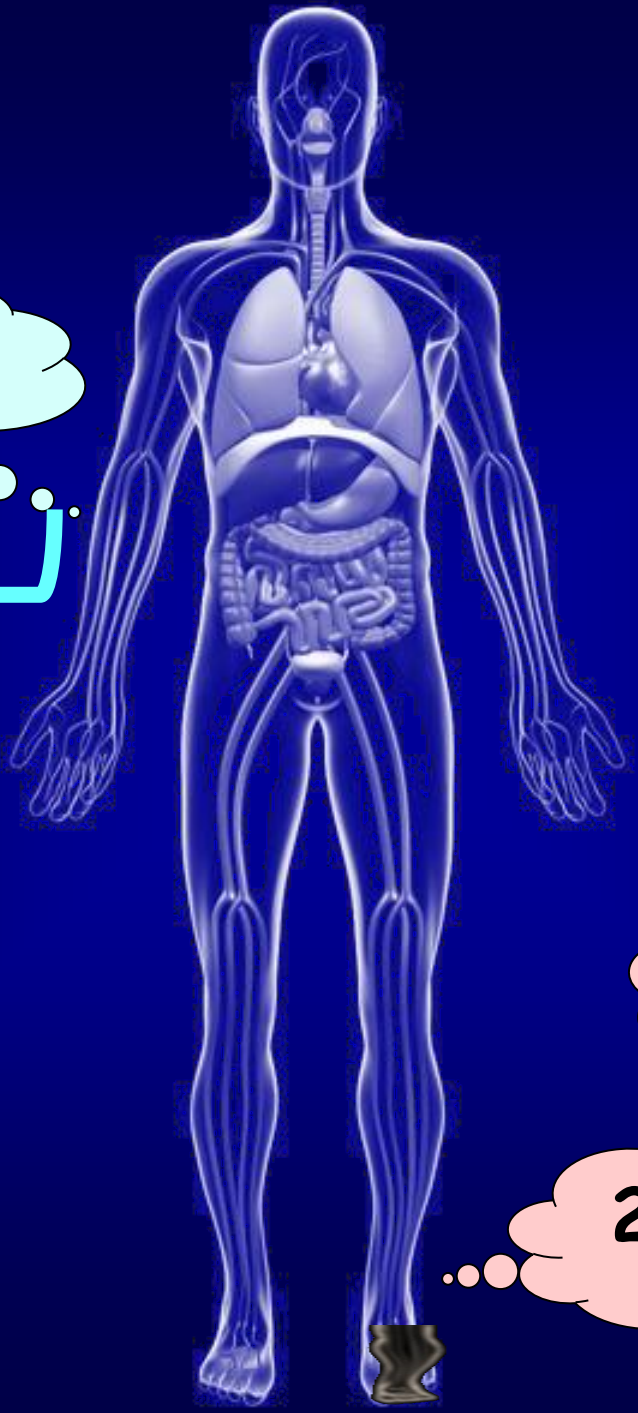
Mikrobom

10^{14}

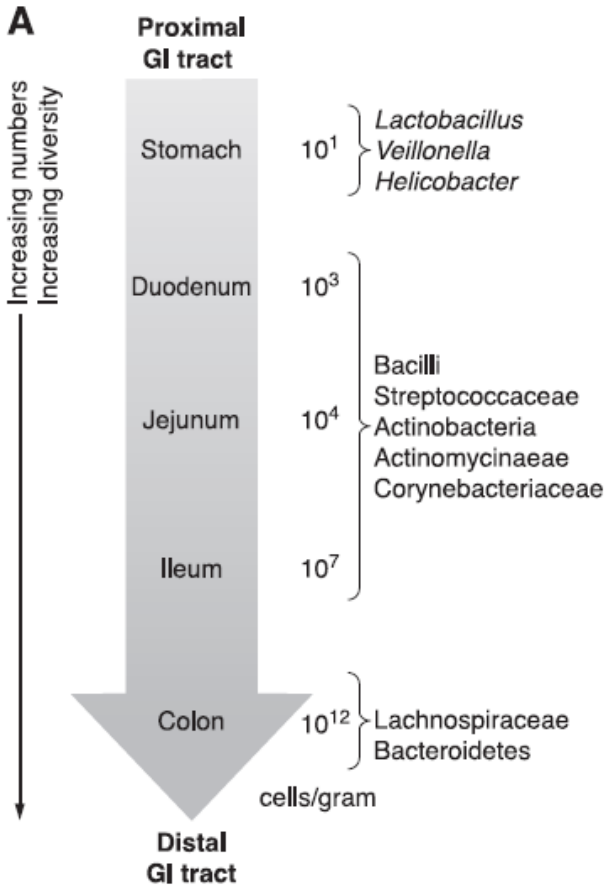
8.000.000

Fonksiyonel bir organımız



10^{13}

23.000



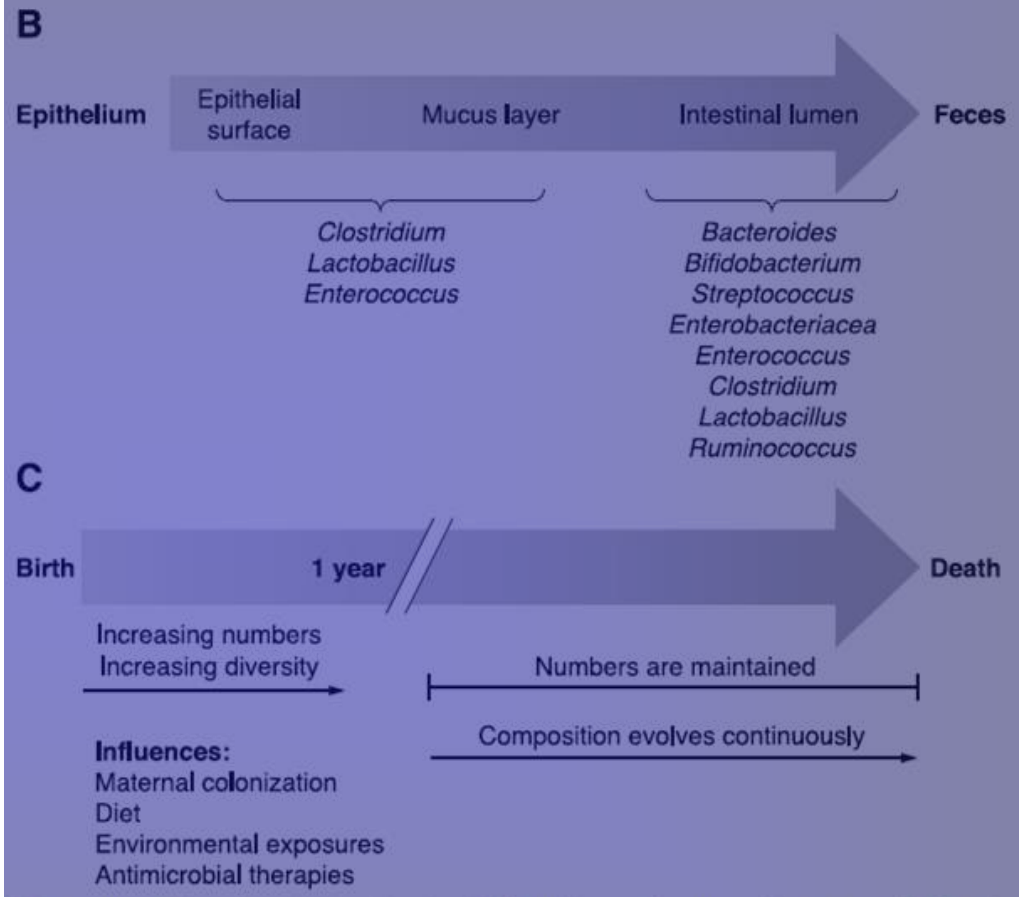
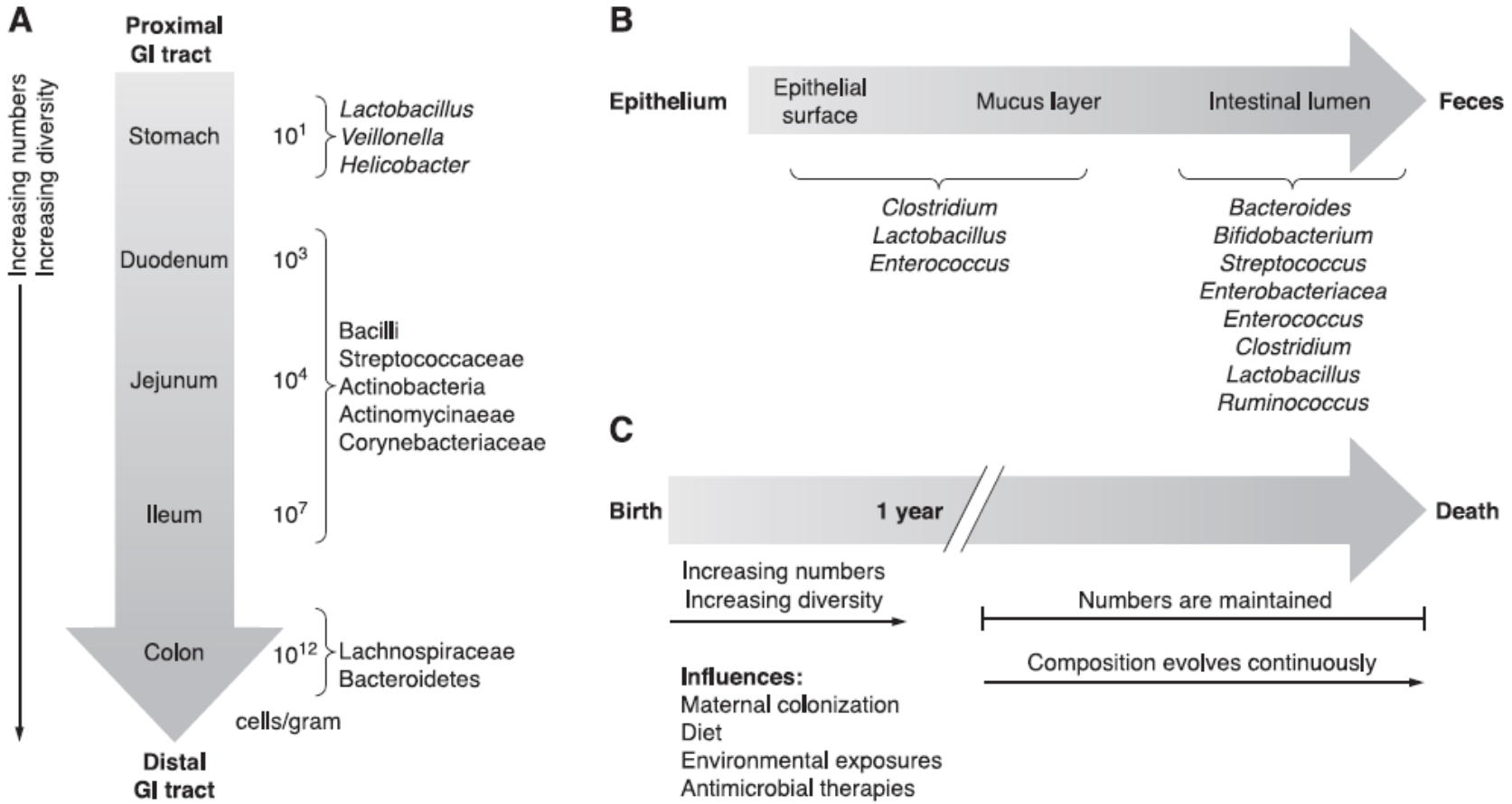


FIG. 2. Spatial and temporal aspects of intestinal microbiota composition. *A*: variations in microbial numbers and composition across the length of the gastrointestinal tract. *B*: longitudinal variations in microbial composition in the intestine. *C*: temporal aspects of microbiota establishment and maintenance and factors influencing microbial composition.



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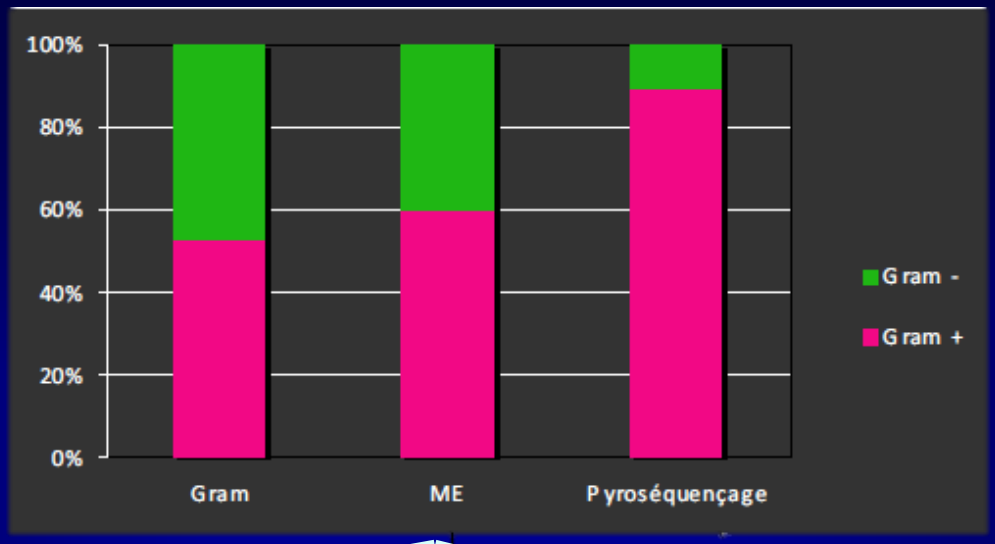
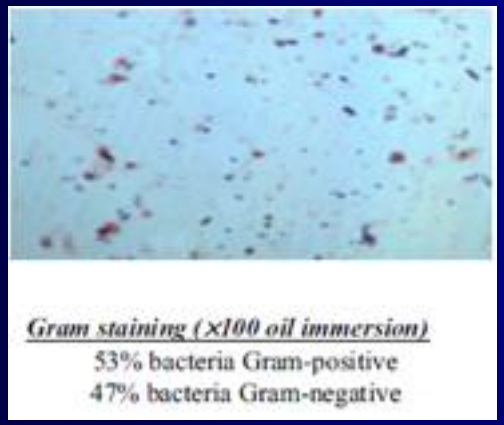
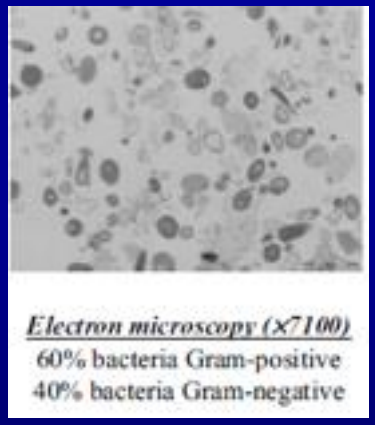




Gram staining (×100 oil immersion)
53% bacteria Gram-positive
47% bacteria Gram-negative



Electron microscopy (×7100)
60% bacteria Gram-positive
40% bacteria Gram-negative

Phylum	Reads	%
Firmicutes	44769	71.12
Actinobacteria	5797	9.21
Other	6627	10.53
Bacteroidetes	3983	6.33
Proteobacteria	1747	2.78
Cyanobacteria	21	0.03
Verrucomicrobia	4	0.01
Total	62948	100

A comparison of Gram staining, electron microscopy, and pyrosequencing to determine the proportion of Gram-positive/Gram-negative bacteria in the same stool sample.

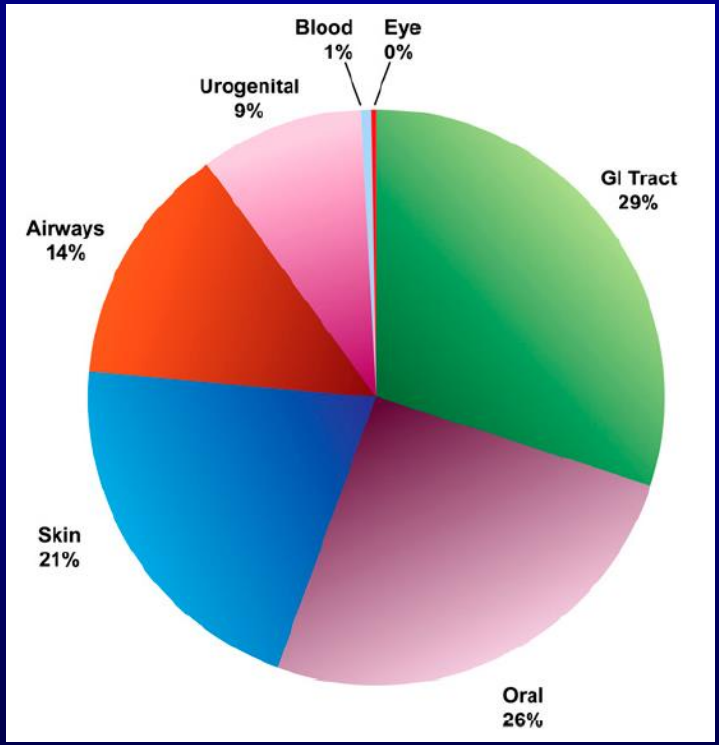
Lagier JL et al: 2012

The NIH Human Microbiome Project

The NIH HMP Working Group[1]

The Human Microbiome Project (HMP), funded as an initiative of the NIH Roadmap for Biomedical Research (http://nihroadmap.nih.gov), is a multi-component community resource. 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; and (3) to provide both a standardized data resource and new technological approaches to enable such studies to be undertaken broadly in the scientific community. The ethical, legal, and social implications of such research are being systematically studied as well. The ultimate

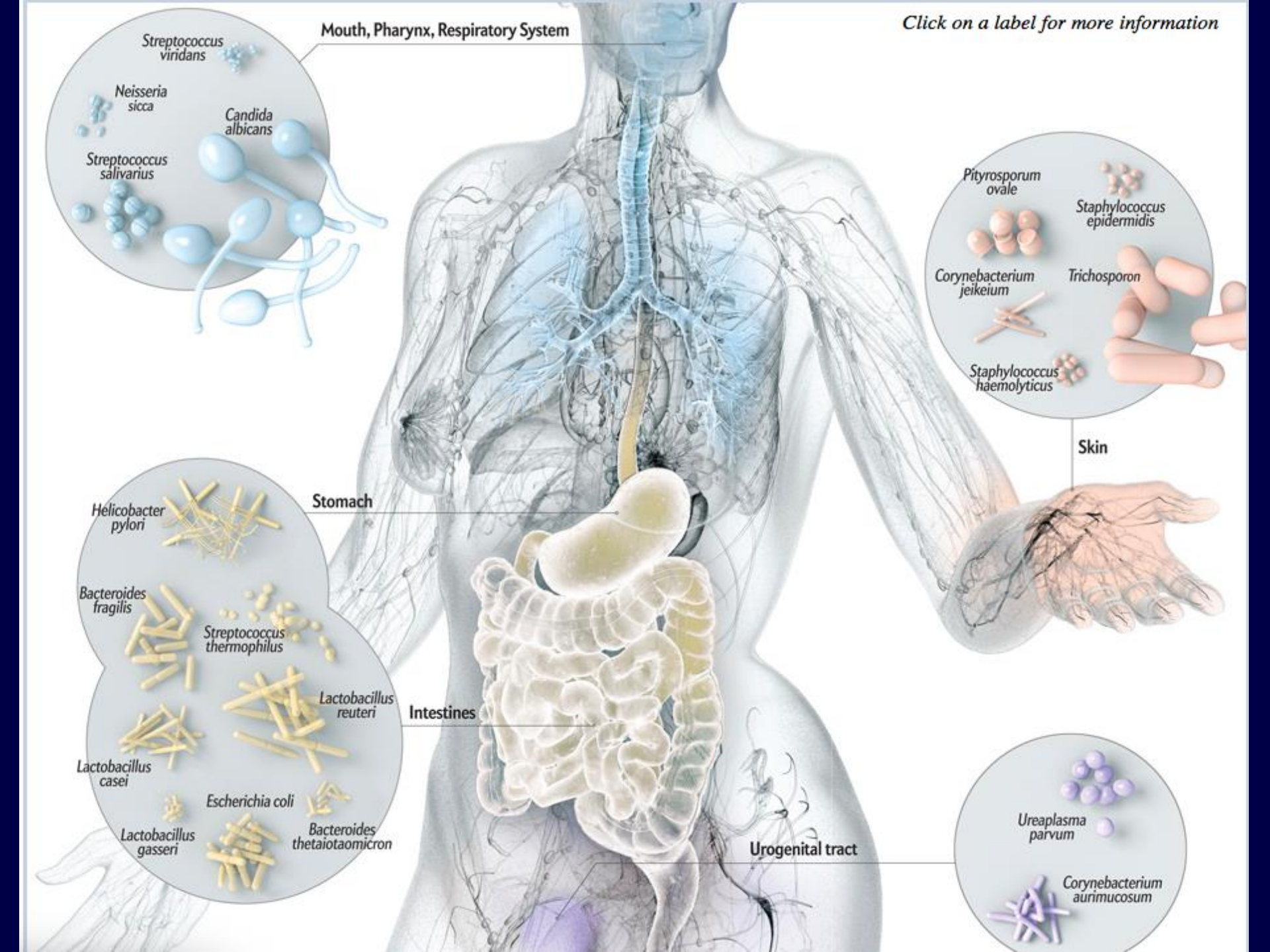
NIH Jumpstart Program	USA
MetaHIT, Metagenomics of the Human Intestinal Tract	EU
MicroObes, Human Intestinal Microbiome in Obesity and Nutritional Transition	France
DACC, Data Analysis and Coordination Center	USA



CMI, Canadian Human Microbiome Initiative	Canada
The Australian Jumpstart Human Microbiome Project	AU
HMP, NIH Human Microbiome Project	USA
Korean Microbiome Diversity, using Korean Twin Cohort Project	Korea

Gut 2013;62:146

Genome Research 2009;19: 2317

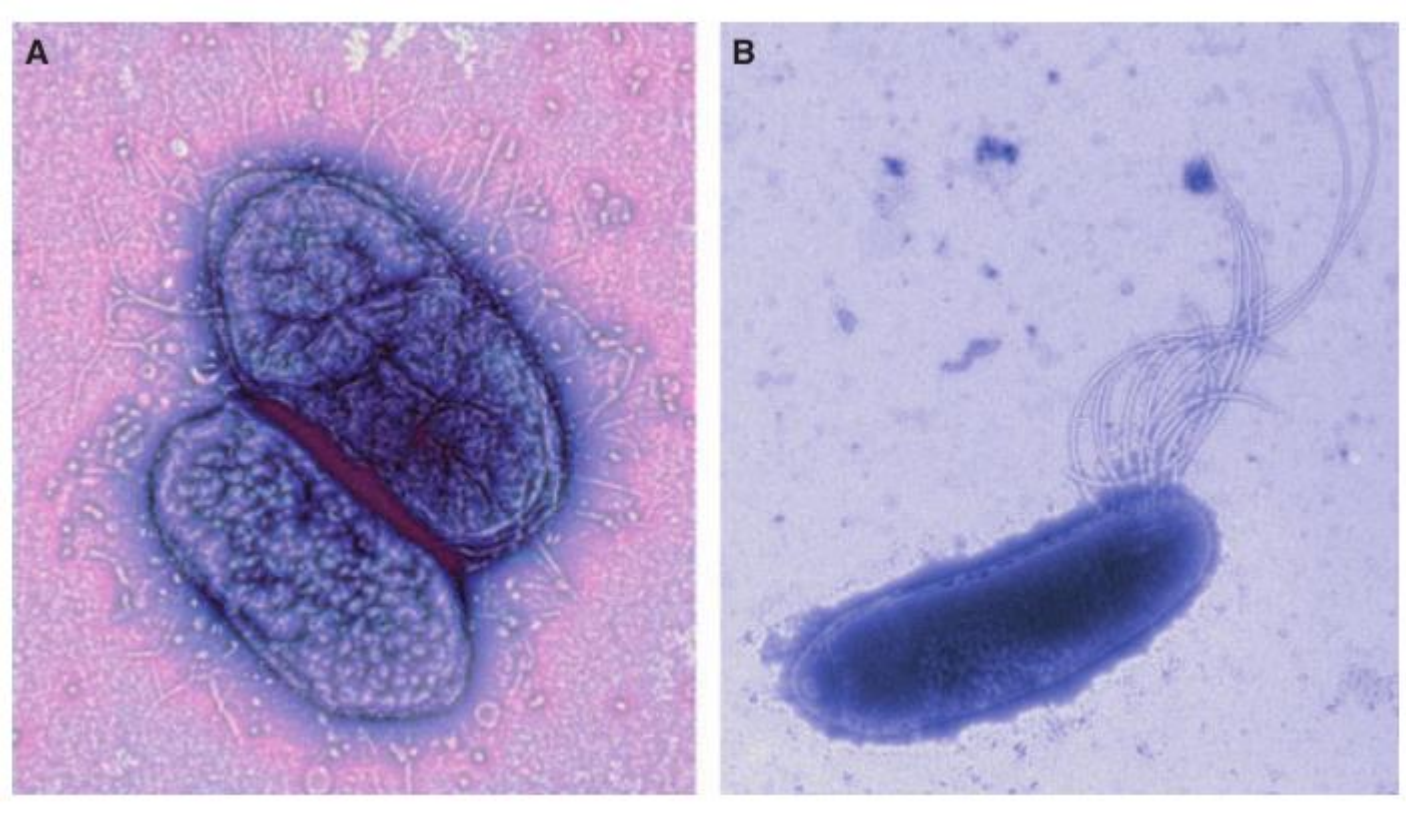

Click on a label for more information
Mouth, Pharynx, Respiratory System
Streptococcus viridans
Neisseria sicca
Candida albicans
Streptococcus salivarius
Pityrosporum ovale
Staphylococcus epidermidis
Corynebacterium jeikeium
Trichosporon
Staphylococcus haemolyticus
Skin
Stomach
Helicobacter pylori
Bacteroides fragilis
Streptococcus thermophilus
Lactobacillus reuteri
Intestines
Lactobacillus casei
Escherichia coli
Lactobacillus gasseri
Bacteroides thetaiotaomicron
Urogenital tract
Ureaplasma parvum
Corynebacterium aurimucosum

İnsan barsak mikrobiyotası bakteriyel bileşenleri

Filum	Kısa tanım	Bileşenler
Firmicutes	G (+); zorunlu anaerop; ileri derecede çeşitli; çoğu üretilemiyor; sıklıkla bol miktarda	Lachnospiraceae Ruminococcaceae Öteki Firmikütler Segmentli filamentöz bakteriler(?)
Bacteroidetes	G (-); zorunlu anaerop; sıklıkla bol miktarda	Alistipes, Bacteroides, Barnesiella, Prevotella, Parabacteroides
Actinobacteria	G (+); zorunlu anaerop ya da mikroaerofil; kimi cinsleri infantlarda bol	Atopobium, Bifidobacterium, Collinsella, Eggerthella
Proteobacteria	G (-); başlıca fakültatif anaerop ; birçok patojen türü içerir	Alcaligenes, Bilophila, Campylobacter, Escherichia, Enterobacter, Desulfovibrio, Hafnia, Helicobacter, Proteus, Klebsiella,Sutterella vb.
Diğerleri	Genellikle az sayıdadırlar	Akkermansia, Fusobacterium, Victivallis

Bacteroidetes

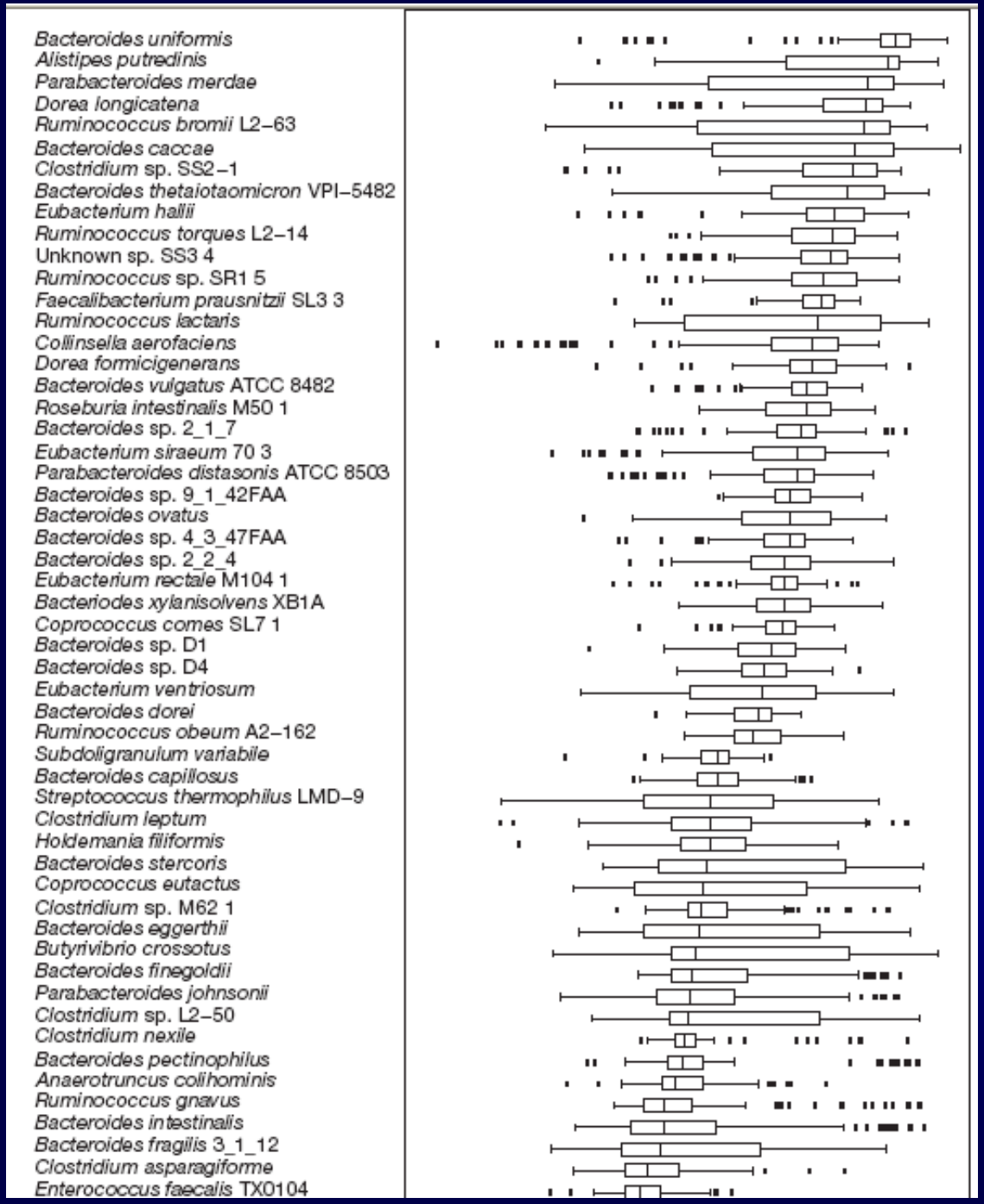
Firmicutes



Bacteroides thetaiotaomicron

Roseburia intestinalis

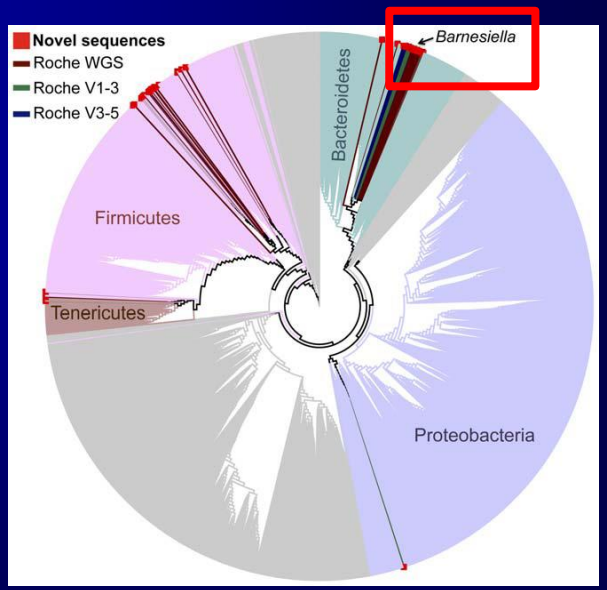
Immunol Rev 2012; 245: 27



A human gut microbial gene catalogue established by metagenomic sequencing

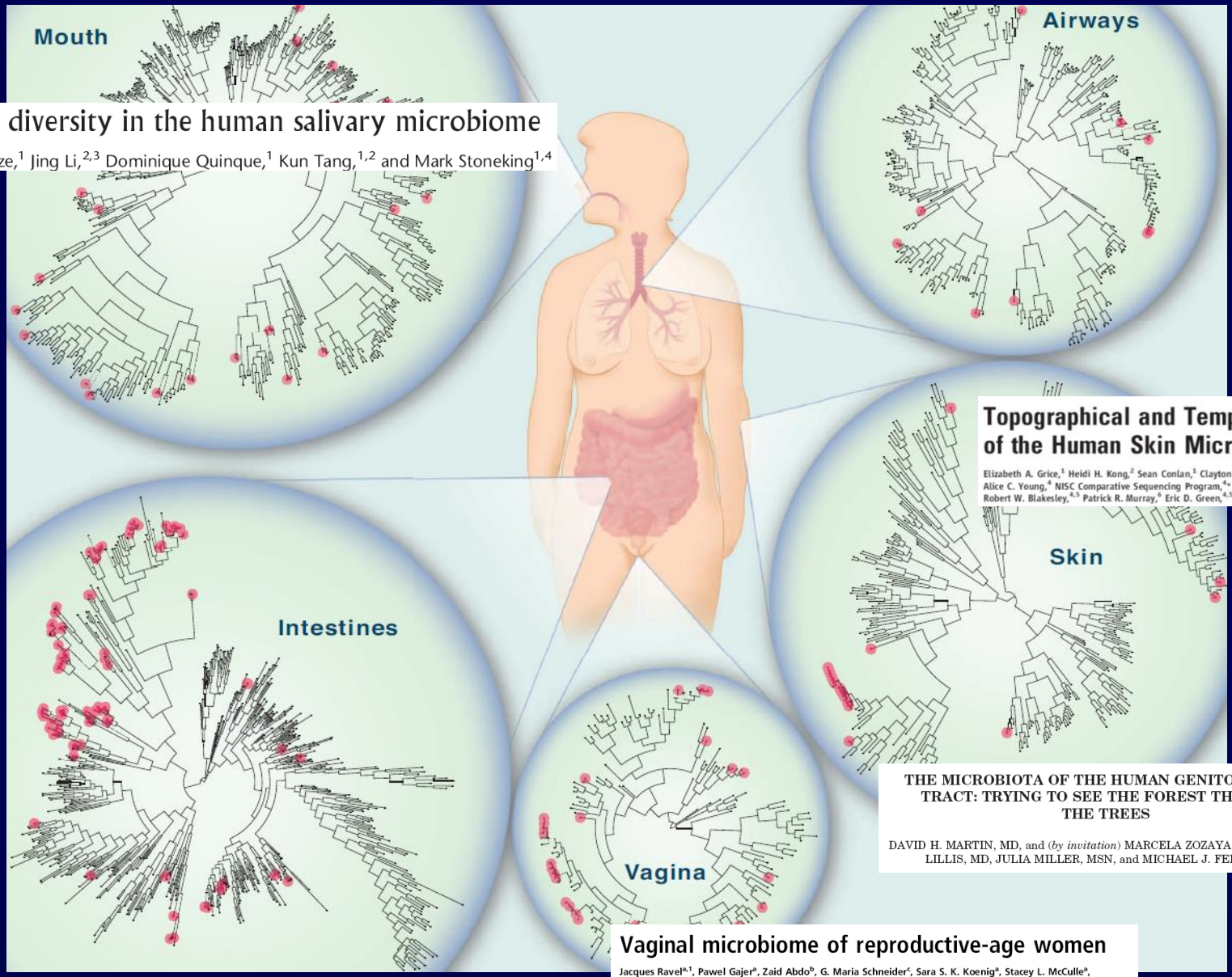
Junjie Qin[1]*, Ruiqiang Li[1]*, Jeroen Raes[2,3], Manimozhiyan Arumugam[2], Kristoffer Solvsten Burgdorf[4], Chaysavanh Manichanh[5], Trine Nielsen[4], Nicolas Pons[6], Florence Levenez[6], Takuji Yamada[2], Daniel R. Mende[2], Junhua Li[1,7], Junming Xu[1], Shaochuan Li[1], Dongfang Li[1,8], Jianjun Cao[1], Bo Wang[1], Huiqing Liang[1], Huisong Zheng[1], Yinlong Xie[1,7], Julien Tap[6], Patricia Lepage[6], Marcelo Bertalan[9], Jean-Michel Batto[6], Torben Hansen[4], Denis Le Paslier[10], Allan Linneberg[11], H. Bjørn Nielsen[9], Eric Pelletier[10], Pierre Renault[6], Thomas Sicheritz-Ponten[9], Keith Turner[12], Hongmei Zhu[1], Chang Yu[1], Shengting Li[1], Min Jian[1], Yan Zhou[1], Yingrui Li[1], Xiuqing Zhang[1], Songgang Li[1], Nan Qin[1], Huanming Yang[1], Jian Wang[1], Søren Brunak[9], Joel Doré[6], Francisco Guarner[5], Karsten Kristiansen[1,3], Oluf Pedersen[4,14], Julian Parkhill[12], Jean Weissenbach[10], MetaHIT Consortium†, Peer Bork[2], S. Dusko Ehrlich[6] & Jun Wang[1,13]

Nature 2010;464: 59



PLoS One 2012;7: e35294

Mikrobiota Sadece Barsakta Değil…



Global diversity in the human salivary microbiome

Ivan Nasidze,[1] Jing Li,[2,3] Dominique Quinque,[1] Kun Tang,[1,2] and Mark Stoneking[1,4]

Topographical and Temporal Diversity of the Human Skin Microbiome

Elizabeth A. Grice,[1] Heidi H. Kong,[2] Sean Conlan,[1] Clayton B. Deming,[1] Joie Davis,[3] Alice C. Young,[4] NISC Comparative Sequencing Program,[4+] Gerard G. Bouffard,[4,5] Robert W. Blakesley,[4,5] Patrick R. Murray,[6] Eric D. Green,[4,5] Maria L. Turner,[2] Julia A. Segre[1]†

THE MICROBIOTA OF THE HUMAN GENITOURINARY TRACT: TRYING TO SEE THE FOREST THROUGH THE TREES

DAVID H. MARTIN, MD, and (*by invitation*) MARCELA ZOZAYA, PhD, REBECCA LILLIS, MD, JULIA MILLER, MSN, and MICHAEL J. FERRIS, PhD

Vaginal microbiome of reproductive-age women

Jacques Ravel[a,1], Pawel Gajer[a], Zaid Abdo[b], G. Maria Schneider[c], Sara S. K. Koenig[a], Stacey L. McCulle[a], Shara Karlebach[d], Reshma Gorle[e], Jennifer Russell[f], Carol O. Tacket[f], Rebecca M. Brotman[a], Catherine C. Davis[g], Kevin Ault[d], Ligia Peralta[e], and Larry J. Forney[c,1]

Science 2010;330: 1768

Mikrobiota da Sadece Bakteriler Yer Almaz…

The human gut virome: Inter-individual variation and dynamic response to diet

Samuel Minot,[1] Rohini Sinha,[1] Jun Chen,[2] Hongzhe Li,[2] Sue A. Keilbaugh,[3] Gary D. Wu,[3] James D. Lewis,[2] and Frederic D. Bushman[1,4]

Genome Res 2011;21: 1616

Immense populations of viruses are present in the human gut and other body sites. Understanding the role of these populations (the human "virome") in health and disease requires a much deeper understanding of their composition and dynamics in the face of environmental perturbation. Here, we investigate viromes from human subjects on a controlled

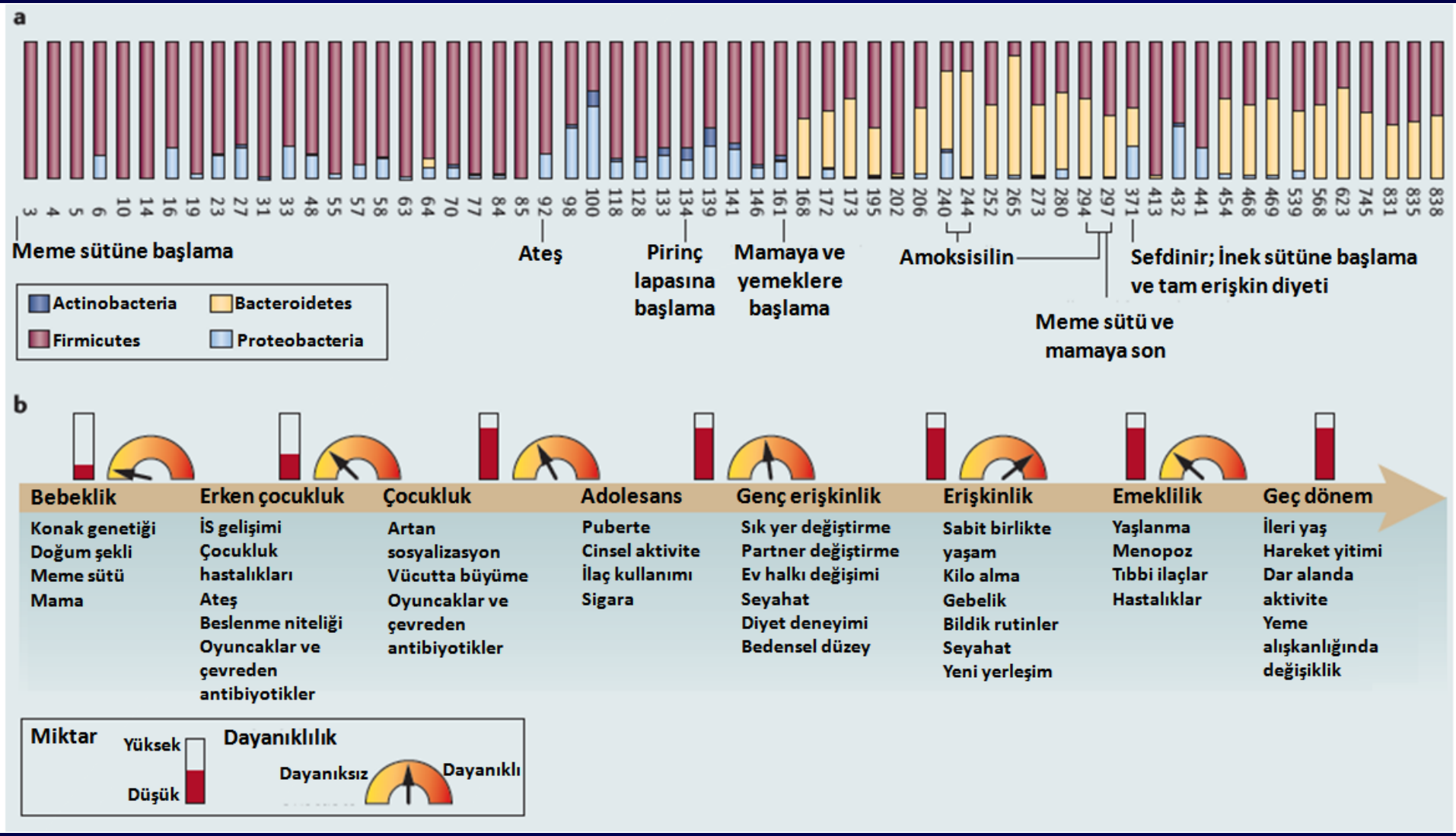
Archaea as emerging organisms in complex human microbiomes

Bédis Dridi, Didier Raoult, Michel Drancourt*

Anaerobe 2011;17:56

In this work, we review the state of knowledge of Archaea associated with the human microbiome. These prokaryotes, initially discovered in extreme environments, were named Archaea because these environments were thought to be the most primitive on Earth. Further research revealed that this terminology is misleading because these organisms were later found in various non-extreme environments, including the human host. Further examination of the human microbiome has enabled the isolation of

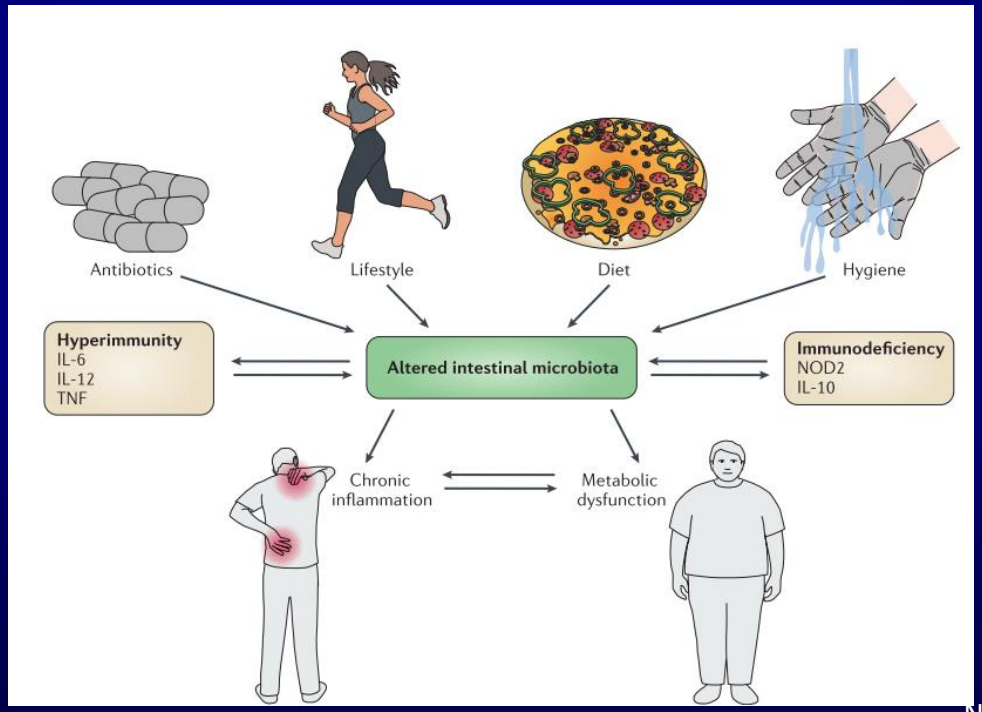
Mikrobiyotanın Gelişimi ve Barsak Mikrobiyomunu Yaşam Boyu Etkileyen Çevresel Faktörler



Nature Rev Microbiol 2011;9: 279

Mikrobiota İçeriğini Etkileyen Faktörler:

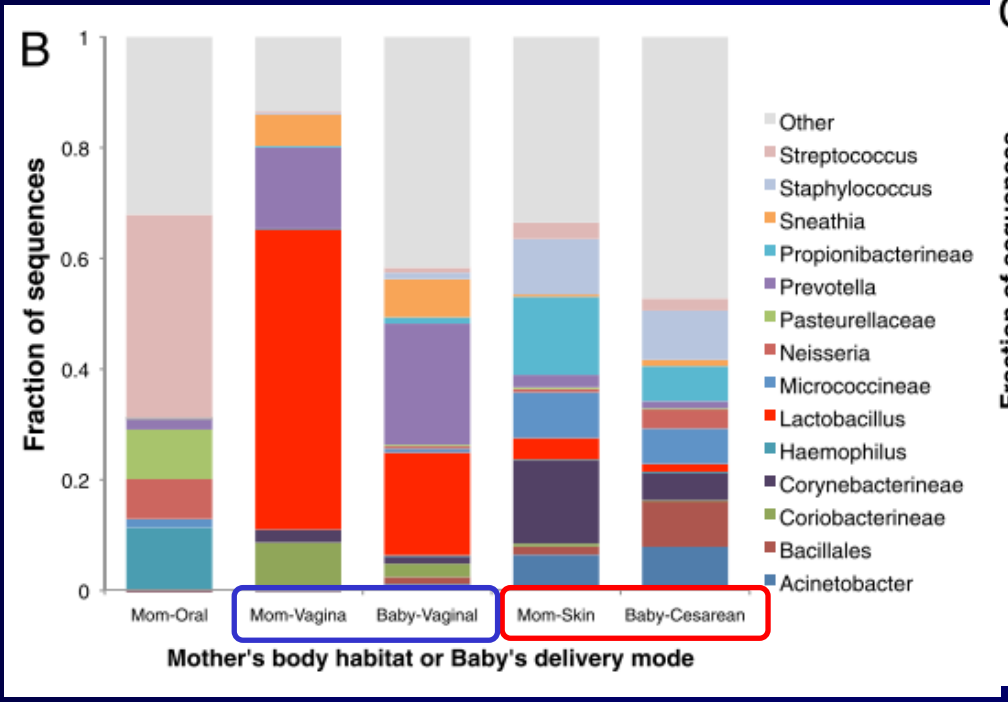
* Maternal kolonizasyon
* Yaş
* Diyet
* Çevresel temaslar
* Antimikrobiyal tedaviler

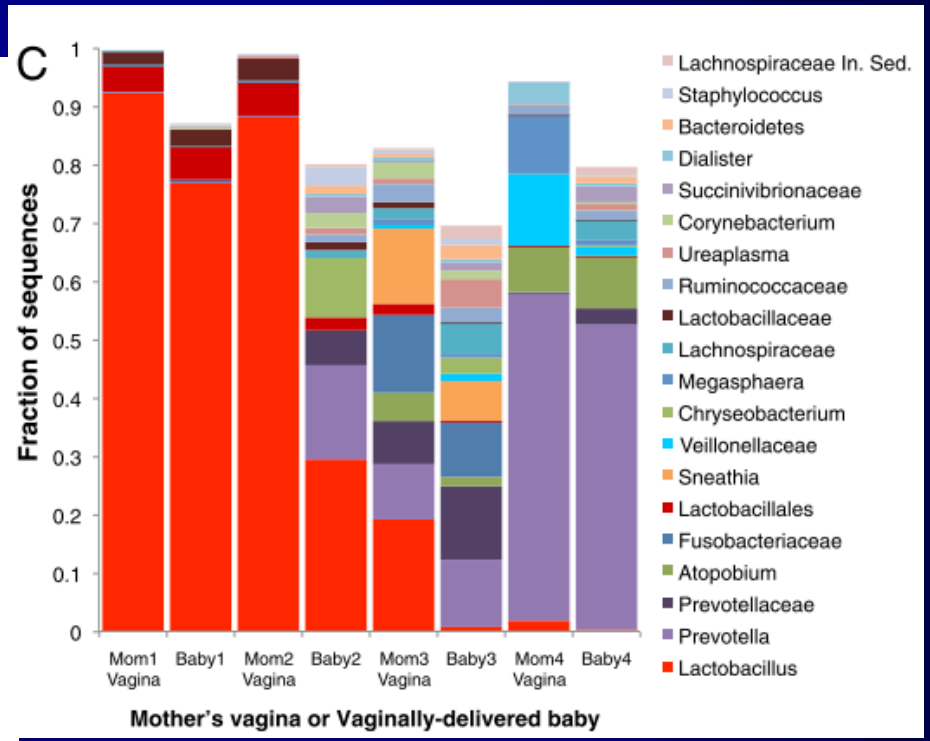


Nature Rev Microbiol 2013;11: 227

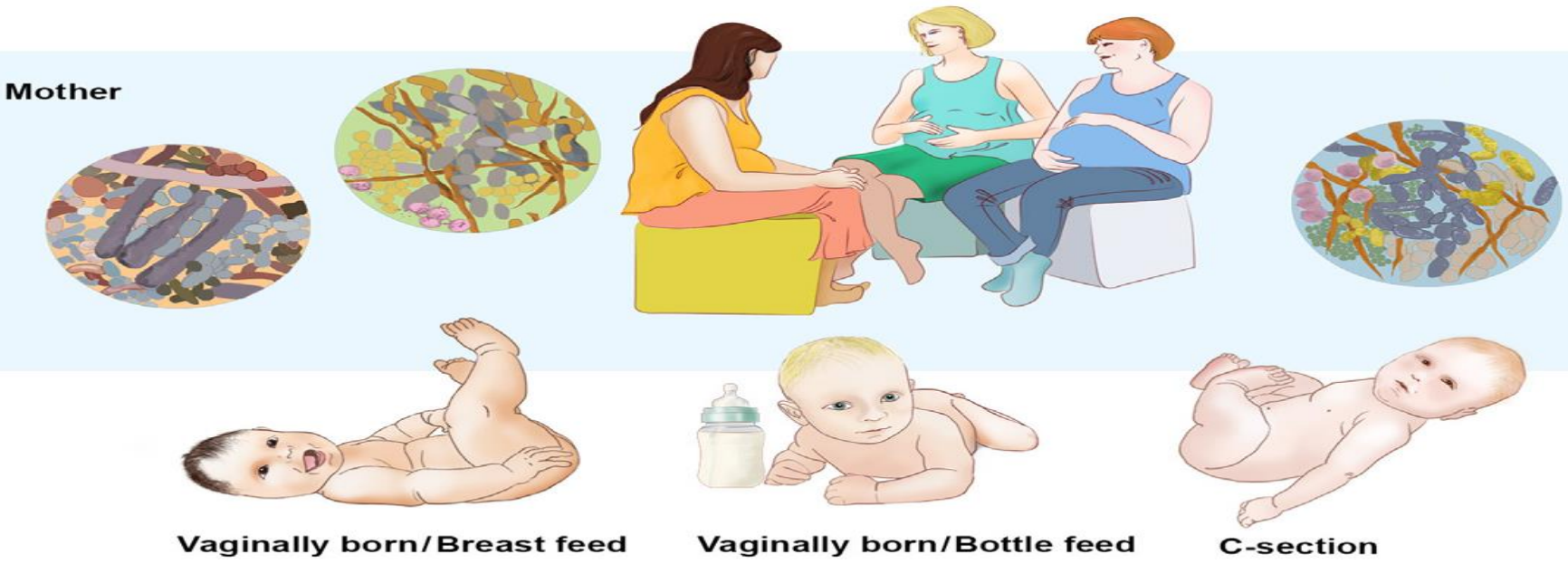
Delivery mode shapes the acquisition and structure of the initial microbiota across multiple body habitats in newborns

Maria G. Dominguez-Bello[a,1,2], Elizabeth K. Costello[b,1,3], Monica Contreras[c], Magda Magris[d], Glida Hidalgo[d], Noah Fierer[e,f], and Rob Knight[b,g]





PNAS 2010;107: 11971


Mother
Vaginally born/Breast feed
Vaginally born/Bottle feed
C-section
4 days
4 month
12 month

THE JOURNAL OF PEDIATRICS • www.jpeds.com

ORIGINAL ARTICLES

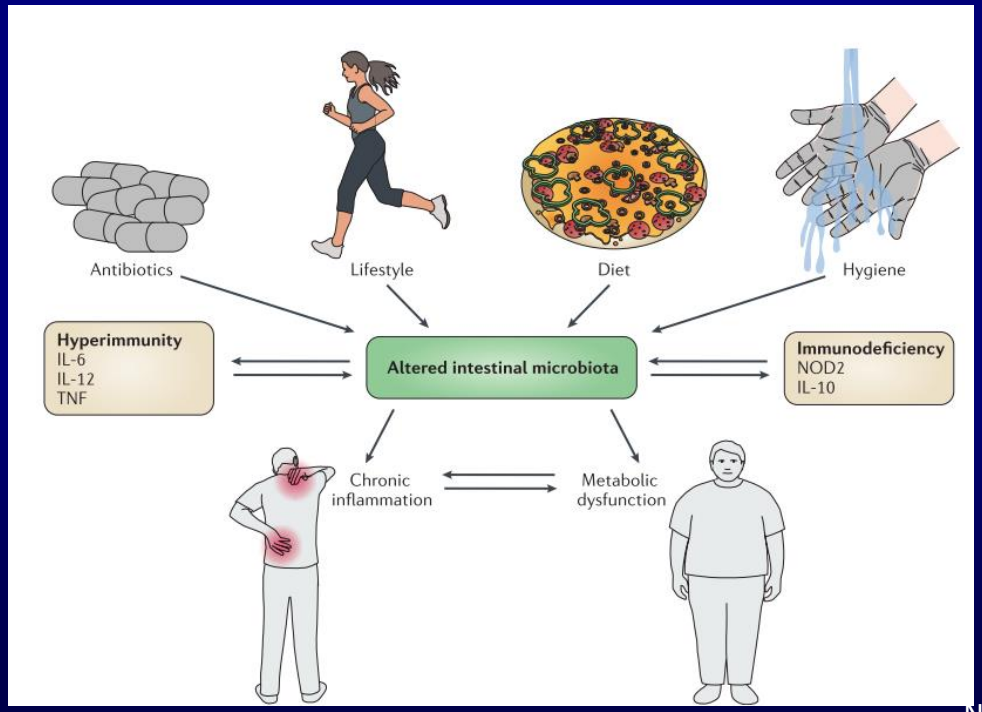
Intestinal Microbiota Development in Preterm Neonates and Effect of Perinatal Antibiotics

Silvia Arboleya, MSc[1], Borja Sánchez, PhD[1,*], Christian Milani, MSc[2], Sabrina Duranti, MSc[2], Gonzalo Solís, PhD[3], Nuria Fernández, PhD[4], Clara G. de los Reyes-Gavilán, PhD[1], Marco Ventura, PhD[2], Abelardo Margolles, PhD[1], and Miguel Gueimonde, PhD[1]

Results Immaturity affects the microbiota as indicated by a reduced percentage of the family *Bacteroidaceae* during the first months of life and by a higher initial percentage of *Lactobacillaceae* in preterm infants compared with full term infants. Perinatal antibiotics, including intrapartum antimicrobial prophylaxis, affects the gut microbiota, as indicated by increased *Enterobacteriaceae* family organisms in the infants.

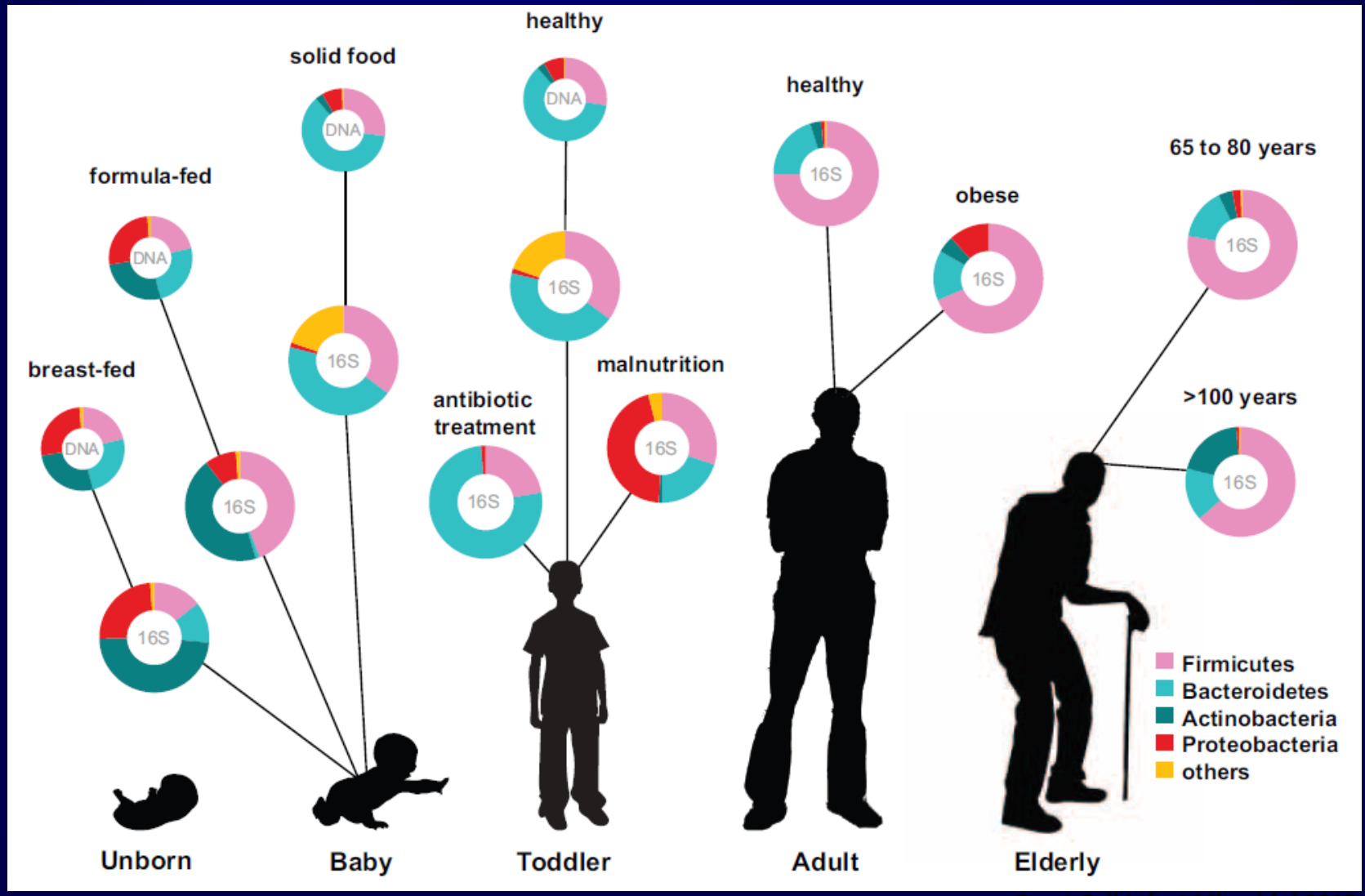
Mikrobiota İçeriğini Etkileyen Faktörler:

* Maternal kolonizasyon
* Yaş
* Diyet
* Çevresel temaslar
* Antimikrobiyal tedaviler



Nature Rev Microbiol 2013;11: 227

İnsan Mikrobiotası: Farklı Yaş dönemlerinde Değişimler



Front Cell Infect Microbiol 2012;2: 104

Mikrobiota İçeriğini Etkileyen Faktörler:

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* Diyet
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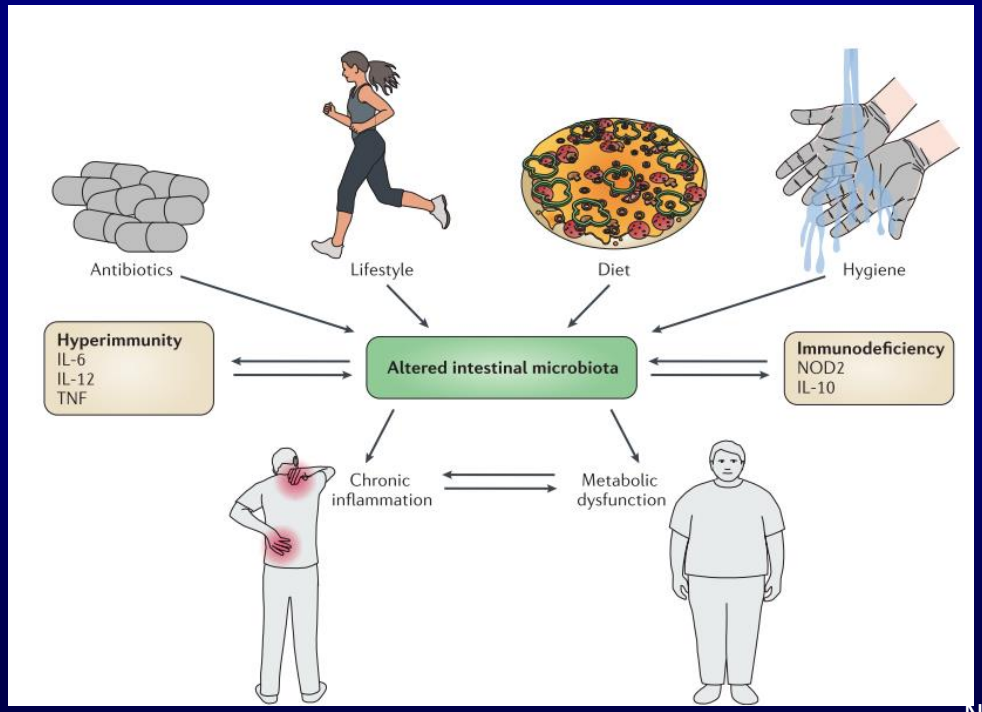
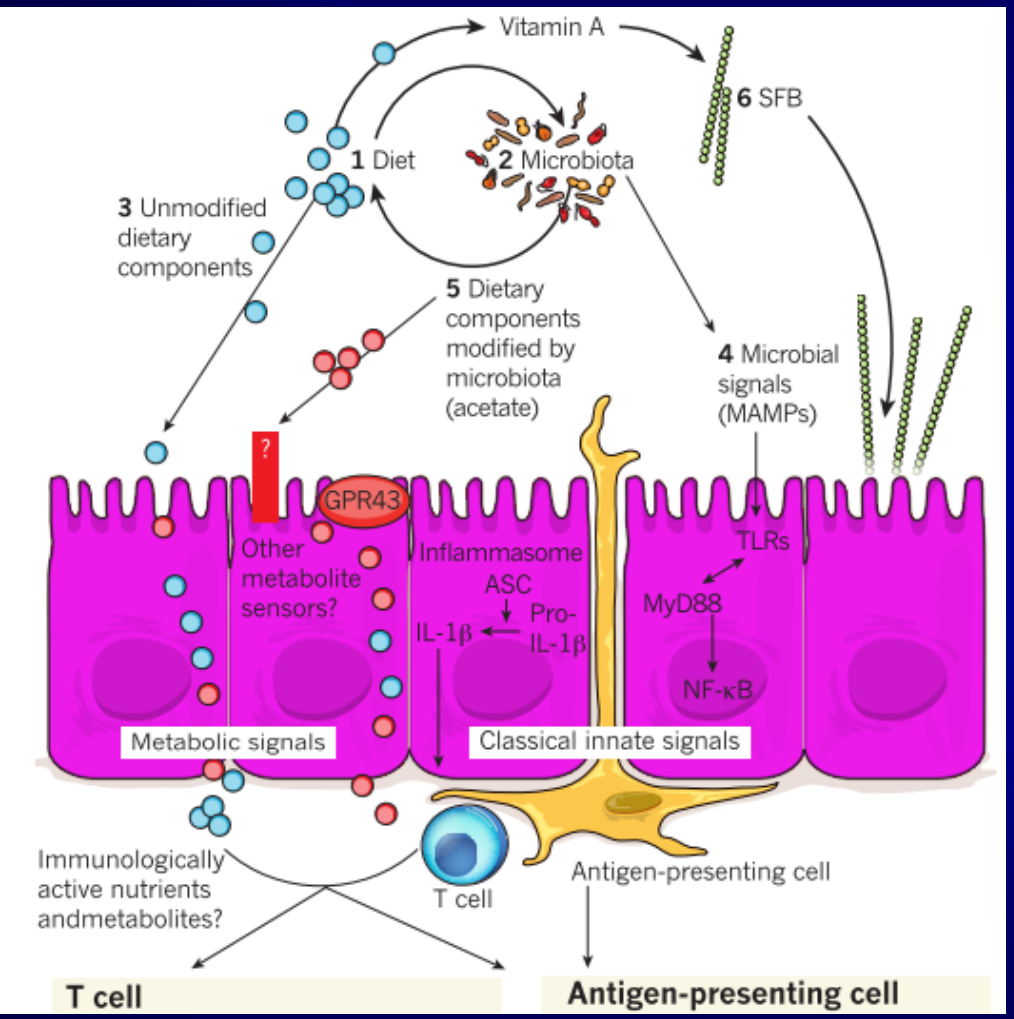


Nature Rev Microbiol 2013;11: 227

Human nutrition, the gut microbiome and the immune system

Andrew L. Kau[1]*, Philip P. Ahern[1]*, Nicholas W. Griffin[1], Andrew L. Goodman[1]† & Jeffrey I. Gordon[1]



T cell

mTOR
Promotes T_H1, T_H2, T_H17 cell differentiation; inhibits T_{reg} cell differentiation

RAR–RXR
Promotes intestinal T-cell homing; promotes T_H2 and T_{reg} cell differentiation

VDR–RXR
Promotes T_{reg} cell differentiation; inhibits T_H1 and T_H17 cell differentiation

AHR
Promotes T_H17 and T_{reg} cell differentiation

LXR and PPAR
Control T-cell differentiation

Antigen-presenting cell

TLRs

Inflammasomes

mTOR
Modulates DC function and differentiation

RAR–RXR and VDR–RXR

AHR
Modulates DC differentiation

PKR
Regulates inflammatory responses

GPR120
Inhibits inflammatory responses in macrophages

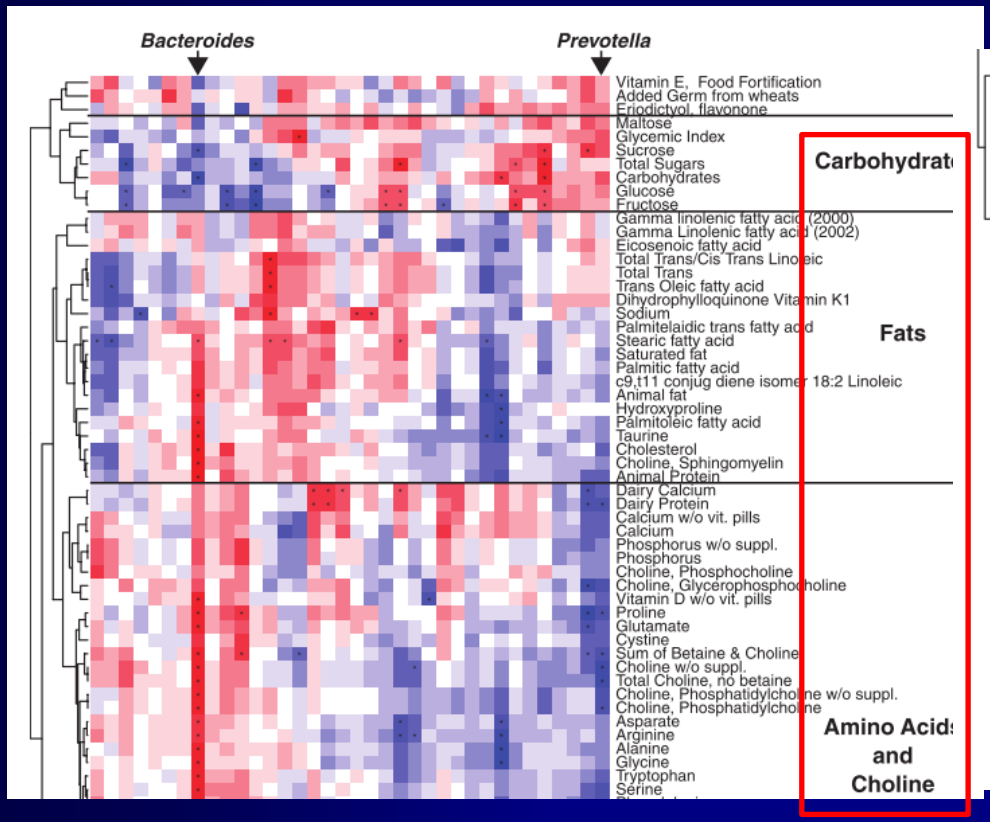
Nature 2011;474: 327

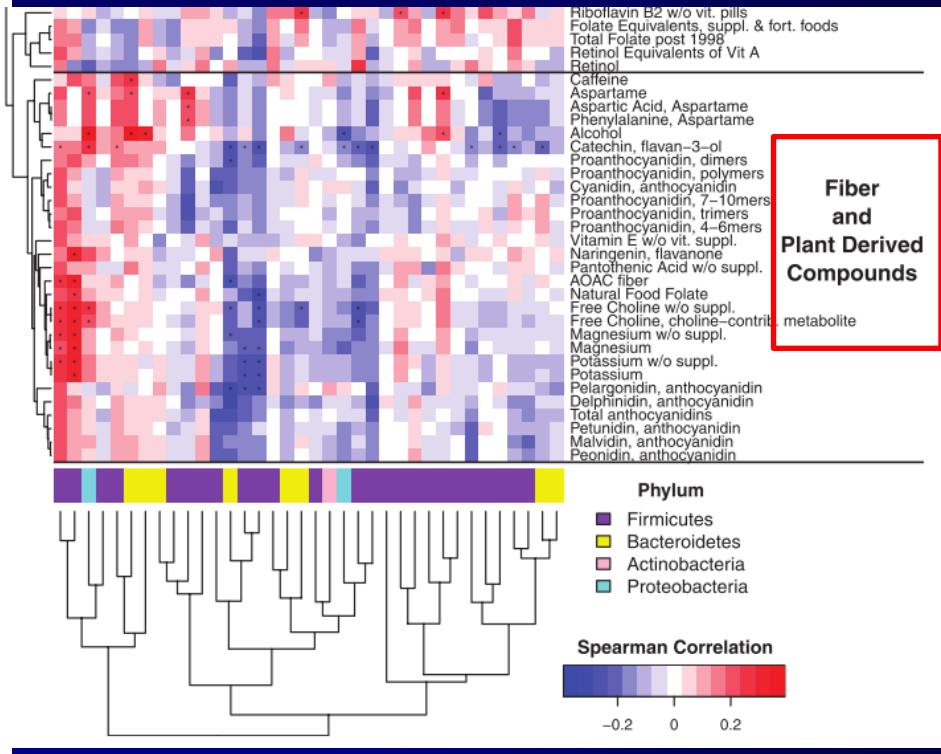
Linking Long-Term Dietary Patterns with Gut Microbial Enterotypes

Gary D. Wu,[1*] Jun Chen,[2,3] Christian Hoffmann,[4,5] Kyle Bittinger,[4] Ying-Yu Chen,[1] Sue A. Keilbaugh,[1] Meenakshi Bewtra,[1,2] Dan Knights,[6] William A. Walters,[7] Rob Knight,[8,9] Rohini Sinha,[4] Erin Gilroy,[2] Kernika Gupta,[10] Robert Baldassano,[10] Lisa Nessel,[2] Hongzhe Li,[2,3] Frederic D. Bushman,[4*] James D. Lewis[1,2,3*]

Diet strongly affects human health, partly by modulating gut microbiome composition. We used diet inventories and 16*S* rDNA sequencing to characterize fecal samples from 98 individuals. Fecal communities clustered into enterotypes distinguished primarily by levels of *Bacteroides* and *Prevotella*. Enterotypes were strongly associated with long-term diets, particularly protein and animal fat (*Bacteroides*) versus carbohydrates (*Prevotella*). A controlled-feeding study of 10 subjects showed that microbiome composition changed detectably within 24 hours of initiating a high-fat/low-fiber or low-fat/high-fiber diet, but that enterotype identity remained stable during the 10-day study. Thus, alternative enterotype states are associated with long-term diet.

Science 2011;334: 105

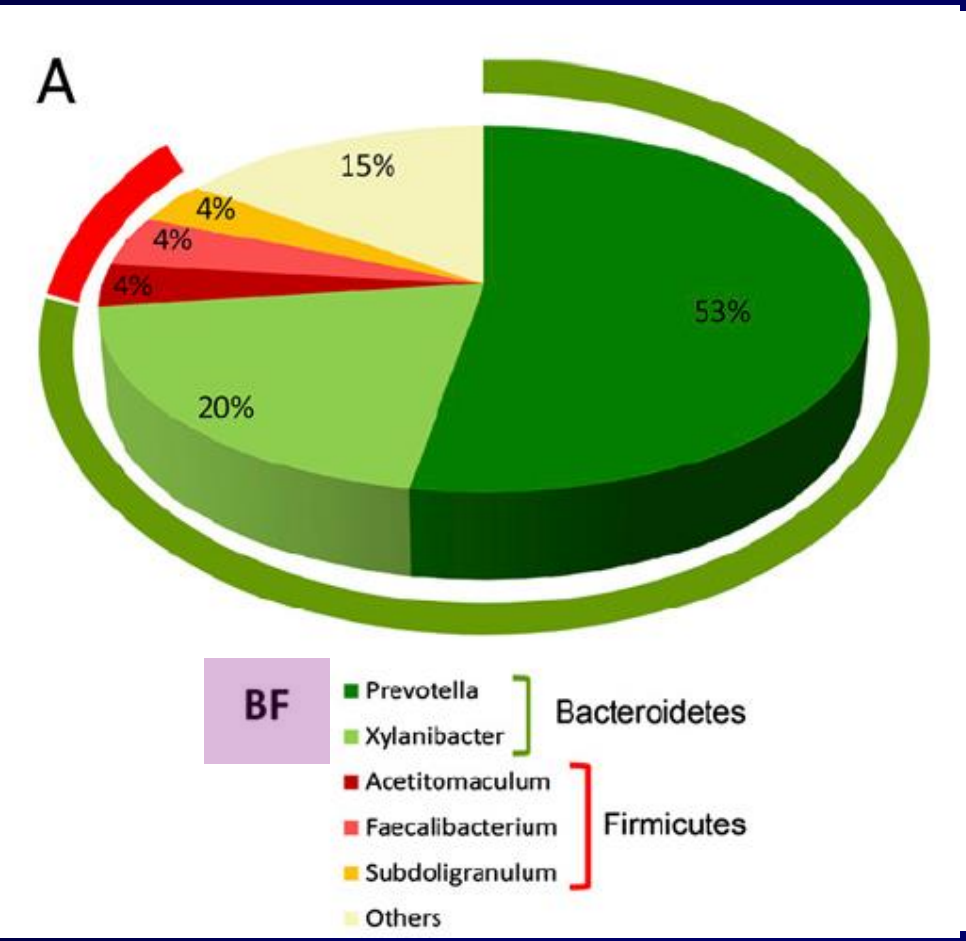

Bacteroides
Prevotella
Vitamin E, Food Fortification
Added Germ from wheats
Eriodictyol, flavonone
Maltose
Glycemic Index
Sucrose
Total Sugars
Carbohydrates
Glucose
Fructose
Carbohydrat
Gamma linolenic fatty acid (2000)
Gamma Linolenic fatty acid (2002)
Eicosenoic fatty acid
Total Trans/Cis Trans Linoleic
Total Trans
Trans Oleic fatty acid
Dihydrophylloquinone Vitamin K1
Sodium
Palmitelaidic trans fatty acid
Stearic fatty acid
Saturated fat
Palmitic fatty acid
c9,t11 conjug diene isomer 18:2 Linoleic
Animal fat
Hydroxyproline
Palmitoleic fatty acid
Taurine
Cholesterol
Choline, Sphingomyelin
Fats
Animal Protein
Dairy Calcium
Dairy Protein
Calcium w/o vit. pills
Calcium
Phosphorus w/o suppl.
Phosphorus
Choline, Phosphocholine
Choline, Glycerophosphocholine
Vitamin D w/o vit. pills
Proline
Glutamate
Cystine
Sum of Betaine & Choline
Choline w/o suppl.
Total Choline, no betaine
Choline, Phosphatidylcholine w/o suppl.
Choline, Phosphatidylcholine
Asparate
Arginine
Alanine
Glycine
Tryptophan
Serine
Amino Acids and Choline

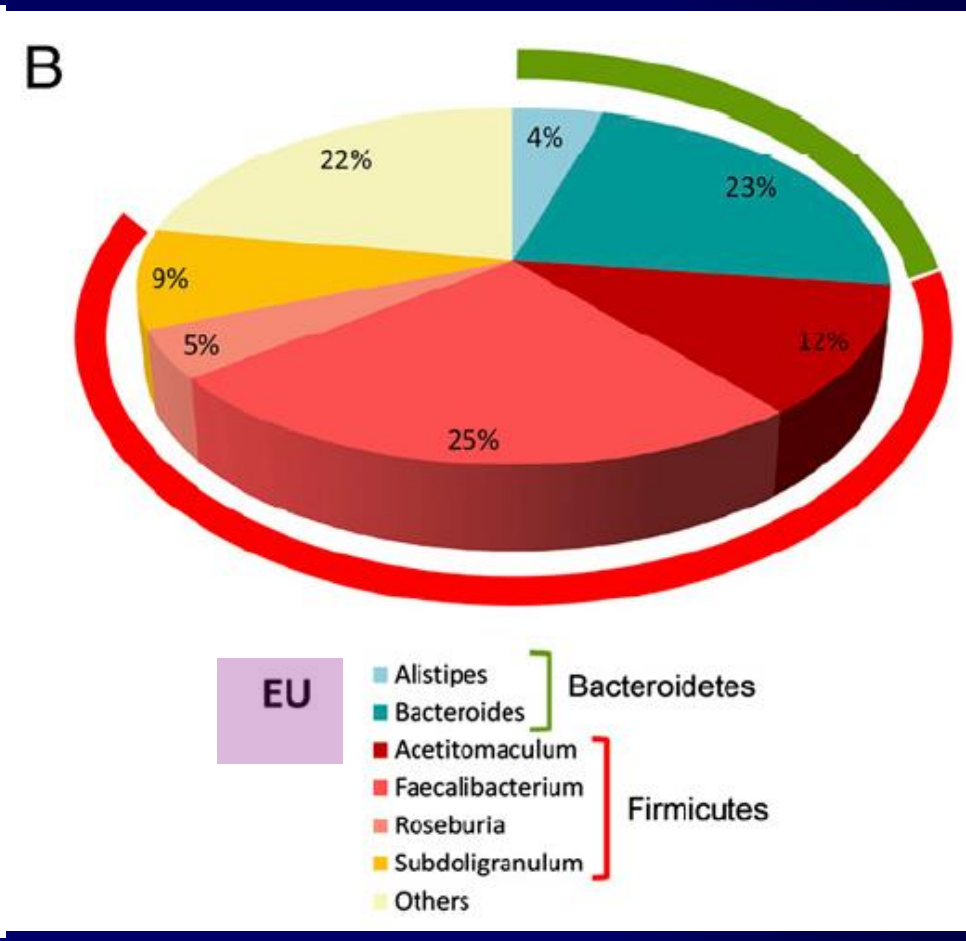

Riboflavin B2 w/o vit. pills
Folate Equivalents, suppl. & fort. foods
Total Folate post 1998
Retinol Equivalents of Vit A
Retinol
Caffeine
Aspartame
Aspartic Acid, Aspartame
Phenylalanine, Aspartame
Alcohol
Catechin, flavan−3−ol
Proanthocyanidin, dimers
Proanthocyanidin, polymers
Cyanidin, anthocyanidin
Proanthocyanidin, 7−10mers
Proanthocyanidin, trimers
Proanthocyanidin, 4−6mers
Vitamin E w/o vit. suppl.
Naringenin, flavanone
Pantothenic Acid w/o suppl.
AOAC fiber
Natural Food Folate
Free Choline w/o suppl.
Free Choline, choline−contrib. metabolite
Magnesium w/o suppl.
Magnesium
Potassium w/o suppl.
Potassium
Pelargonidin, anthocyanidin
Delphinidin, anthocyanidin
Total anthocyanidins
Petunidin, anthocyanidin
Malvidin, anthocyanidin
Peonidin, anthocyanidin
Fiber and Plant Derived Compounds
Phylum
Firmicutes
Bacteroidetes
Actinobacteria
Proteobacteria
Spearman Correlation
−0.2
0
0.2

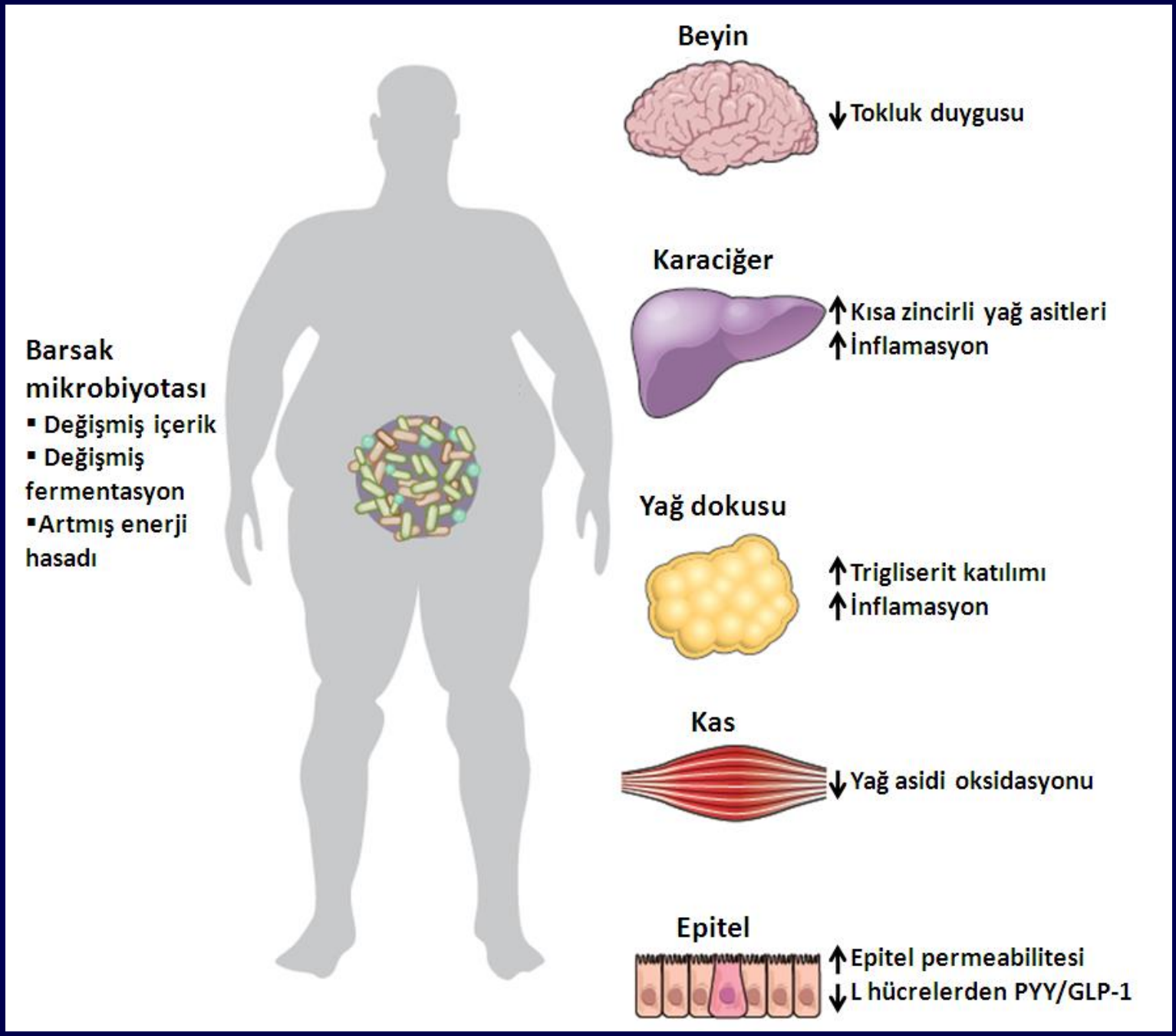
Impact of diet in shaping gut microbiota revealed by a comparative study in children from Europe and rural Africa

Carlotta De Filippo[a], Duccio Cavalieri[a], Monica Di Paola[b], Matteo Ramazzotti[c], Jean Baptiste Poullet[d], Sebastien Massart[d], Silvia Collini[b], Giuseppe Pieraccini[e], and Paolo Lionetti[b,1]

Gut microbial composition depends on different dietary habits just as health depends on microbial metabolism, but the association of microbiota with different diets in human populations has not yet been shown. In this work, we compared the fecal microbiota of European children (EU) and that of children from a rural African village of Burkina Faso (BF), where the diet, high in fiber content, is similar to that of early human settlements at the time of the birth of agriculture. By using high-throughput 16S rDNA sequencing and biochemical analyses, we found significant differences in gut microbiota between the two groups. BF children showed a significant enrichment in Bacteroidetes and depletion in Firmicutes ($P < 0.001$), with a unique abundance of bacteria from the genus *Prevotella* and *Xylanibacter*, known to contain a set of bacterial genes for cellulose and xylan hydrolysis, completely lacking in the EU children. In addition, we found significantly more short-chain fatty acids ($P < 0.001$) in BF than in EU children. Also, *Enterobacteriaceae* (*Shigella* and *Escherichia*) were significantly underrepresented in BF than in EU children ($P < 0.05$). We hypothesize that gut microbiota coevolved with the polysaccharide-rich diet of BF individuals, allowing them to maximize energy intake from fibers while also protecting them from inflammations and noninfectious colonic diseases. This study investigates and compares human intestinal microbiota from children characterized by a modern western diet and a rural diet, indicating the importance of preserving this treasure of microbial diversity from ancient rural communities worldwide.


A
15%
4%
4%
4%
53%
20%
BF
Prevotella
Xylanibacter
Bacteroidetes
Acetitomaculum
Faecalibacterium
Subdoligranulum
Firmicutes
Others


B
22%
4%
23%
9%
5%
12%
25%
EU
Alistipes
Bacteroides
Bacteroidetes
Acetitomaculum
Faecalibacterium
Roseburia
Subdoligranulum
Firmicutes
Others



Nature 2012;489: 242

Mikrobiota İçeriğini Etkileyen Faktörler:

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* Yaş
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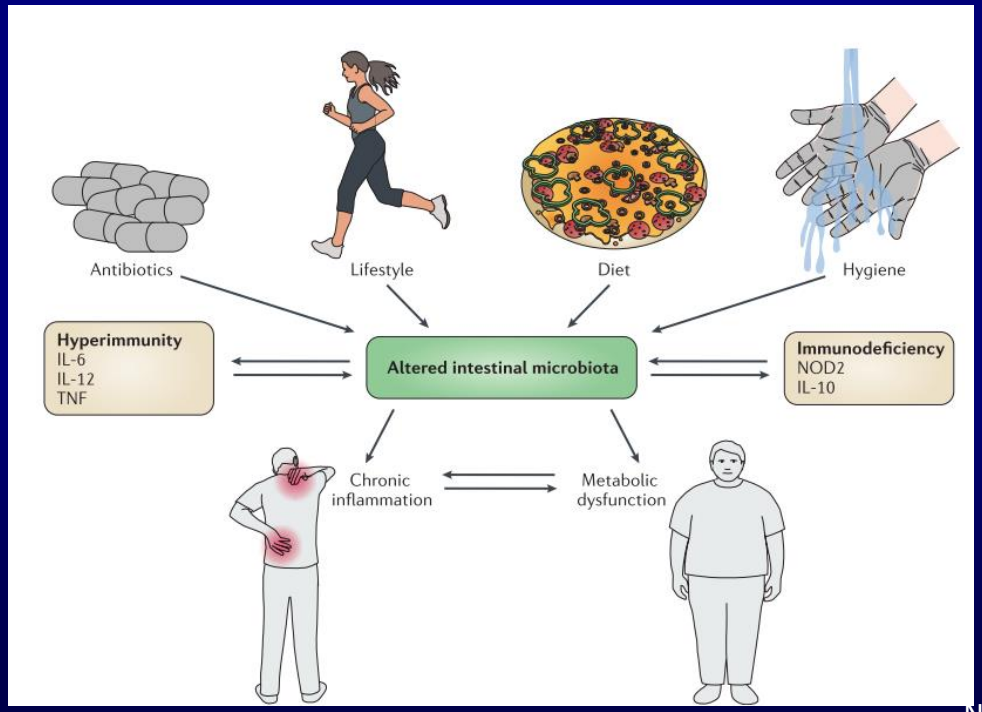
* Antimikrobiyal tedaviler



Nature Rev Microbiol 2013;11: 227

Differences in Fecal Microbiota in Different European Study Populations in Relation to Age, Gender, and Country: a Cross-Sectional Study

Susanne Mueller,[1]† Katiana Saunier,[2]† Christiana Hanisch,[3] Elisabeth Norin,[4] Livia Alm,[4] Tore Midtvedt,[4] Alberto Cresci,[5] Stefania Silvi,[5] Carla Orpianesi,[5] Maria Cristina Verdenelli,[5] Thomas Clavel,[1,2] Corinna Koebnick,[3] Hans-Joachim Franz Zunft,[3] Joël Doré,[2] and Michael Blaut[1]*

A cross-sectional study on intestinal microbiota composition was performed on 230 healthy subjects at four European locations in France, Germany, Italy, and Sweden. The study participants were assigned to two age groups: 20 to 50 years (mean age, 35 years; $n = 85$) and >60 years (mean age, 75 years; $n = 145$). A set of 14 group- and species-specific 16S rRNA-targeted oligonucleotide probes was applied to the analysis of fecal samples by fluorescence in situ hybridization coupled with flow cytometry. Marked country-age interactions were observed for the German and Italian study groups. These interactions were inverse for the predominant bacterial groups *Eubacterium rectale-Clostridium coccoides* and *Bacteroides-Prevotella*. Differences between European populations were observed for the *Bifidobacterium* group only. Proportions of bifidobacteria were two- to threefold higher in the Italian study population than in any other study group, and this effect was independent of age. Higher proportions of enterobacteria were found in all elderly volunteers independent of the location. Gender effects were observed for the *Bacteroides-Prevotella* group, with higher levels in males than in females. In summary, age-related differences in the microbiota makeup were detected but differed between the study populations from the four countries, each showing a characteristic colonization pattern.

App Env Microbiol 2006;72: 1027

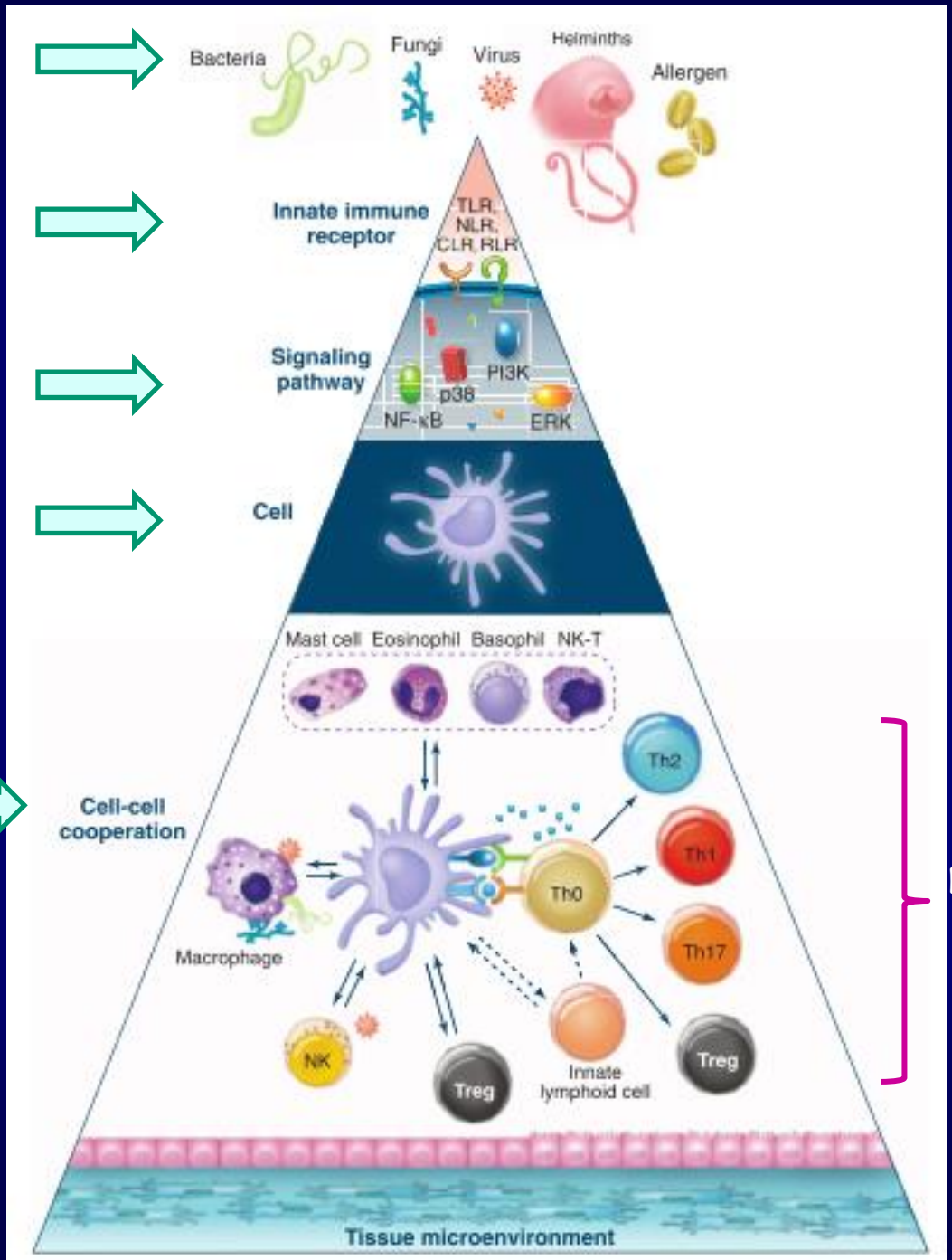
Yabancı Mikroorganizma

Reseptör

Sinyal iletisi

Doğal Bağışıklık Hücresi

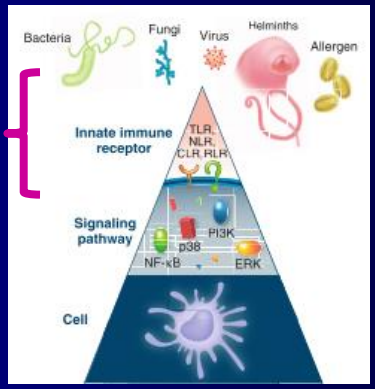
Hücreler arası ilişki



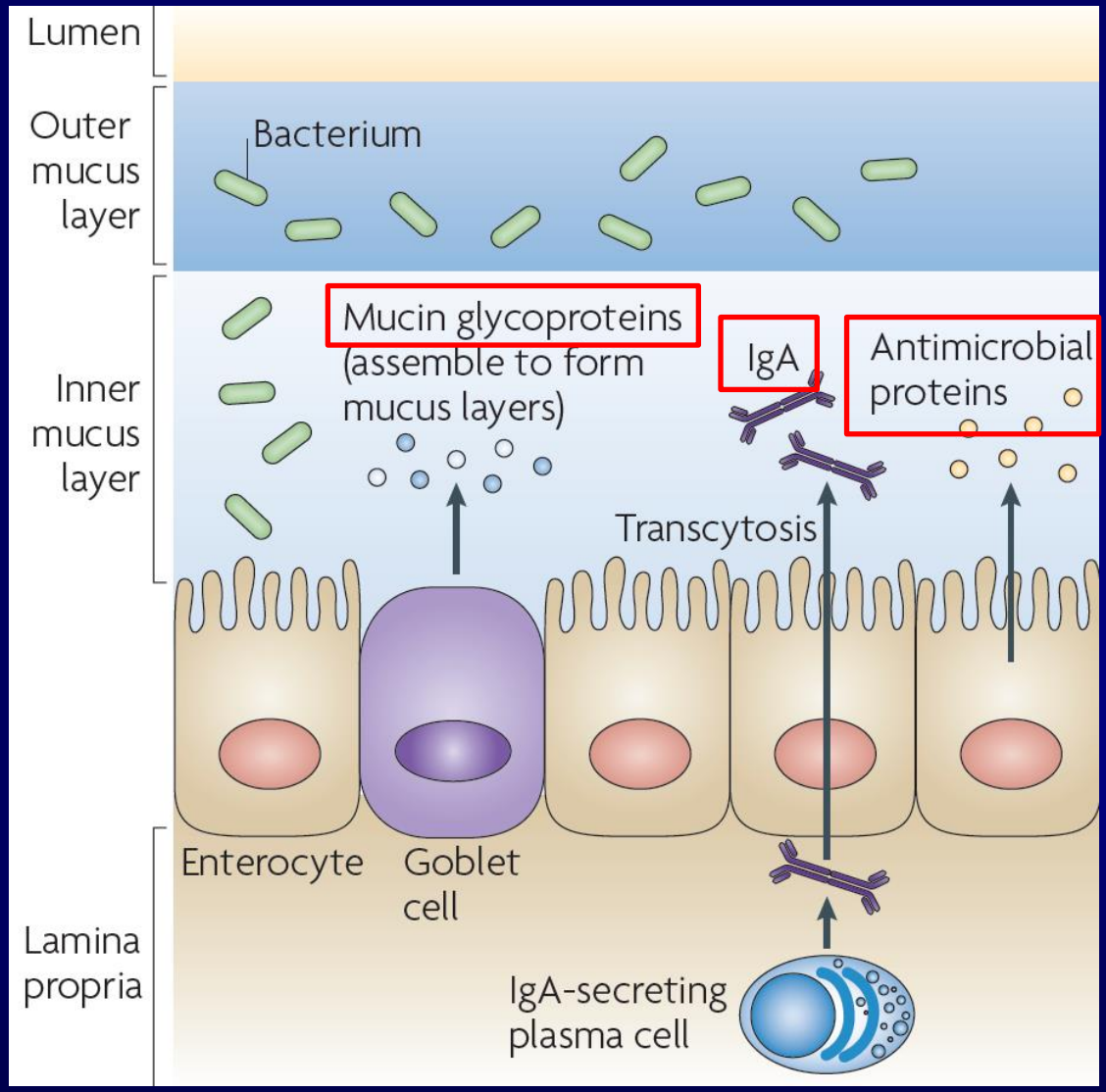
Naif $CD4^+$ T hücrelerinin Farklılaşması

Science 2012;337: 431

Tanıma


Bacteria
Fungi
Virus
Helminths
Allergen
Innate immune receptor
TLR, NLR, CLR, RLR
Signaling pathway
PI3K
p38
NF-κB
ERK
Cell

Bakteri-Epitel Hücre Direkt Temasını Sınırlayan/Engelleyen Yapılar



Nature Rev Immunol 2010;10: 159

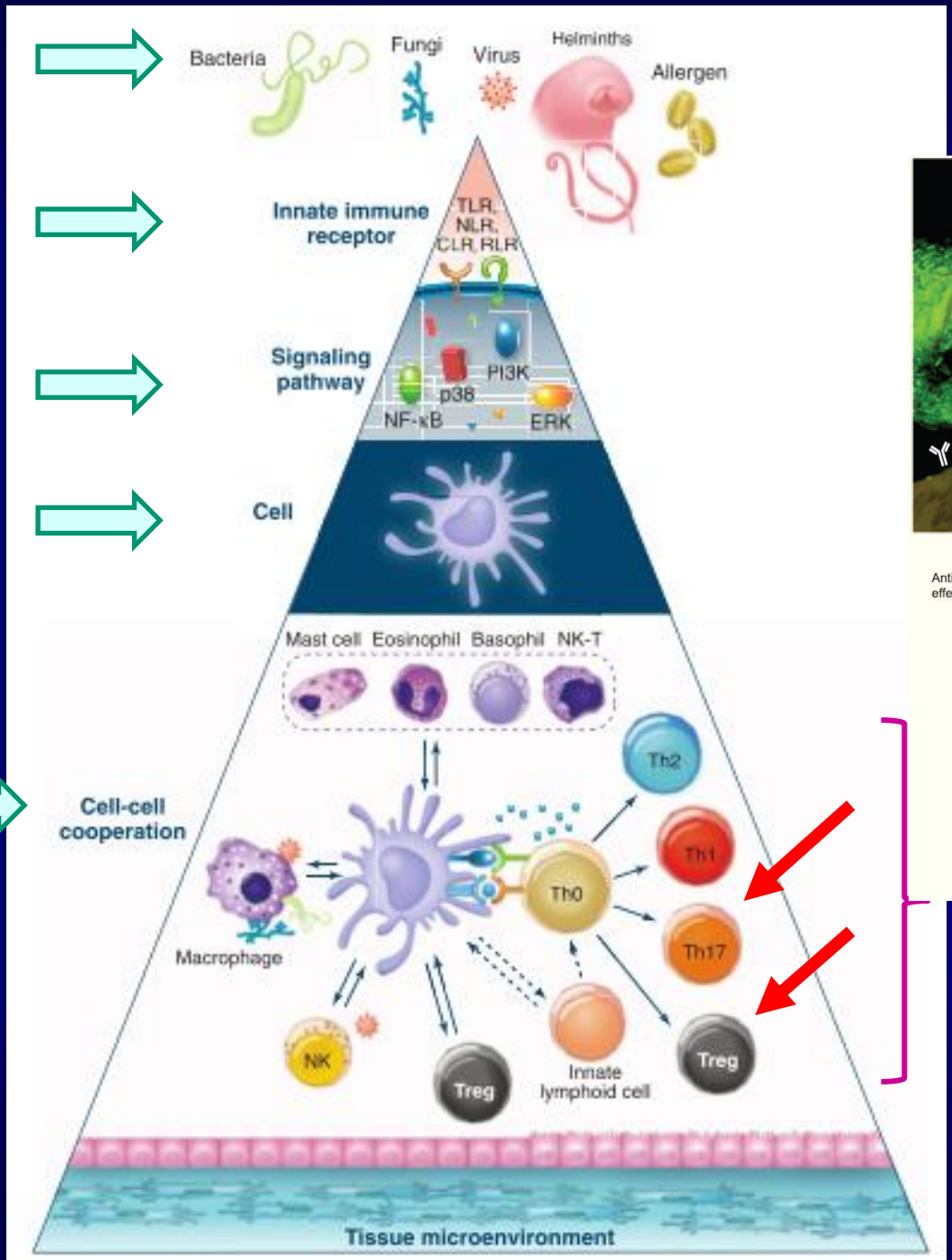
Yabancı Mikroorganizma

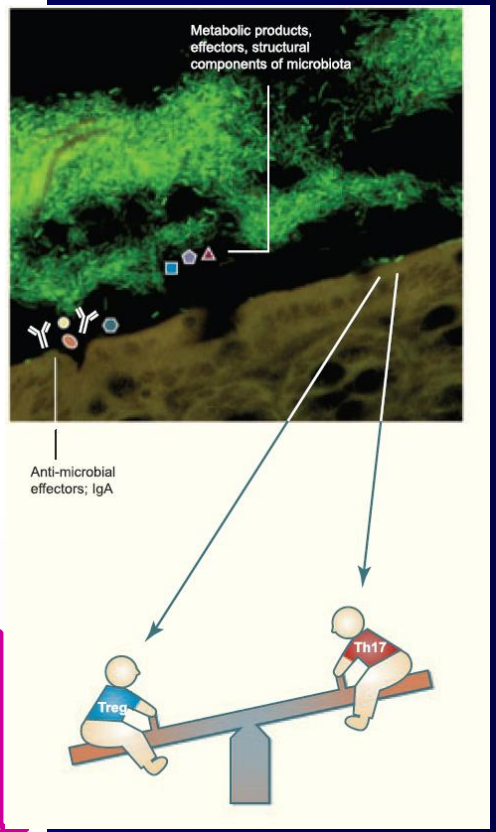
Reseptör

Sinyal iletisi

Doğal Bağışıklık Hücresi

Hücreler arası ilişki



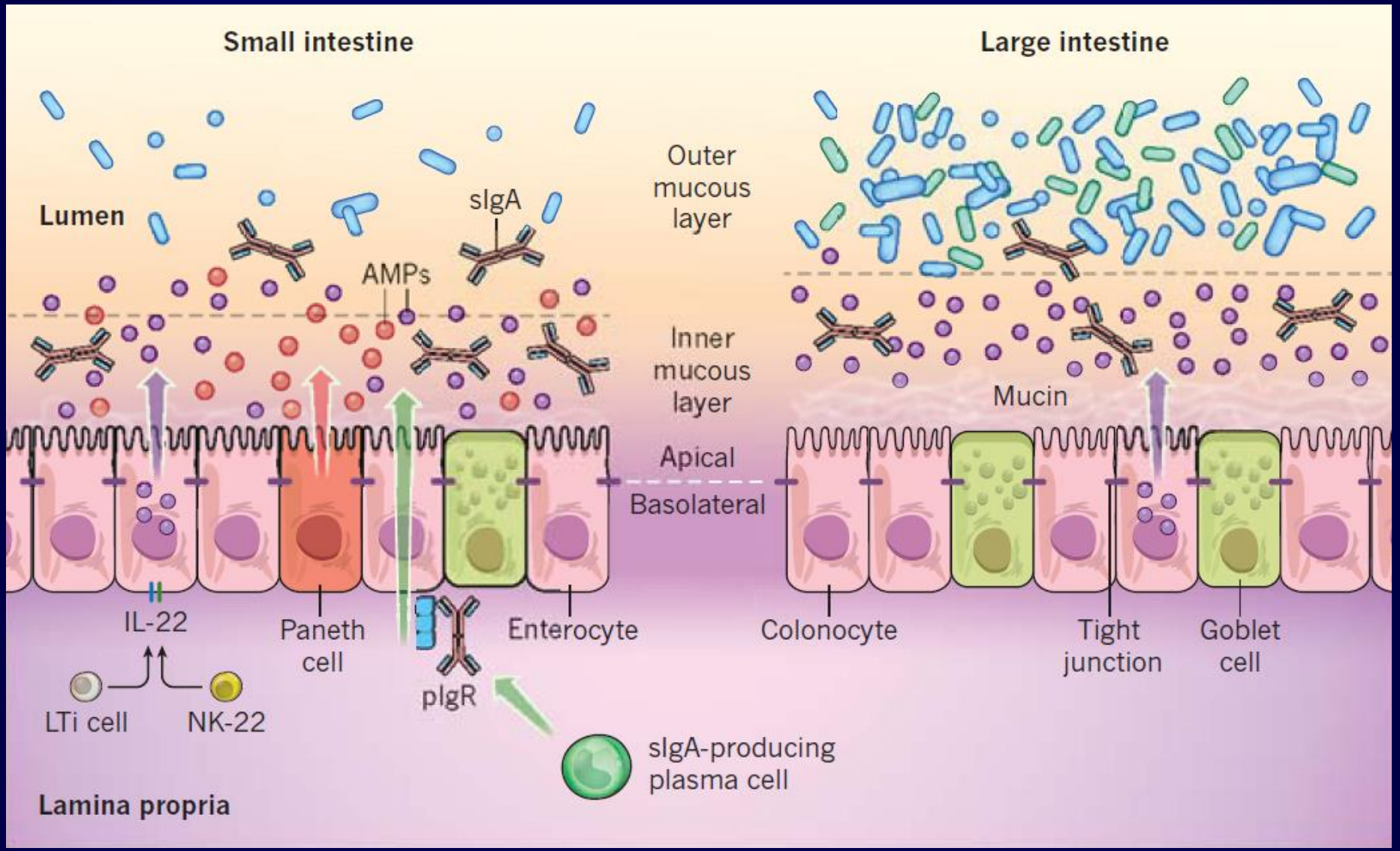


Immunol Rev 2012;245: 7

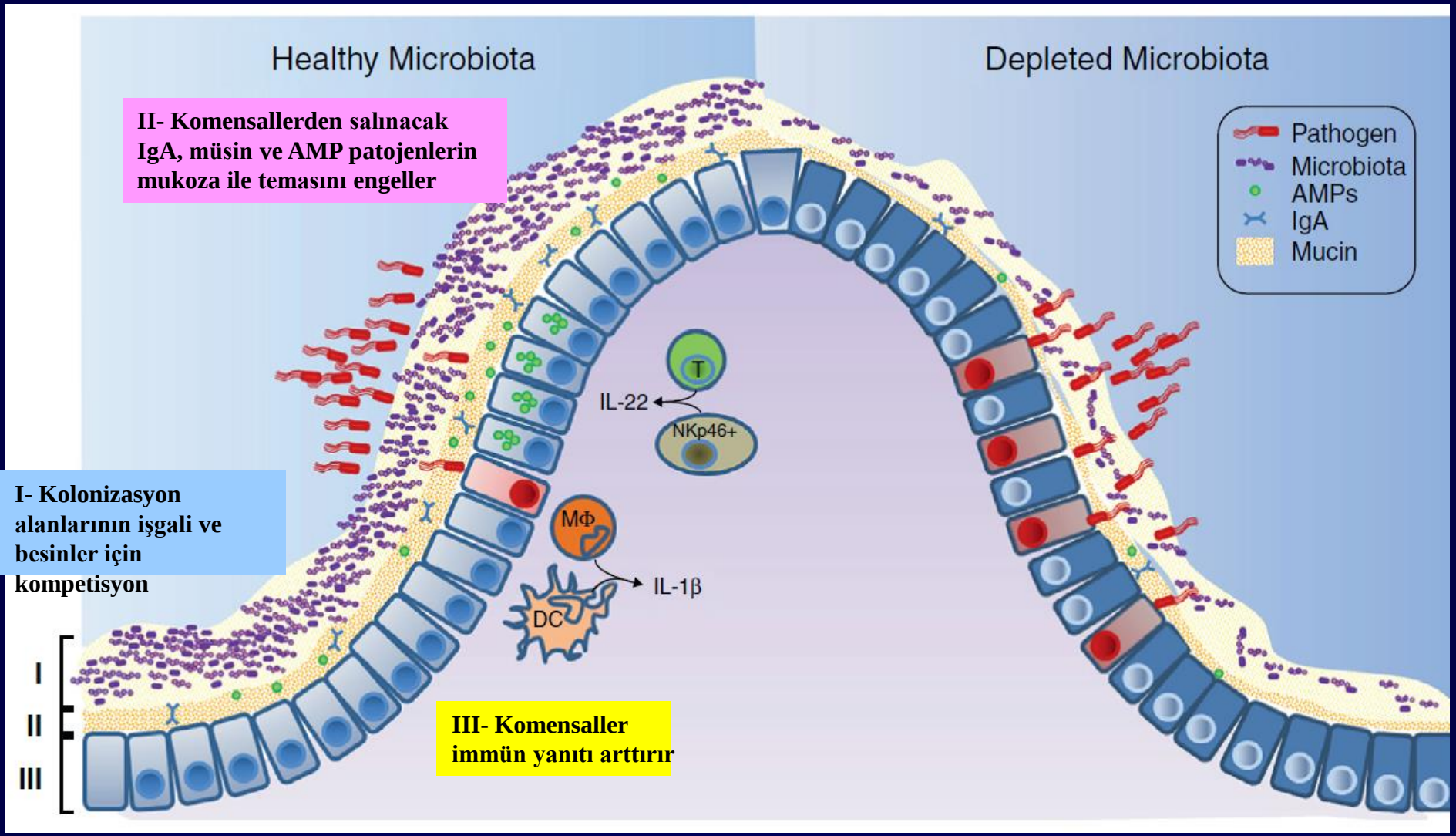
Science 2012;337: 431

Science 2012;337: 431

Barsak Epitel tabakasının Bariyer İşlevi



Nature 2012;489: 231



Curr Opinion Microbiol 2013;16: 221

1850

Her dört bebekte
Birisi ölüyor

2010

Bir yaşından önce
1000'de 6

1850

Her dört bebekte
Birisi ölüyor

2010

Bir yaşından önce
1000'de 6

1990

Obez oranı %12

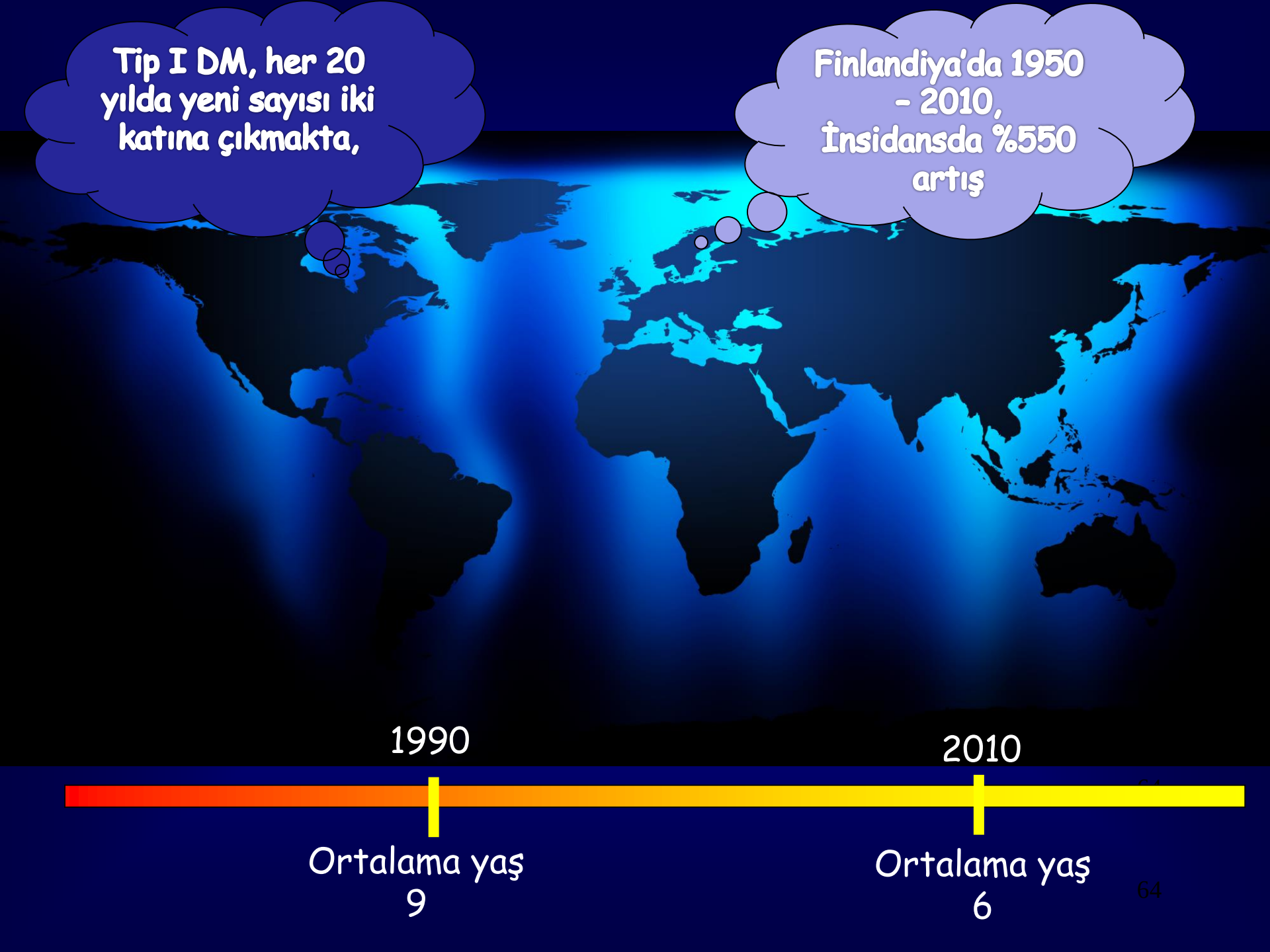
2010

Obez oranı %30

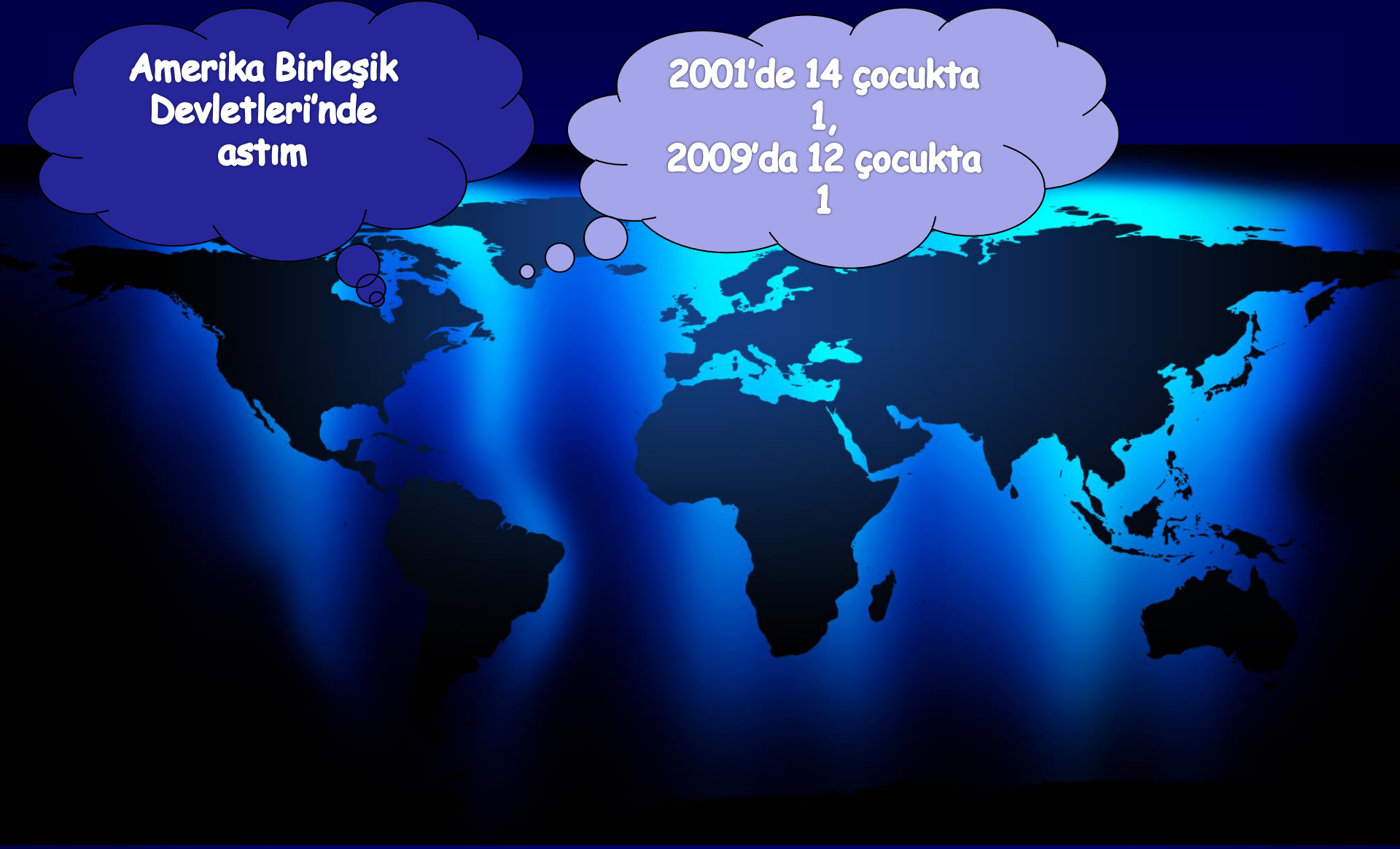
Dünya genelinde 1.5 milyar insan kilolu, 200 milyon erkek ve 300 milyon kadın obez

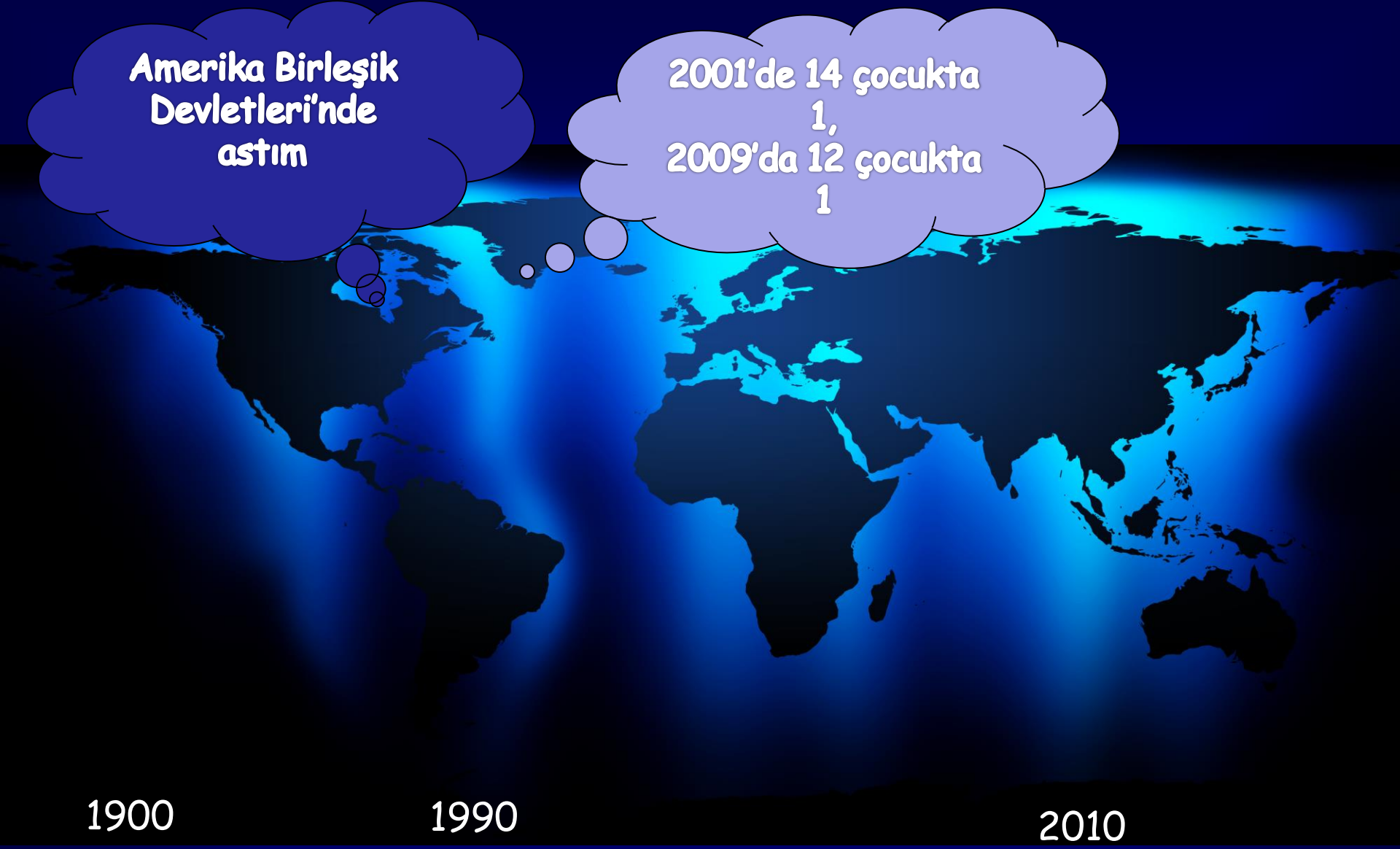

Tip I DM, her 20 yılda yeni sayısı iki katına çıkmakta,

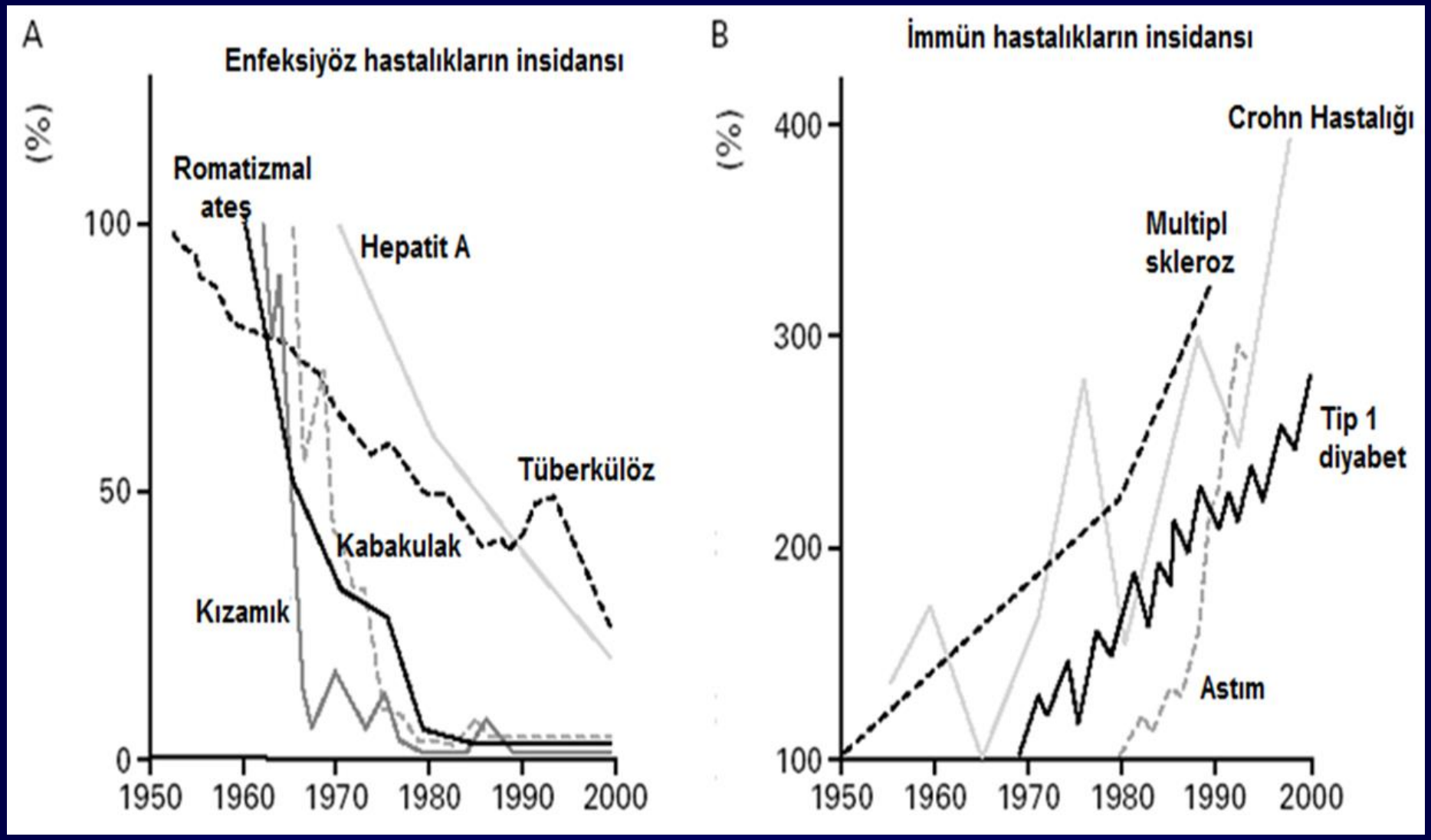

Tip I DM, her 20 yılda yeni sayısı iki katına çıkmakta,
Finlandiya'da 1950 – 2010, İnsidansda %550 artış


Tip I DM, her 20 yılda yeni sayısı iki katına çıkmakta,
Finlandiya'da 1950 – 2010, İnsidansda %550 artış
1990
2010
Ortalama yaş 9
Ortalama yaş 6


Amerika Birleşik Devletleri'nde astım


Amerika Birleşik Devletleri'nde astım
2001'de 14 çocukta 1,
2009'da 12 çocukta 1


Amerika Birleşik Devletleri'nde astım
2001'de 14 çocukta 1,
2009'da 12 çocukta 1
1900
1990
2010
Gıda allerjileri
Egzema
İnflamatuar barsak hastalıkları


A
Enfeksiyöz hastalıkların insidansı
(%)
100
50
0
Romatizmal ateş
Hepatit A
Tüberkülöz
Kabakulak
Kızamık
1950
1960
1970
1980
1990
2000
B
İmmün hastalıkların insidansı
(%)
400
300
200
100
Crohn Hastalığı
Multipl skleroz
Tip 1 diyabet
Astım
1950
1960
1970
1980
1990
2000

Clinical Microbiology
NEWSLETTER

CMN
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Stay Informed.

CMN
Vol. 35, No. 20
October 15, 2013
www.cmnewsletter.com

The Oral Microbiome: Its Role in Health and in Oral and Systemic Infections

Frank A. Scannapieco, D.M.D., Ph.D., Professor and Chair, Department of Oral Biology, School of Dental Medicine, University at Buffalo, State University of New York, Foster Hall, Buffalo, New York

Clin
Mic
NEWS

CMN
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CMN
Vol. 35, No. 20
October 15, 2013
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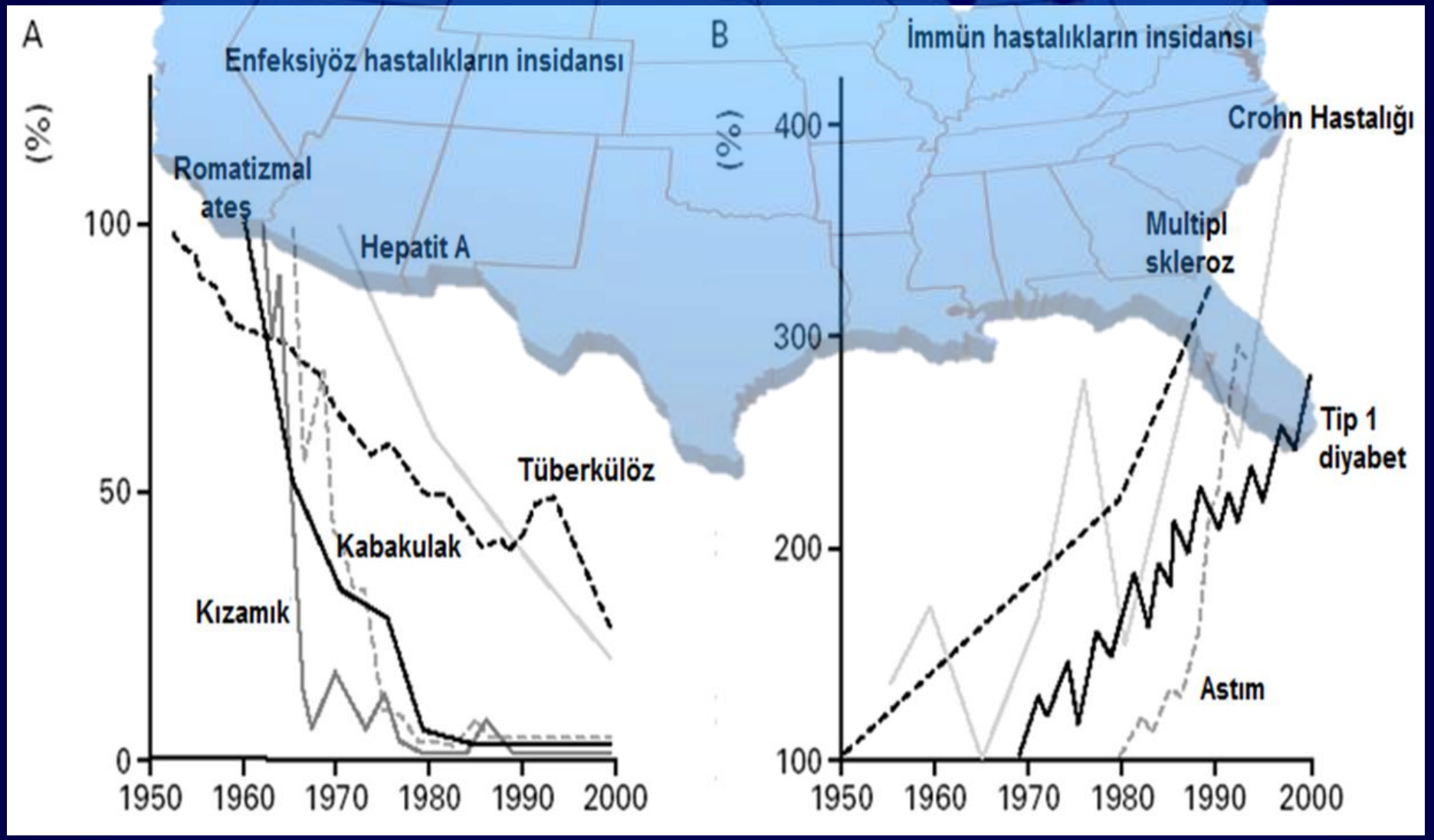
ffalo, New York


A
(%)
Enfeksiyöz hastalıkların insidansı
Romatizmal ateş
Hepatit A
Tüberkülöz
Kabakulak
Kızamık
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1950
1960
1970
1980
1990
2000
B
İmmün hastalıkların insidansı
(%)
400
300
200
100
Crohn Hastalığı
Multipl skleroz
Tip 1 diyabet
Astım
1950
1960
1970
1980
1990
2000

Contents lists available at ScienceDirect

International Journal of Pediatric Otorhinolaryngology

journal homepage: www.elsevier.com/locate/ijporl

Chorda tympani nerve function in children: Relationship to otitis media and body mass index☆

Raewyn M. Seaberg[a,*], Neil K. Chadha[b], Bradley J. Hubbard[a], Karen A. Gordon[a], Brooke A. Allemang[a], Brittany J. Harrison[a], Blake C. Papsin[a]

[a] Department of Otolaryngology – Head and Neck Surgery, Hospital for Sick Children, University of Toronto, Toronto, Ontario, Canada
[b] Division of Pediatric Otolaryngology, BC Children's Hospital, University of British Columbia, Vancouver, Canada

ORIGINAL ARTICLE

Changes in Taste Function Related to Obesity and Chronic Otitis Media With Effusion

Il Ho Shin, MD; Dong Choon Park, MD; Chul Kwon, MD; Seung Geun Yeo, MD, PhD

Objective: To evaluate changes in taste threshold in patients with chronic otitis media with effusion (COME) and their relationship with body mass index. A relationship has been suggested between pediatric obesity and COME, and we hypothesized that changes in taste function may occur in children with COME and that such changes may be associated with changes in body weight.

Design: A prospective, nonrandomized, case-control study.

Setting: A university tertiary care center.

Subjects: The experimental group comprised 42 children with COME who underwent tympanostomy tube insertion, and the control group, 42 children without otitis media with effusion. Patients were enrolled between September 2007 and August 2009.

Main Outcome Measure: Taste threshold was measured by electrogustometry, and 4 standard taste solutions (sucrose, sodium chloride, citric acid, and quinine hydrochloride) were used in chemical taste tests.

Results: Body mass index was significantly higher in the COME than in the control group ($P=.02$). Electrogustometry showed that the anterior part of the tongue had a significantly higher taste threshold in the COME than in the control group (anterior right, $P=.03$; anterior left, $P=.04$), and chemical taste test results showed that sweet and salty tastes were significantly lower in the COME group (sweet, $P=.02$; salty, $P=.04$).

Conclusion: These results showed that COME can cause changes in taste and that these changes may be related to pediatric obesity.

Arch Otolaryngol Head Neck Surg. 2011;137(3):242-246

ORIGINAL ARTICLE

Relationship Between Pediatric Obesity and Otitis Media With Effusion

Jong Bin Kim, MD; Dong Choon Park, MD, PhD; Chang Il Cha, MD, PhD; Seung Geun Yeo, MD, PhD

Objective: To investigate the relationship between pediatric otitis media with effusion and obesity, as determined by body mass index (BMI) (calculated as weight in kilograms divided by height in meters squared) and serum triglyceride (TG) and total cholesterol (TC) concentrations.

Design: A prospective, nonrandomized, case-control study.

Setting: University-affiliated hospital.

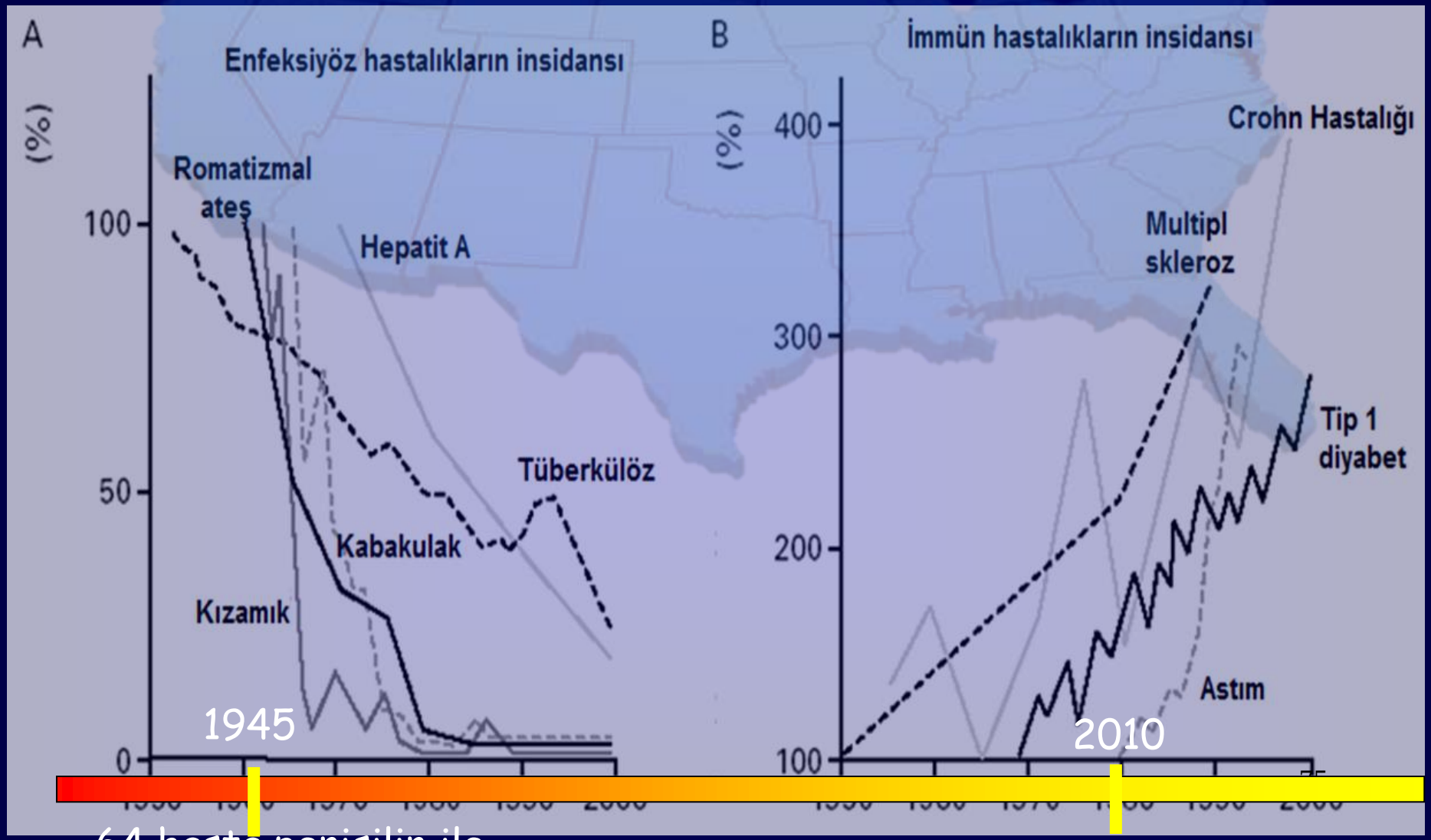
Subjects: The experimental group comprised 155 children aged 2 to 7 years, who received unilateral or bilateral ventilation tube insertion for the treatment of otitis media with effusion. The control group comprised 118 children with no history of otitis media with effusion, who underwent operations for conditions other than ear diseases. Based on BMI and serum TG and TC concentrations, we divided the experimental group into 2 subgroups, those who were and were not obese.

Main Outcome Measures: We determined the difference between the experimental and control groups in BMI and serum TG and TC concentrations and the difference between the obese and nonobese subgroups in frequency of ventilation tube insertion.

Results: Mean±SD BMI (22.0±3.4 vs 16.3±2.4) ($P=.01$) and mean±SD TC level (195.0±31.0 mg/dL vs 159.3±26.9 mg/dL [5.05±0.80 mmol/L vs 4.13±0.70 mmol/L]) ($P=.04$), but not mean serum TG level (109.4±40.4 mg/dL vs 90.0±52.3 mg/dL [1.24±0.46 mmol/L vs 1.02±0.59 mmol/L]) ($P=.13$), were significantly higher in the experimental group than in the control group. Frequency of ventilation tube insertion, however, did not differ significantly between the obese and nonobese subgroups, whether divided by BMI ($P=.10$) or serum TG ($P=.12$) or TC ($P=.07$) concentration.

Conclusion: Childhood obesity may be associated with the occurrence of otitis media with effusion.

Arch Otolaryngol Head Neck Surg. 2007;133:379-382



64 hasta penisilin ile
Tedavi edildi

250 milyon antibiyotik kürü

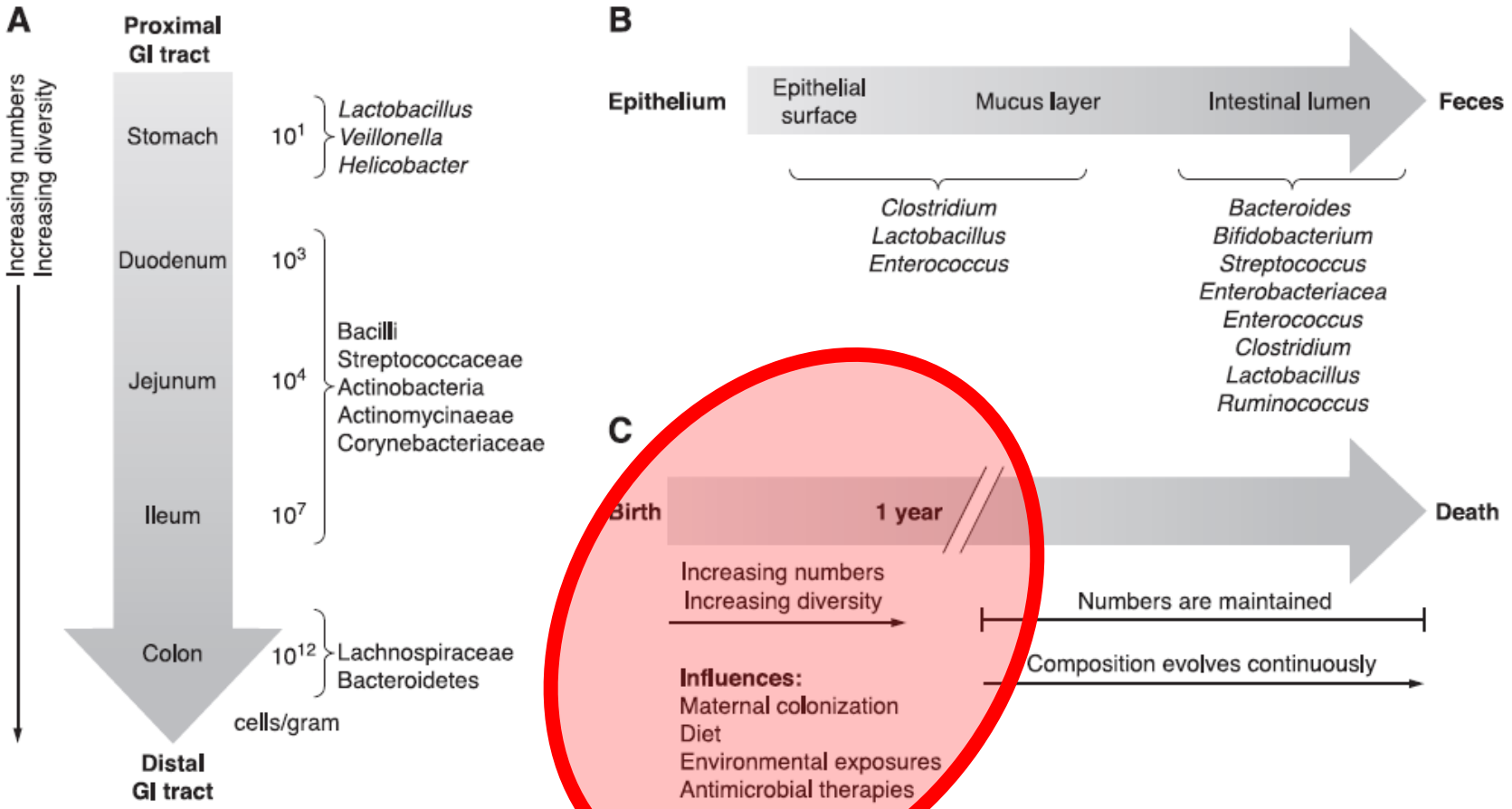
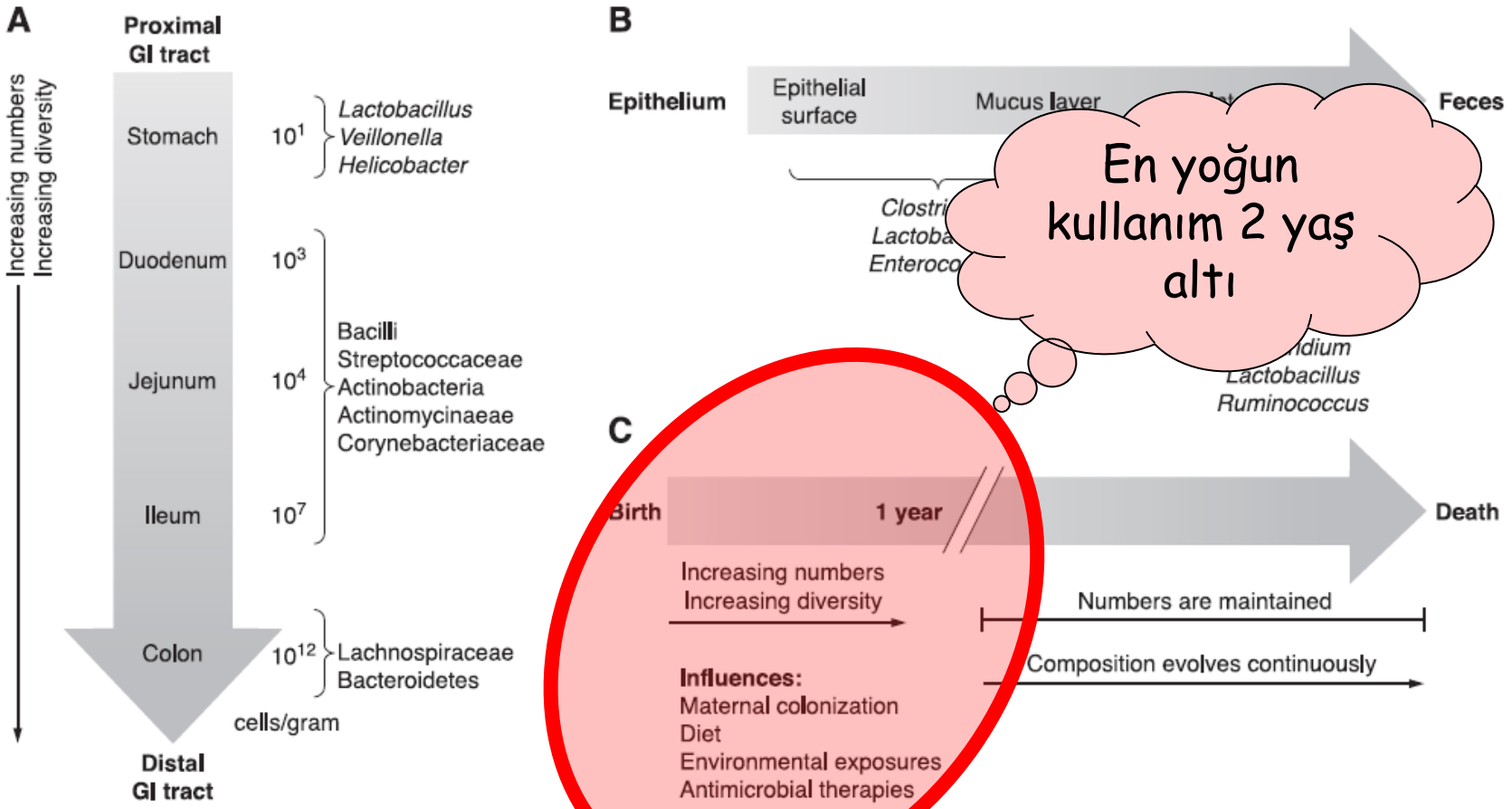


FIG. 2. Spatial and temporal aspects of intestinal microbiota composition. *A*: variations in microbial numbers and composition across the length of the gastrointestinal tract. *B*: longitudinal variations in microbial composition in the intestine. *C*: temporal aspects of microbiota establishment and maintenance and factors influencing microbial composition.



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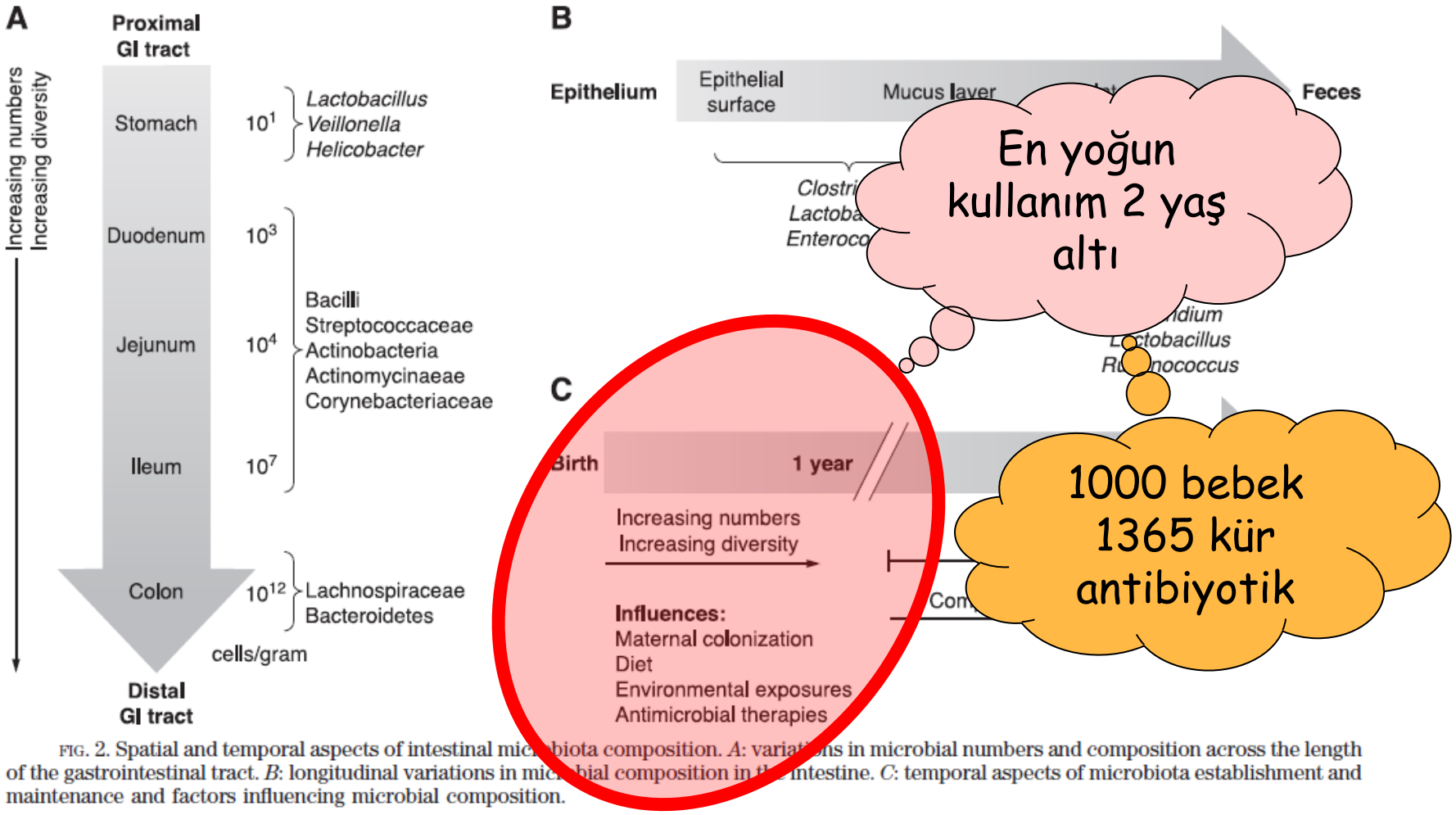


FIG. 2. Spatial and temporal aspects of intestinal microbiota composition. *A*: variations in microbial numbers and composition across the length of the gastrointestinal tract. *B*: longitudinal variations in microbial composition in the intestine. *C*: temporal aspects of microbiota establishment and maintenance and factors influencing microbial composition.

TABLE 1. Trends in the Therapeutic use of antimcrobial comp... ds[1] in food animals in Denmark (WHO, 20...

Compound	1994	1996	1998				2[2]
Tetracyclines	36,500	12,900	12,100				,300
Penicillins, β-lactamase sensitive	9,400	7,200	14,300				16,900
Other penicillins, cephalosporins	4,400	5,800	6,700	6,6		,700	9,800
Sulfonamides and trimethoprim	9,500	4,800	7,700	6,8	7,000	9,400	10,400
Sulfonamides	5,600	2,100	1,000	,000	1,000	900	850
Macrolides, lincosamides, tiamulin	11,400	7,600	7,100	8,700	15,600	9,900	21,200
Aminoglycosides	8,600	7,100	7,800	7,500	10,400		
Others			650	350			
Total				61,900			

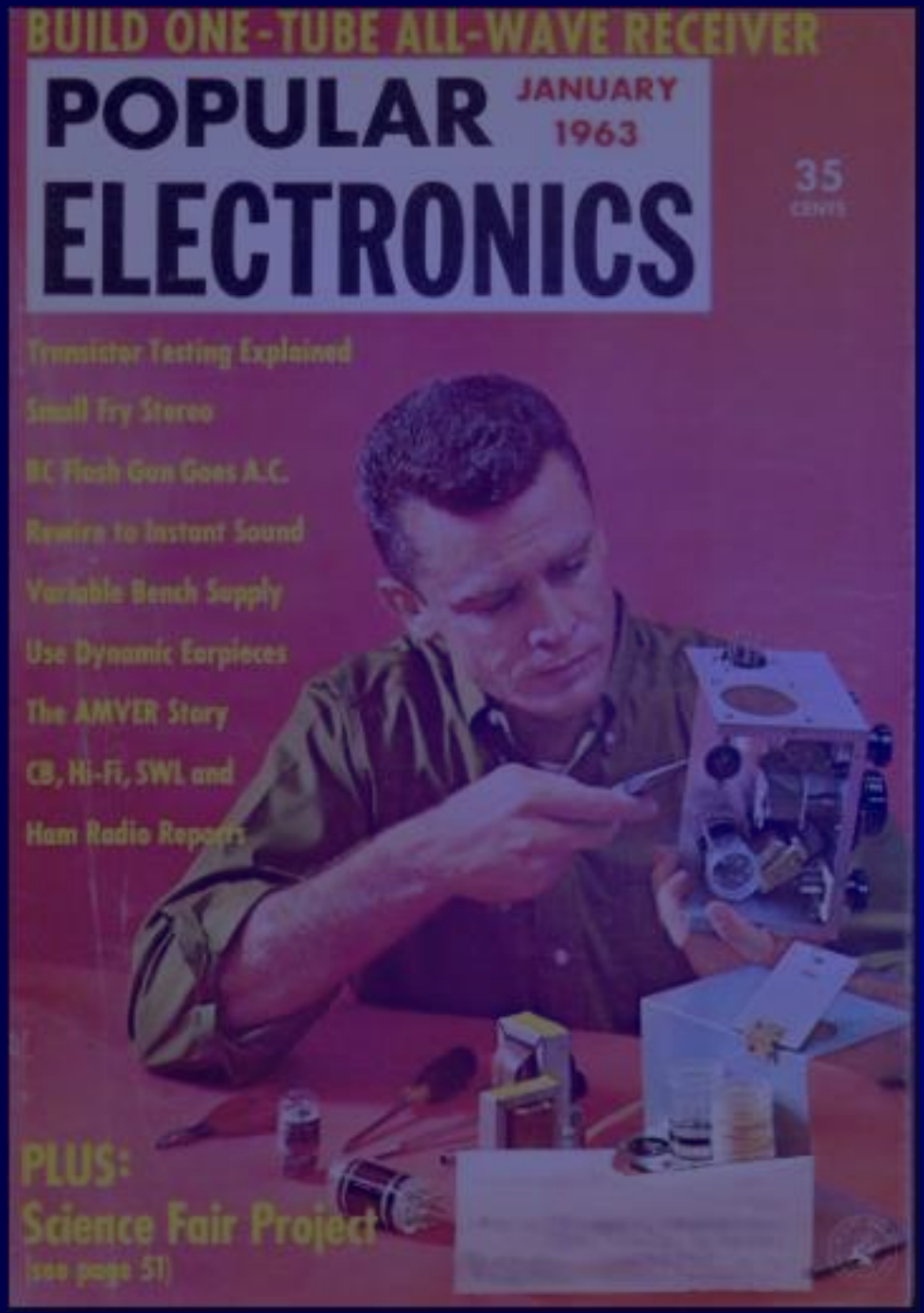
[1]On... [2]D... ...sed in pe...

1950'li yıllarda ilk kullanım

%5 -%10 -%15 ekstra kilo kazanımı

Aralık 2008, Amerikan Kongresi tarafından ret ediliyor

Amerika Birleşik Devletleri'nde kullanılan antibiyotiklerin %70-80'ı

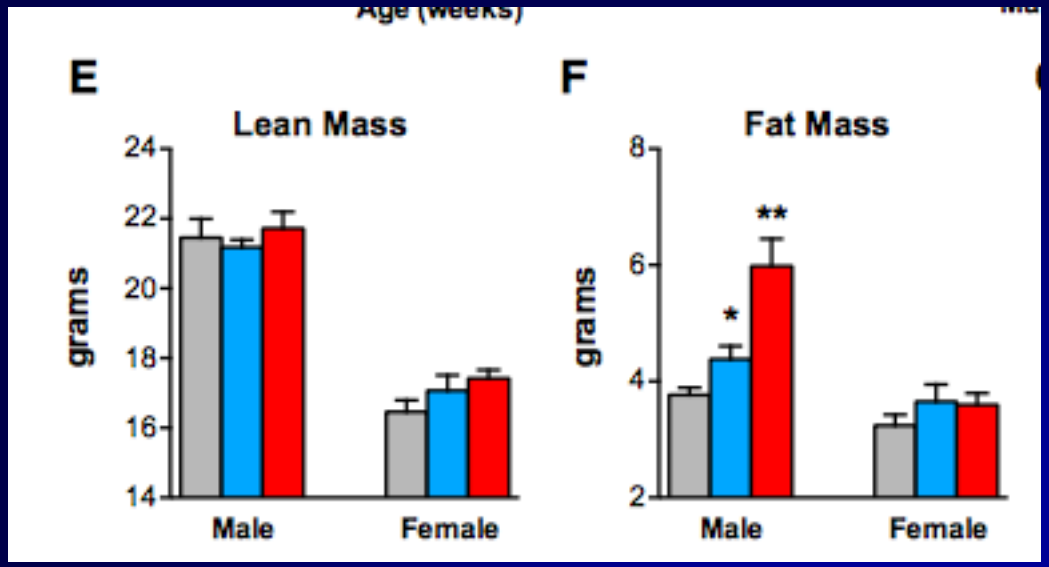


Normal beslenme

Germ free

Germ free + Antibiyotik

Antibiyotik



Normal beslenme

Yüksek kalorili yağlı beslenme

Yüksek kalorili yağlı + Antibiyotik

Antibiyotik

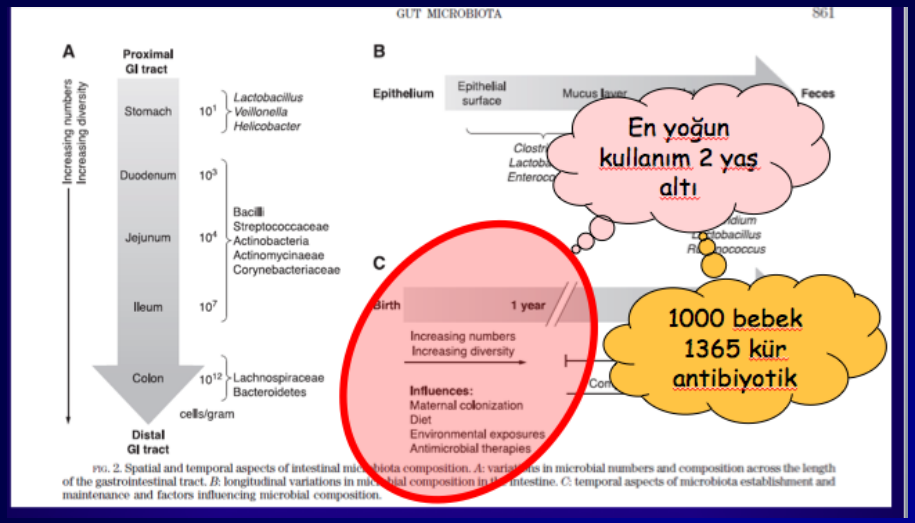


FIG. 2. Spatial and temporal aspects of intestinal microbiota composition. *A*: variations in microbial numbers and composition across the length of the gastrointestinal tract. *B*: longitudinal variations in microbial composition in the intestine. *C*: temporal aspects of microbiota establishment and maintenance and factors influencing microbial composition.

4 hafta

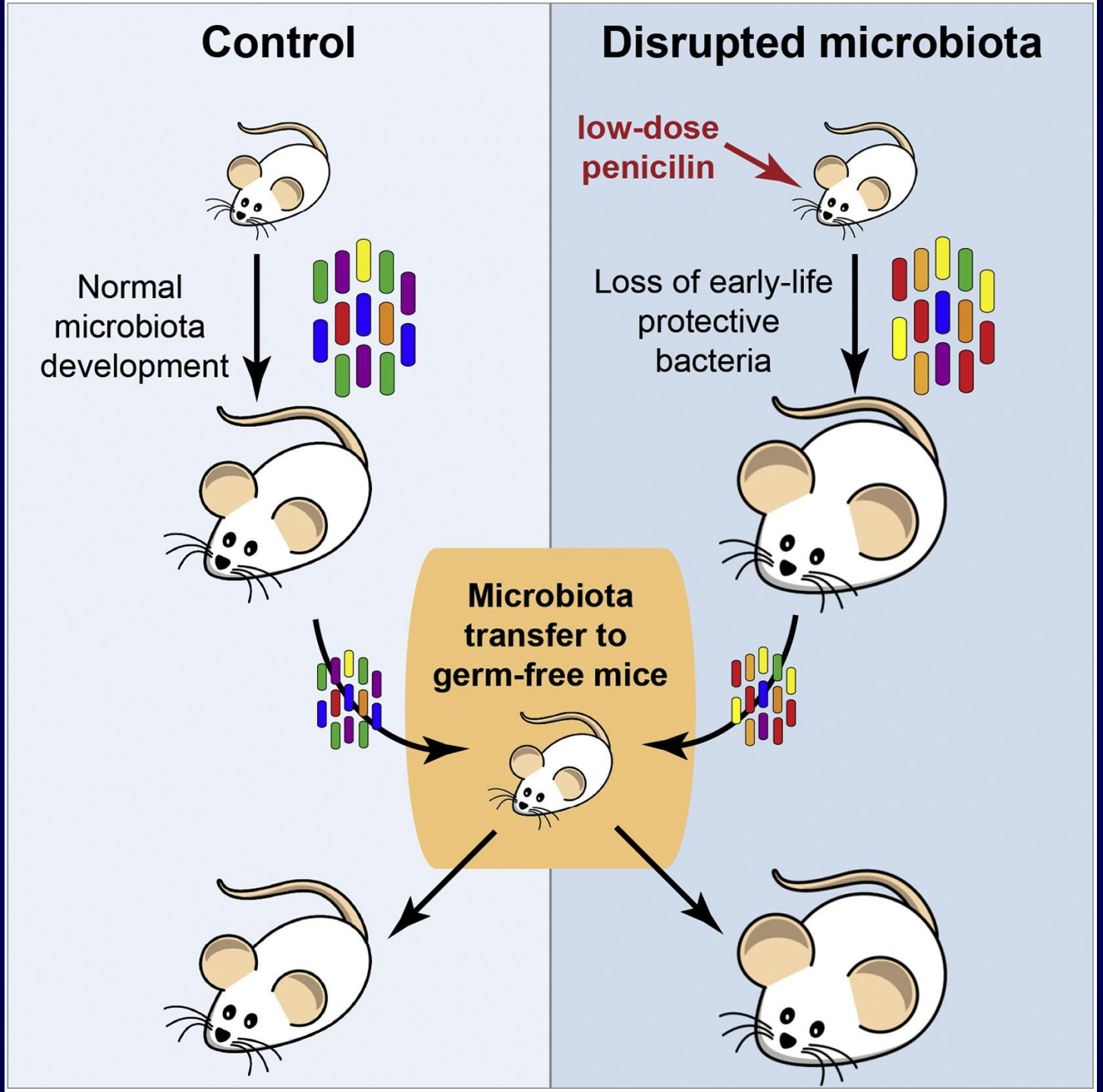
12 - 20 hafta

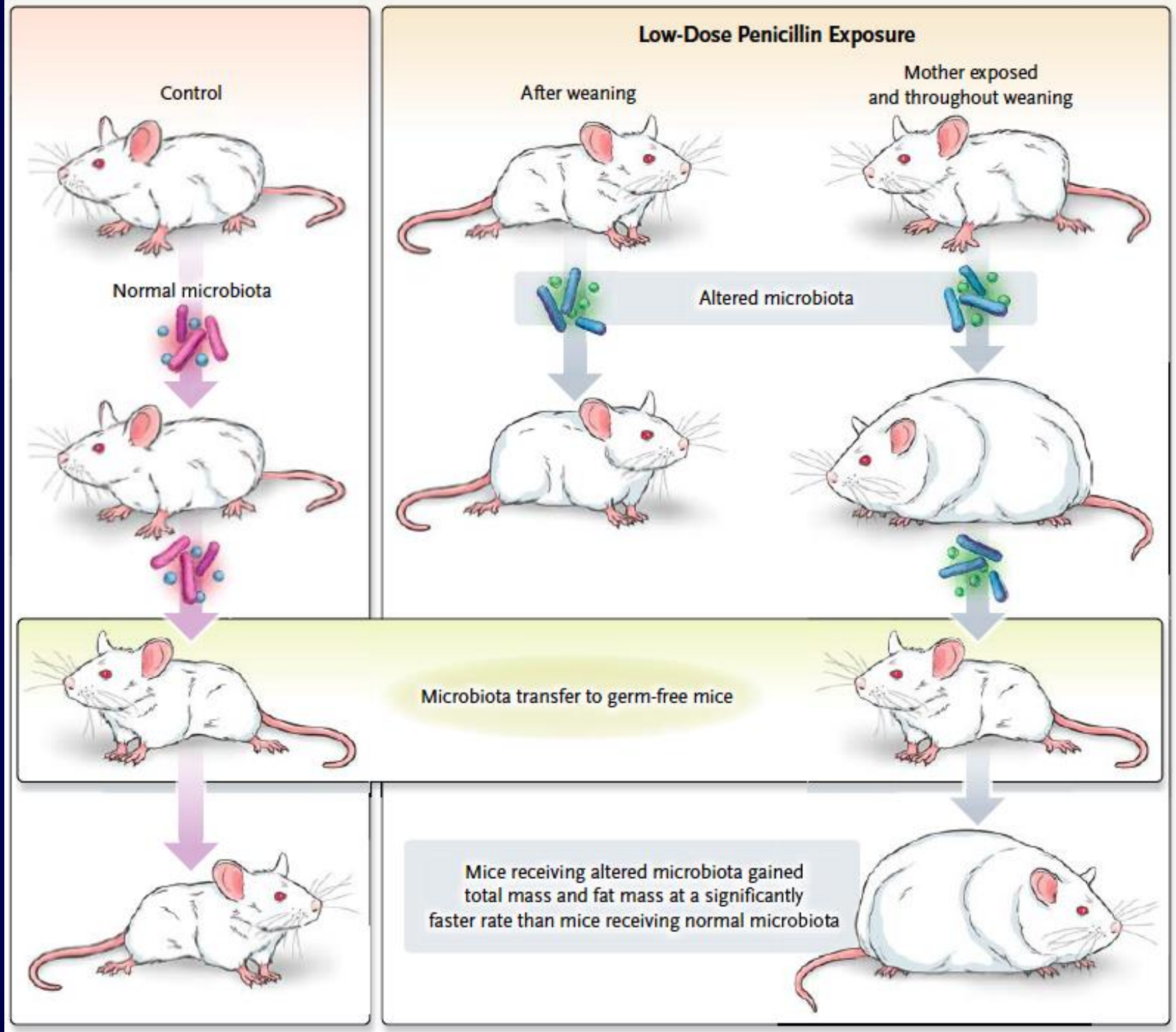
Normal beslenme

Normal beslenme

Antibiyotik

Antibiyotik

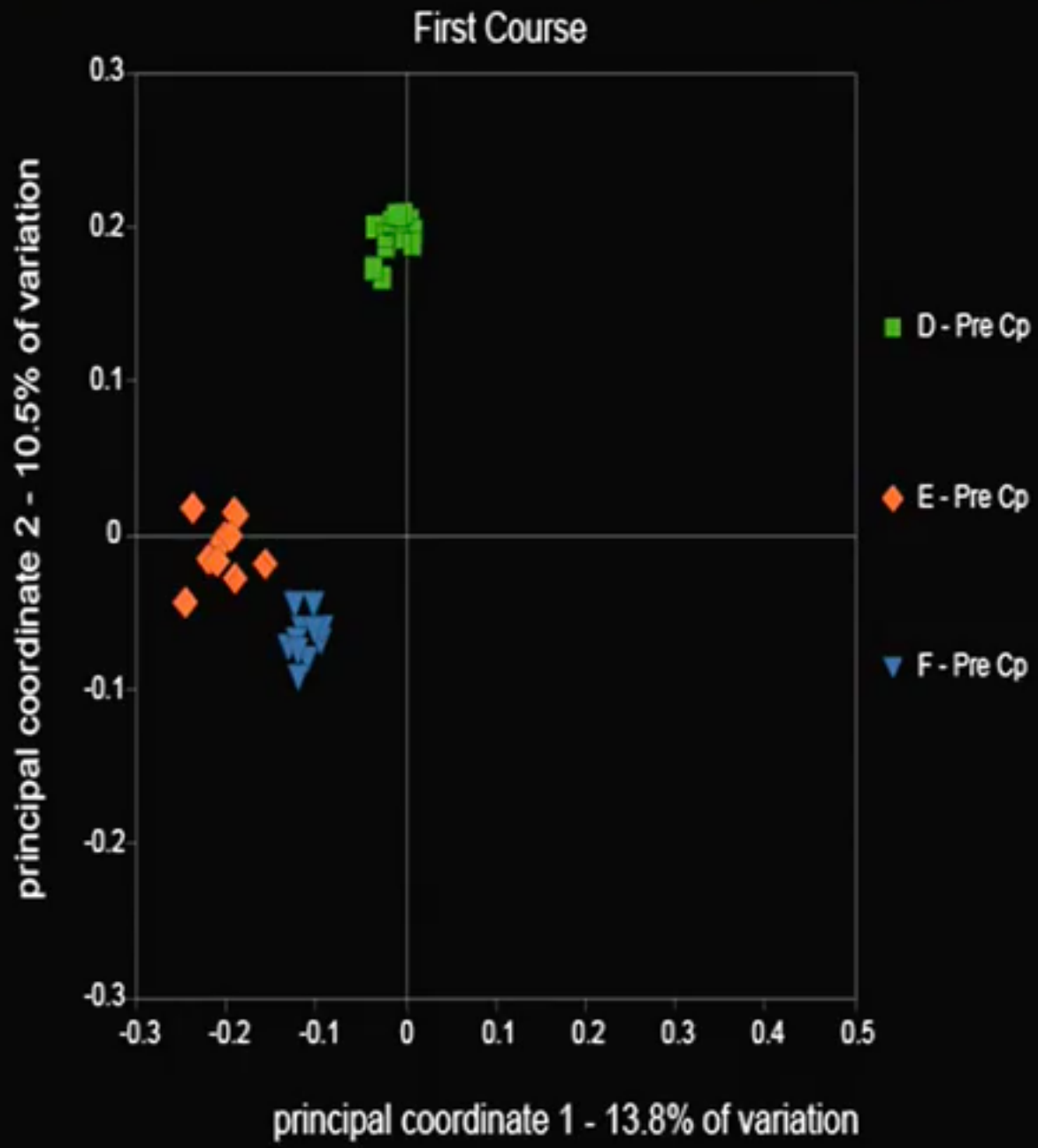

Control
Disrupted microbiota
low-dose penicillin
Normal microbiota development
Loss of early-life protective bacteria
Microbiota transfer to germ-free mice


Low-Dose Penicillin Exposure
Control
After weaning
Mother exposed and throughout weaning
Normal microbiota
Altered microbiota
Microbiota transfer to germ-free mice
Mice receiving altered microbiota gained total mass and fat mass at a significantly faster rate than mice receiving normal microbiota

16S rDNA data

Unweighted Unifrac Analysis

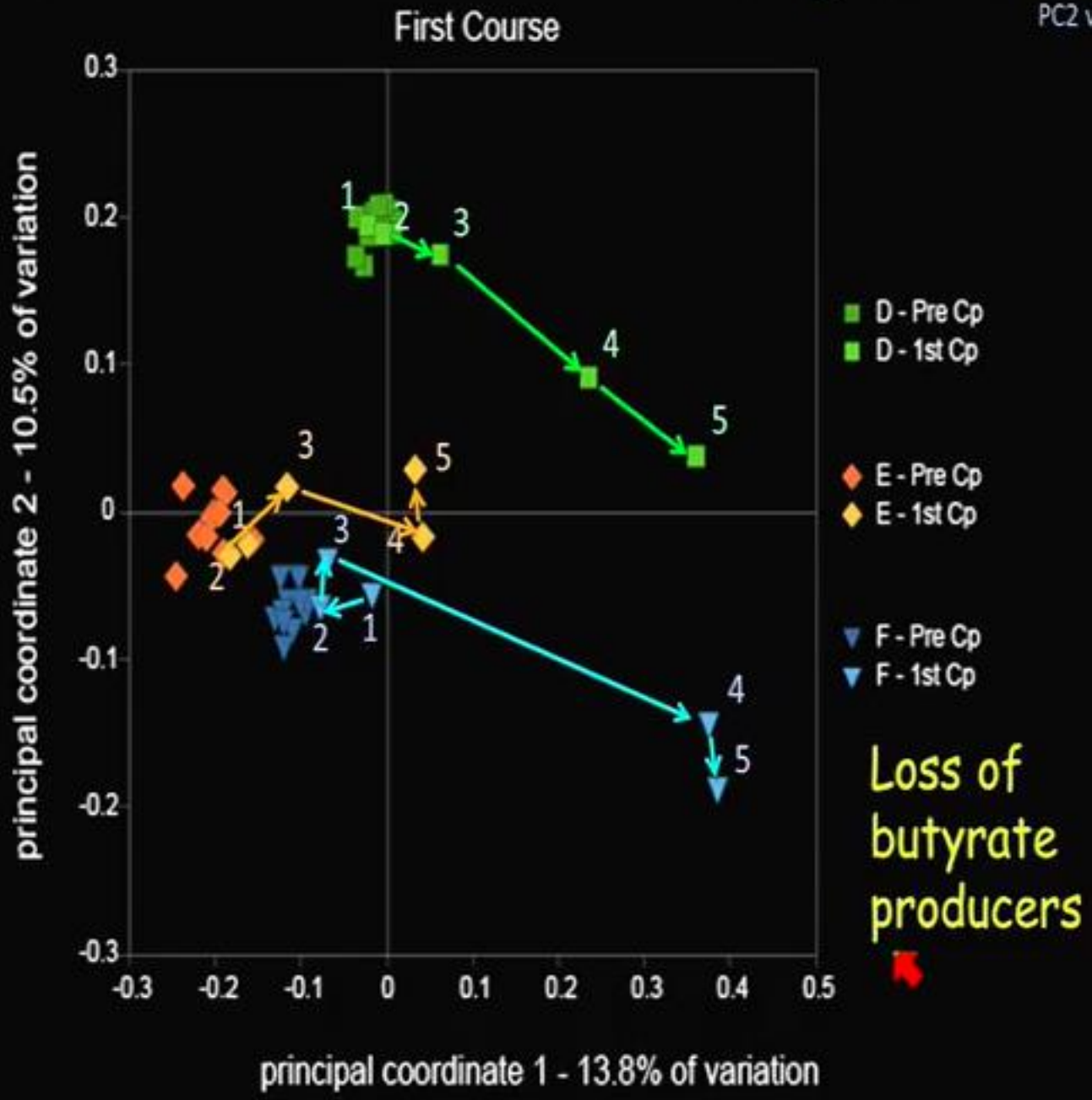
PC2 vs PC1



16S rDNA data

Unweighted Unifrac Analysis

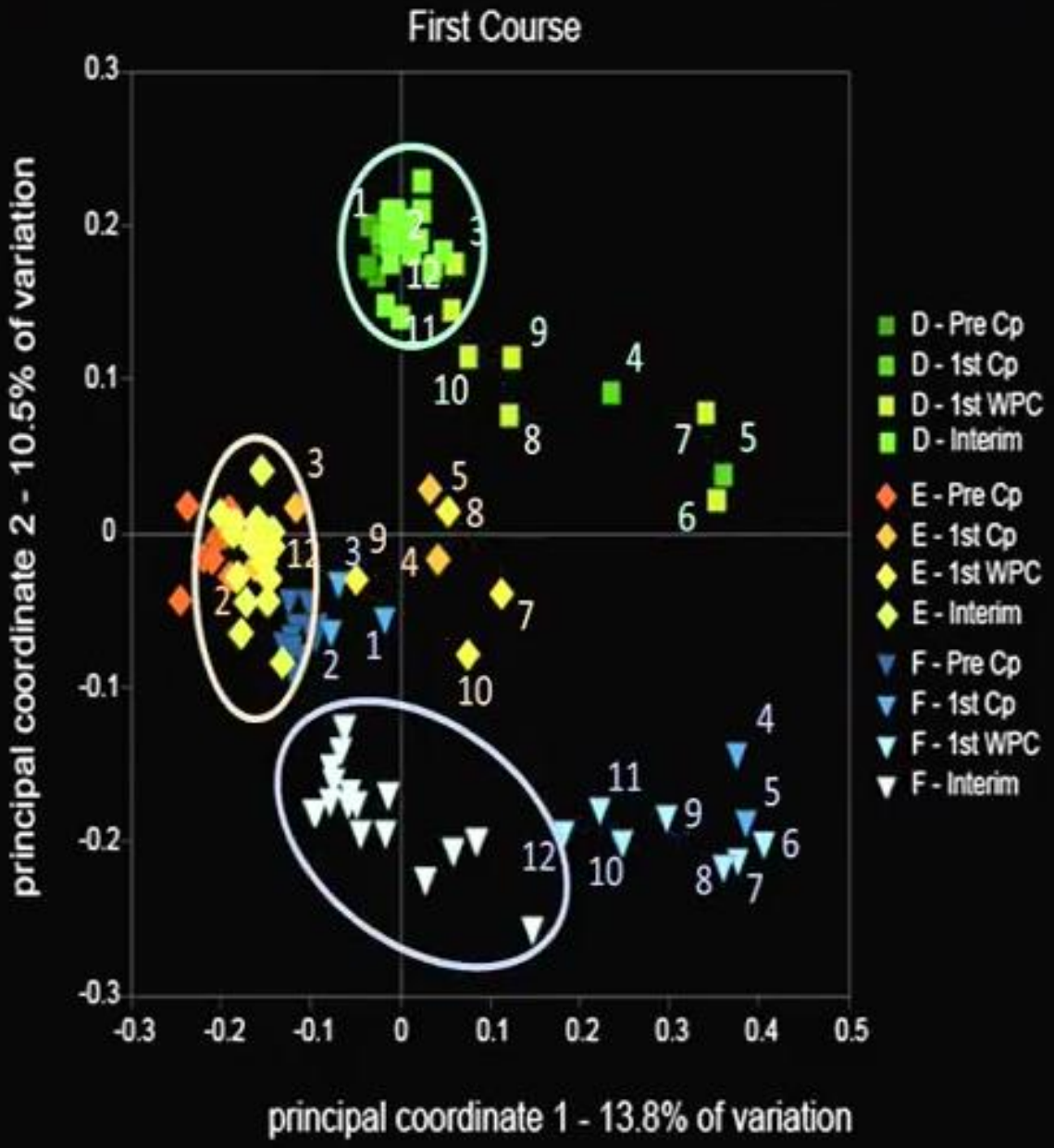
PC2 vs PC1



16S rDNA data

Unweighted Unifrac Analysis

PC2 vs PC1

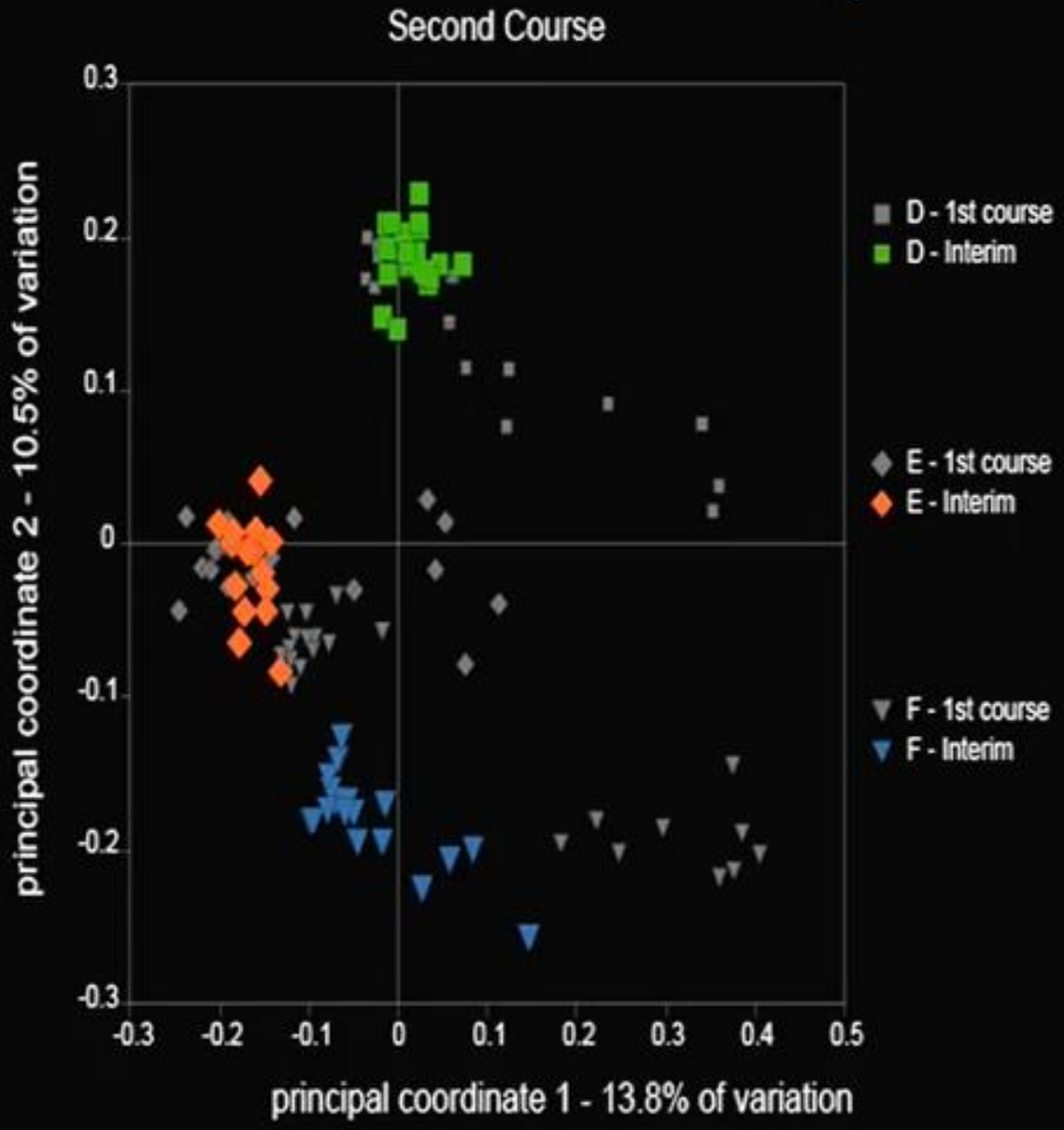


PLoS Biology 2008; 6:e280. PNAS 2011; 108:4554-61

16S rDNA data

Unweighted Unifrac Analysis

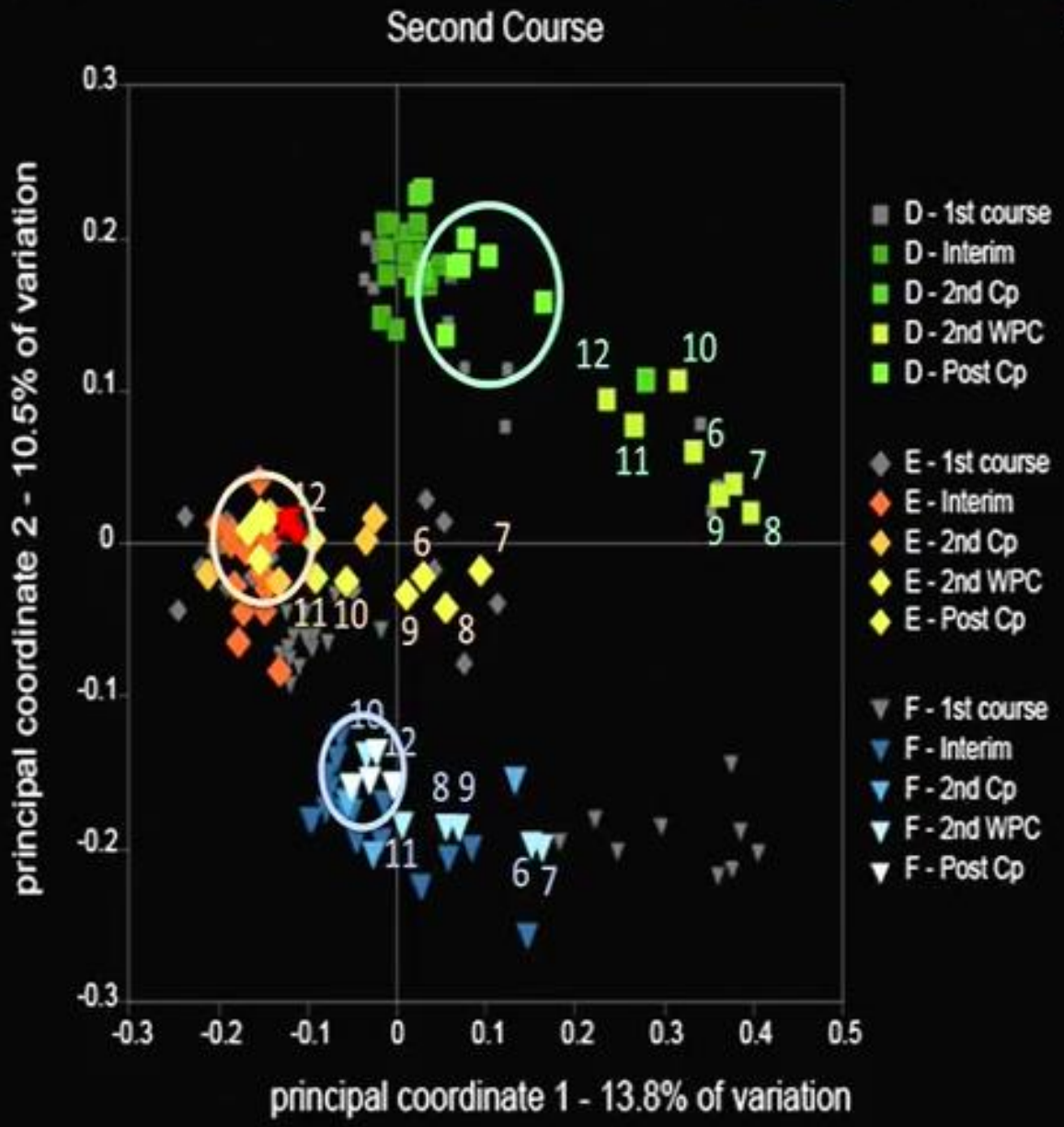
PC2 vs PC1



16S rDNA data

Unweighted Unifrac Analysis

PC2 vs PC1



International Journal of Obesity

Yaşamın ilk 6 ayında

Original Article

International Journal of Obesity , (21 August 2012) | doi:10.1038/ijo.2012.

Infant antibiotic exposures and early-life body mass

L Trasande, J Blustein, M Liu, E Corwin, L M Cox and M J Blaser

Objectives:

To examine the associations of antibiotic exposures during the first 2 years of life and the development of body mass over the first 7 years of life.

Design:

Longitudinal birth cohort study.

Subjects:

A total of 11 532 children born at ⩾2500 g in the Avon Longitudinal Study of Parents and Children (ALSPAC), a population-based study of children born in Avon, UK in 1991–1992.

ADC Online First, published on May 15, 2014 as 10.1136/archdischild-2014-306698

ARCHIVIST

Do antibiotics make children grow?

Accepted 3 May 2014

Arch Dis Child 2014;**0**:1. doi:10.1136/archdischild-2014-306698

ADC Online First, published on May 15, 2014 as 10.1136/archdischild-2014-306698

ARCHIVIST

Do antibiotics make children grow?

promote growth and increase profits. Could the same principle apply to humans? An international team of authors, acknowledging the important link between sustained growth and favourable health outcomes, examined the evidence for whether this principle could apply to children in developing countries (Gough EK and colleagues. *BMJ* 2014;348:g2267). Perhaps surprisingly, they found 10 trials of sufficient quality, spanning 6 decades, to be included in their meta-analysis. There was a wide variety of inclusion criteria and antibiotics used. Nine studies compared to placebo, and one to nothing. Treatment and follow-up periods varied enormously. Only one involved HIV–positive children. The net cumulative beneficial effects on height amounted to 0.04 cm/month, and on weight to 23.8g/month. The effect seemed greater for weight than for height, for younger children, and for studies done in Africa. If this effect was sustained over a whole 15 years of growth, antibiotics could, in theory, make children 7.2 cm taller and 4.3 kg heavier.

A recent randomised controlled trial not included in this meta-analysis came from Malawi, where researchers added antibiotics (amoxicillin or cefdinir) or placebo to their existing severe acute malnutrition treatment regime (Trehan I and colleagues. *N Engl J Med* 2013;368:425–35). The study involved over 2750 children less than 3 years of age. Antibiotics produced a significant improvement in mortality (RR of death for placebo vs. cefdinir 1.8; 95% CI 1.22–2.64), and improved recovery rates. Weight gain was modestly but significantly superior for the antibiotic-treated groups.

Antibiotic Exposure in Infancy and Risk of Being Overweight in the First 24 Months of Life

Antti Saari, MD[a,b], Lauri J. Virta MD, PhD[c], Ulla Sankilampi MD, PhD[b], Leo Dunkel MD, PhD[d], Harri Saxen MD, PhD[e]

PEDIATRICS Volume 135, number 4, April 2015

WHAT THIS STUDY ADDS: The weight-promoting effect of antibiotics is most pronounced when the exposure occurs at <6 months of age or repeatedly during infancy. Increased body mass is distinctly associated with exposure to cephalosporins and macrolides, especially in boys.

İNTESTİNAL MİKROBİYOTA
Obesite-Diabetes 2015

Mezenterik viseral yağ dokuda bakteri DNA örnekleri saptanmış

(omentum ve diğer viseral adipoz doku örneklerinde yok)

RALSTONİA PICKETTI

Gram negatif çomak, proteobakter

İNTESTİNAL MİKROBİYOTA
Obesite-Diabetes 2015

RALSTONİA PICKETTI

1- Viseral dokuda *R. picektti* yükü ile sistemik inflamasyon arasında pozitif korelasyon mevcut

2- Fecal *R. picketti* düzeyi ile insülin rezistansı olduğu gösterilmiş.

3- Deneysel çalışmada 4 hafta süre ile oral *R. picketti* içeren gavaj alan ratlarda kilo alımının olduğu, OGTT'nin bozulduğu gösterilmiş.

4- *R. picektti* için geliştirilmiş AŞI uygulanan ratlarda insülin rezistansı gelişiminde azalma!!

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OFFICIAL JOURNAL OF THE AMERICAN ACADEMY OF PEDIATRICS

Corrin

Pediatrics 2012;130;e794; originally published online September 24, 2012;
DOI: 10.1542/peds.2011-3886

PEDIATRICS®
OFFICIAL JOURNAL OF THE AMERICAN ACADEMY OF PEDIATRICS

Antibiotic Exposure and IBD Development Among Children: A Population-Based Cohort Study

WHAT'S KNOWN ON THIS SUBJECT: Inflammatory bowel disease pathogenesis is incompletely understood. Previous pediatric studies suggested associations between antibiotic use and inflammatory bowel disease development but were limited by recall bias, lack of controls, incomplete antibiotic capture, or included exposures between symptom onset and diagnosis.

WHAT THIS STUDY ADDS: Our population-based cohort study suggests that certain childhood antibiotic exposures are associated with an increased risk of developing inflammatory bowel disease. Our findings have implications for understanding the condition's pathogenesis and provide additional stimulus for reducing unnecessary childhood antibiotic use.

AUTHORS: Matthew P. Kronman, MD, MSCE,[a] Theoklis E. Zaoutis, MD, MSCE,[b,c] Kevin Haynes, PharmD, MSCE,[c] Rui Feng, PhD,[c] and Susan E. Coffin, MD, MPH[b,c]

[a]Division of Infectious Diseases, Seattle Children's Hospital, University of Washington, Seattle, Washington; [b]Division of Infectious Diseases, The Children's Hospital of Philadelphia, Philadelphia, Pennsylvania; and [c]Department of Biostatistics and Epidemiology, the Center for Clinical Epidemiology and Biostatistics, Perelman School of Medicine at the University of Pennsylvania, Philadelphia, Pennsylvania

KEY WORDS
antimicrobials, epidemiology, inflammatory bowel disease, pediatric, population-based studies

ABBREVIATIONS
aHR—adjusted hazard ratio
CI—confidence interval

DOI: 10.1542/peds.2011-3880

PEDIATRICS®

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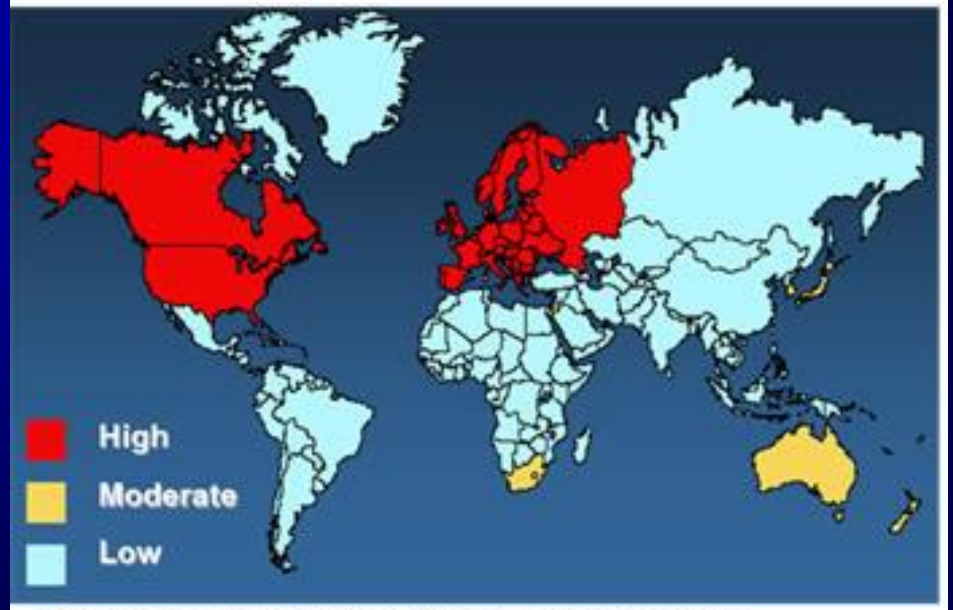
Helminths infestation incidence

Helminths infestation incidence

Autoimmune disorders incidence



Personal communication from Dr. Joel Weinstock

For a better start in life

start COLA earlier!

How soon is too soon?

Not soon enough. Laboratory tests over the last few years have proven that babies who start drinking soda during that early formative period have a much higher chance of gaining acceptance and "fitting in" during those awkward pre-teen and teen years. So, do yourself a favor. Do your child a favor. Start them on a strict regimen of sodas and other sugary carbonated beverages right now, for a lifetime of **guaranteed** happiness.

The Soda Pop Board of America
1515 W. Hart Ave. - Chicago , ILL.


ALO 171 SİGARA BIRAKMA HATTI MI ?
EVET BUYRUN...
ADRESİ VERİYORUM 2 PAKET BIRAKIRSINIZ
DÜÜTT.....
Şahin GÜNEŞ

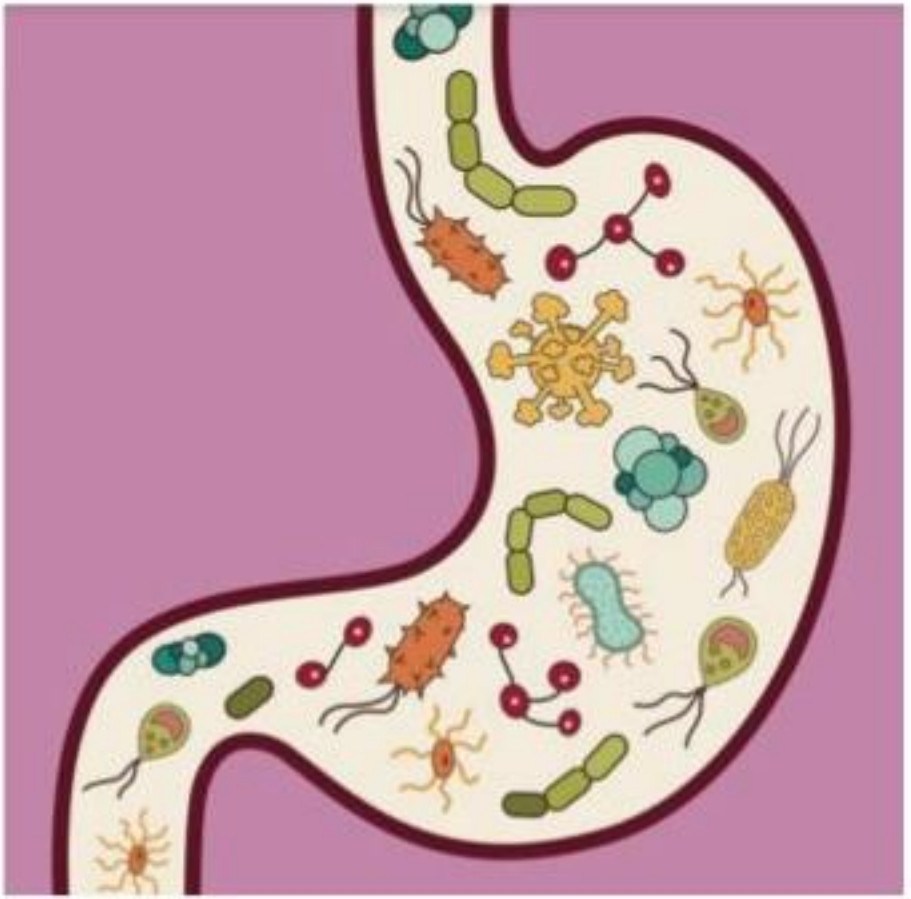
Medical News & Perspectives

Unraveling the Influence of Gut Microbes on the Mind

5 May 2015

M. J. Friedrich

JAMA®
The Journal of the American Medical Association



THE DAILY BEAST

David Perlmutter, MD

The Cure for Brain Diseases Is in Your Gut

28 April 2015

Melancholic microbes or how the microbiota can affect our mood

January 27, 2014, 13:52

- Dinan et al.
- University College Cork
- Deneysel çalışmalarda intestinal mikrobiyota kompozisyonunda değişikliğin depresyon ve anksiyete arasında ilişki olduğu gösterilmiştir.
- Bazı bakterilerin bulunmamasının serotonin bağırsak ve beyinde yeterli düzeyde üretilmediği gösterilmiş (mutluluk?)
- Tedavide probiyotikle

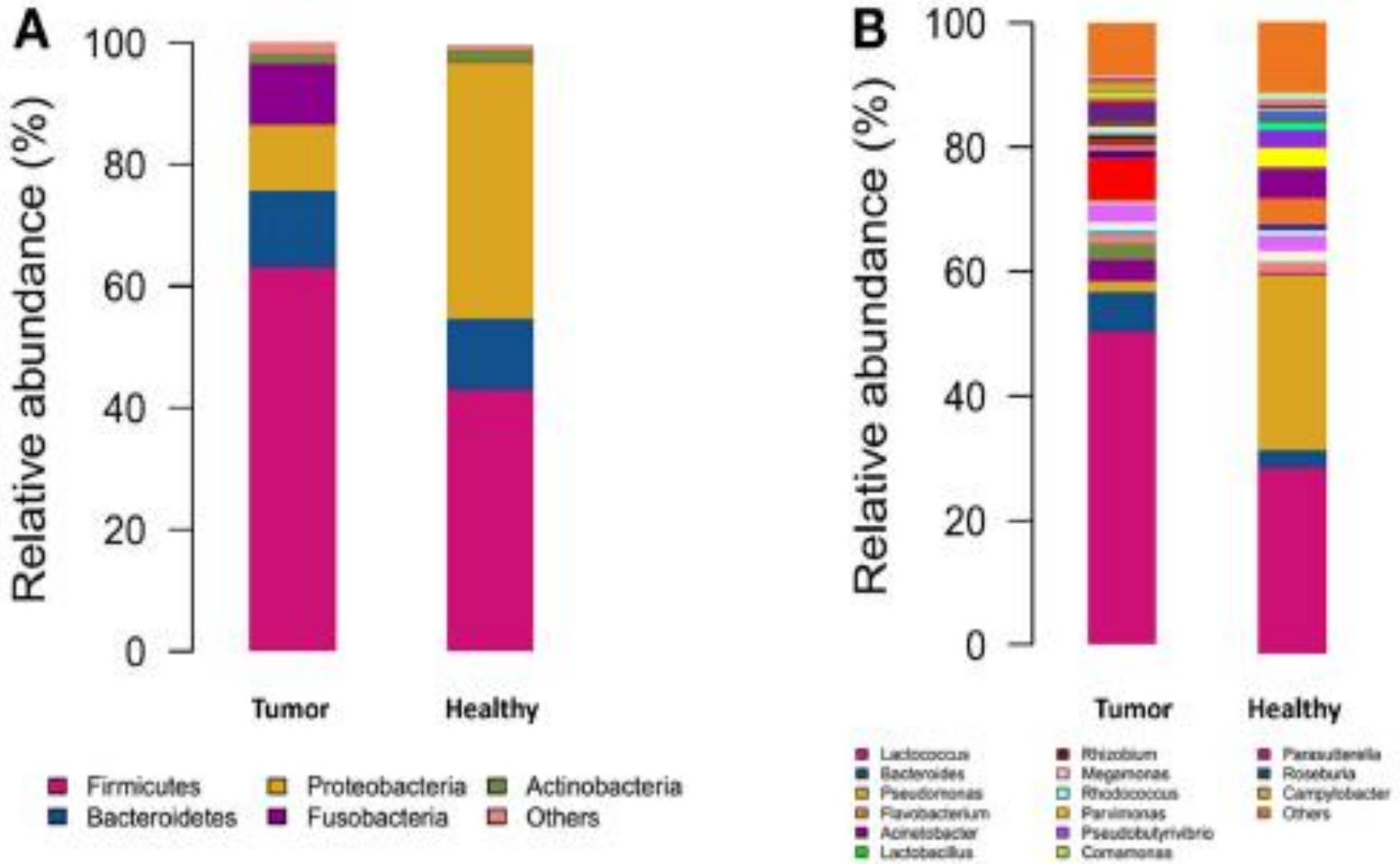
frontiers in MICROBIOLOGY

ORIGINAL RESEARCH ARTICLE
published: 02 February 2015
doi: 10.3389/fmicb.2015.00020

Microbiota disbiosis is associated with colorectal cancer

*Zhiguang Gao†, Bomin Guo†, Renyuan Gao†, Qingchao Zhu and Huanlong Qin**

Department of General Surgery, Shanghai Jiao Tong University Affiliated Sixth People's Hospital, Shanghai, China



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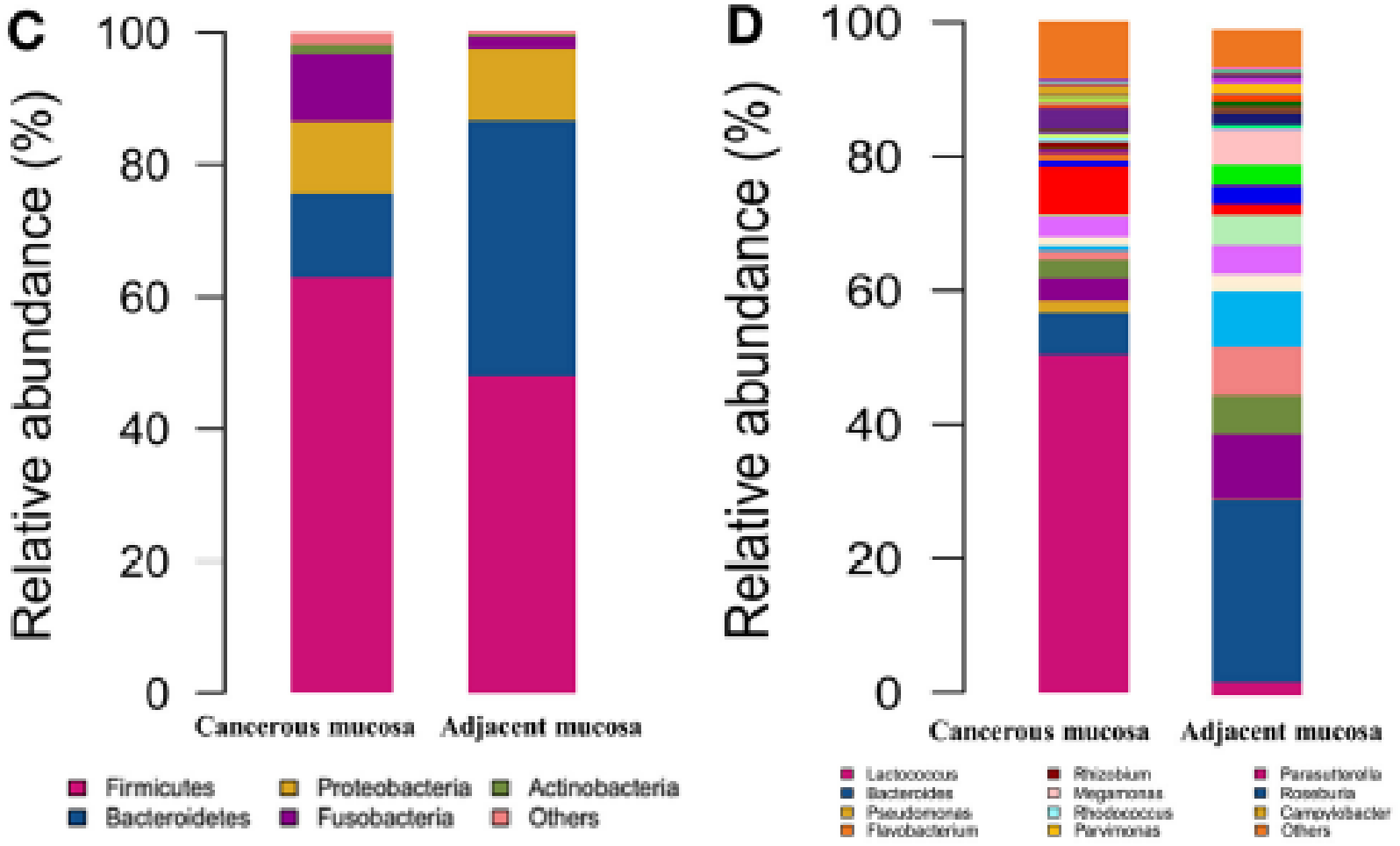
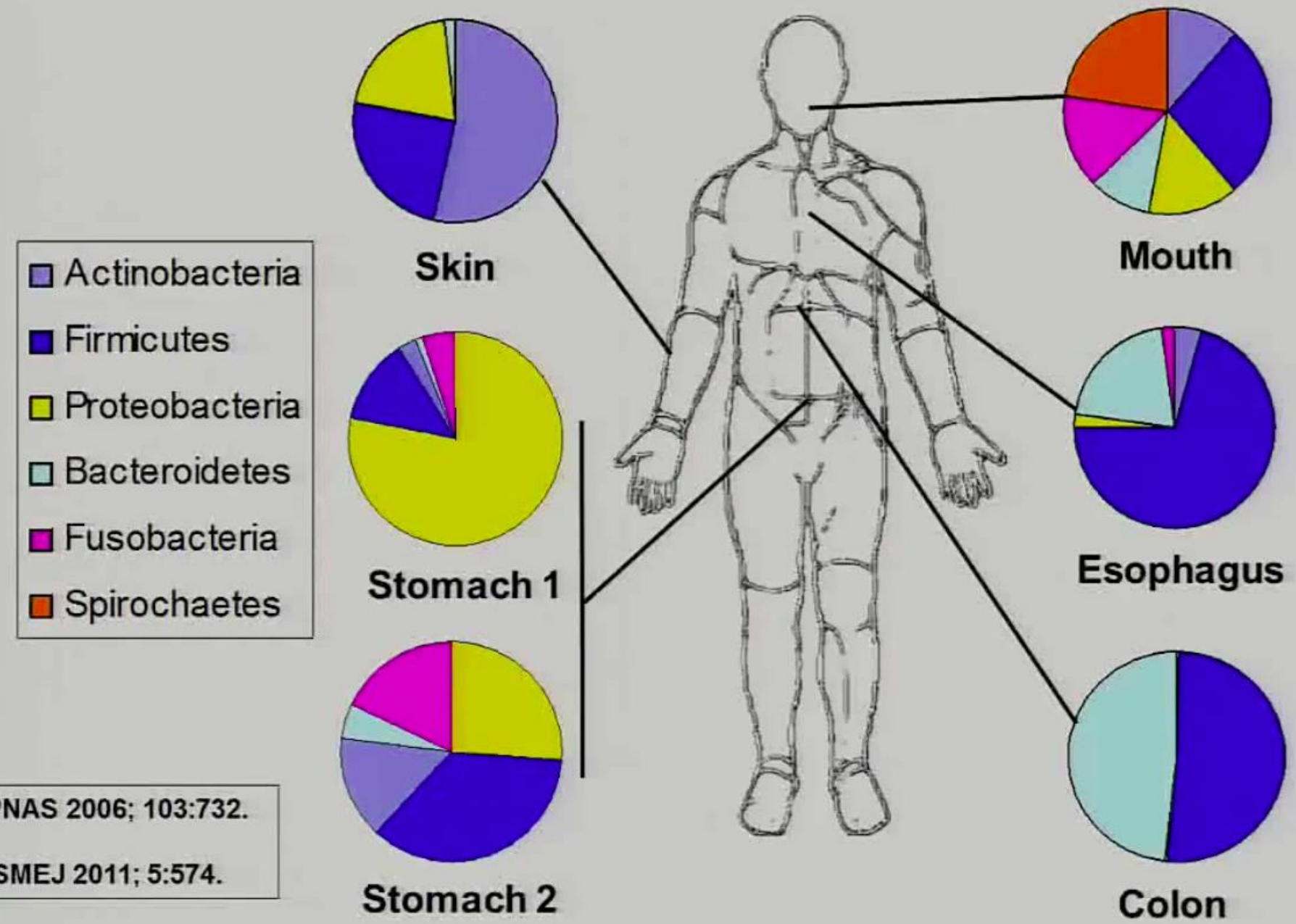


Effects of *H. pylori* loss on gastric microbiome



PNAS 2006; 103:732.

ISMEJ 2011; 5:574.