



Antibiyotikler ve Mikrobiyom

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Original Article

β-lactam antibiotic resistance in aerobic commensal fecal flora of newborns

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The only risk factor for colonization with ESBL-producing bacteria after discharge from the hospital was failure to feed breast milk (relative risk [RR], 7.6; 95% confidence interval [CI], 1.24–47.58; *P* = 0.028).

Table 4 Risk factors for colonization with ESBL-producing microorganisms

Risk factors	RR	95%CI	<i>P</i>
Gestational age	–	–	0.750
Birthweight (<1500 g)	22.02	1.60–309.90	0.021
Vaginal delivery	3.52	1.25–9.92	0.017
Sex (male)	2.61	1.08–6.28	0.031
Failure to feed breast milk	–	–	0.818
Maternal antibiotic usage	3.81	1.07–13.50	0.038
Antibiotic usage of infant	14.05	1.19–164.62	0.035
Intravenous application	–	–	0.647
Total parenteral feeding	–	–	0.834
Nasogastric feeding	0.05	0.004–0.064	0.021
Ventilatory therapy	–	–	0.862
Premature rupture of membrane	7.41	1.19–45.90	0.031
Duration of hospitalization (>5 days)	–	–	0.744
Groups			
Control group (references)			
Neonatal ward group	–	–	0.544
NICU group	–	–	0.804



2010



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

nature

ARTICLES

A human gut microbial gene catalogue established by metagenomic sequencing



2012



ARTICLE

doi:10.1038/nature11209

A framework for human microbiome research

The Human Microbiome Project Consortium*

A map of diversity in the human microbiome

Lactobacillus species (*L. gasseri*, *L. jensenii*, *L. crispatus*, *L. iners*) are predominant but mutually exclusive in the **vagina**

Staphylococcus epidermidis colonizes external body sites



○ Commensal microbes
★ Potential pathogens

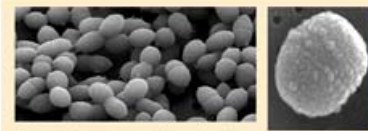
The four most abundant phyla

- Actinobacteria
- Bacteroidetes
- Firmicutes
- Proteobacteria

Low abundance phyla

- Chloroflexi
- Cyanobacteria
- Euryarchaeota
- Fusobacteria
- Lentisphaerae
- Spirochaetes
- Synergistetes
- Tenericutes
- Thermi
- Verrucomicrobia

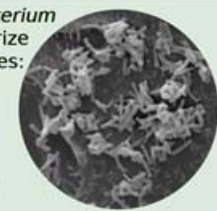
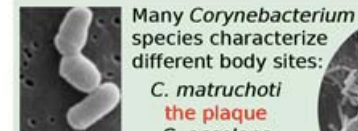
Streptococcus dominates the oral cavity with *S. mitis* > 75% in the **cheek**



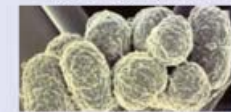
Propionibacterium acnes lives on the skin and **nose** of most people



Many *Corynebacterium* species characterize different body sites:
C. matruchoti the **plaque**
C. accolens the **nose**
C. croppenstedtii the **skin**



Several *Prevotella* species are present in the gastrointestinal tract. *P. copri* is present in 19% of the subjects and dominates the **intestinal** flora when present



Microscopy from <http://bacmap.wishartlab.com>

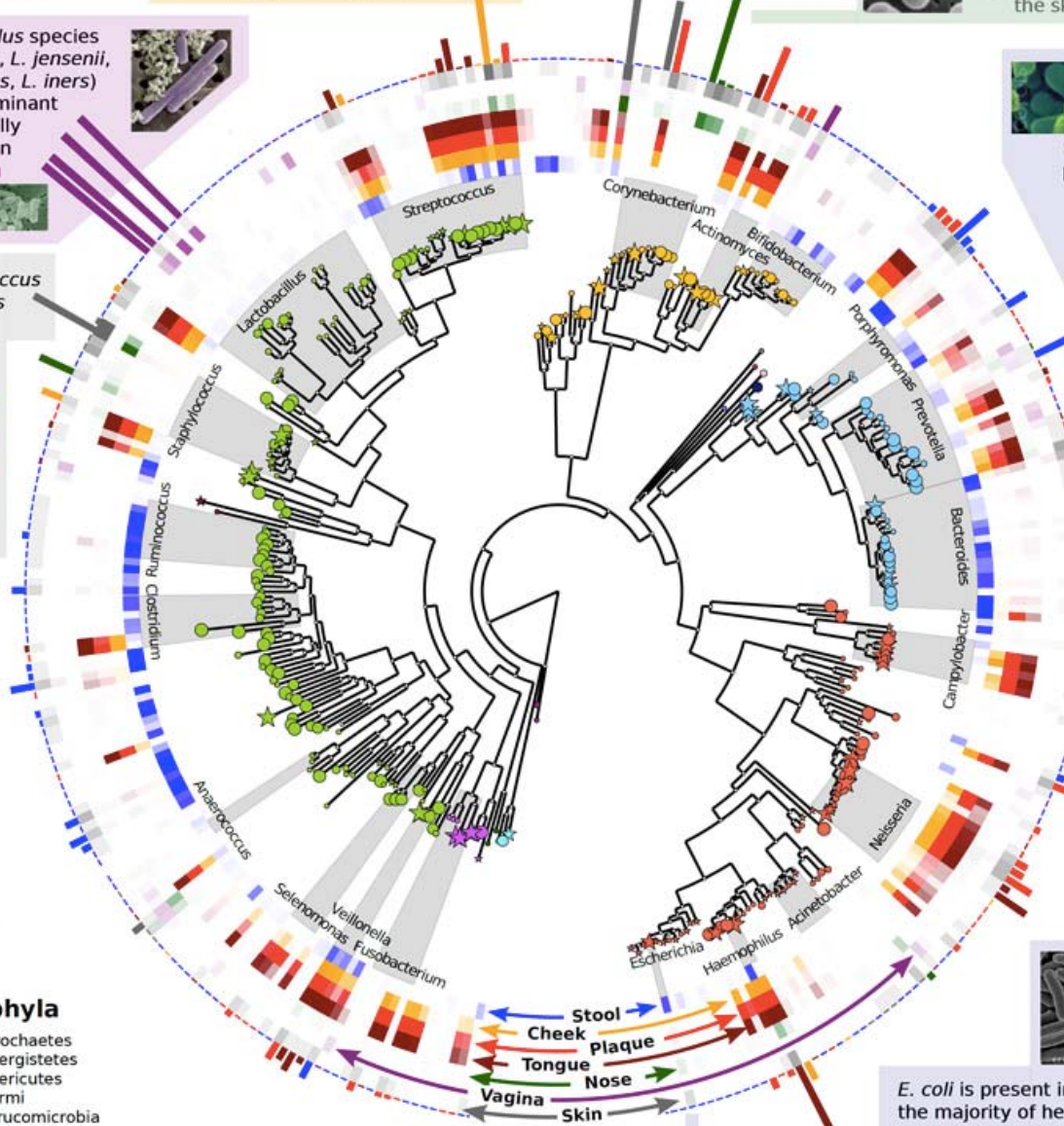
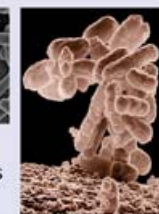
Bacteroides is the most abundant genus in the **gut** of almost all healthy subjects



Campylobacter includes opportunistic pathogens, but members live in the oral cavities of most healthy people in the cohort

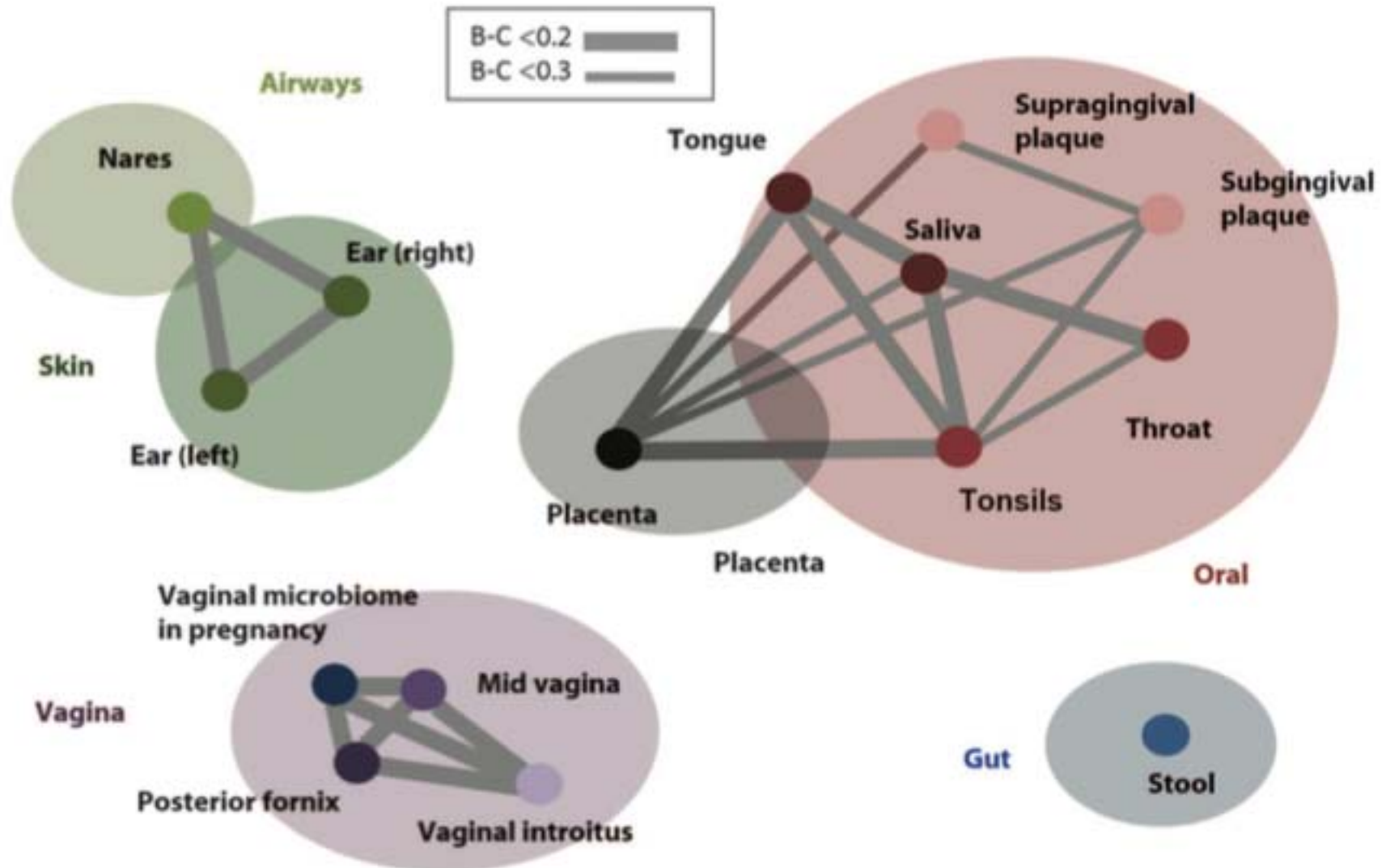


E. coli is present in the **gut** of the majority of healthy subjects but at very low abundance



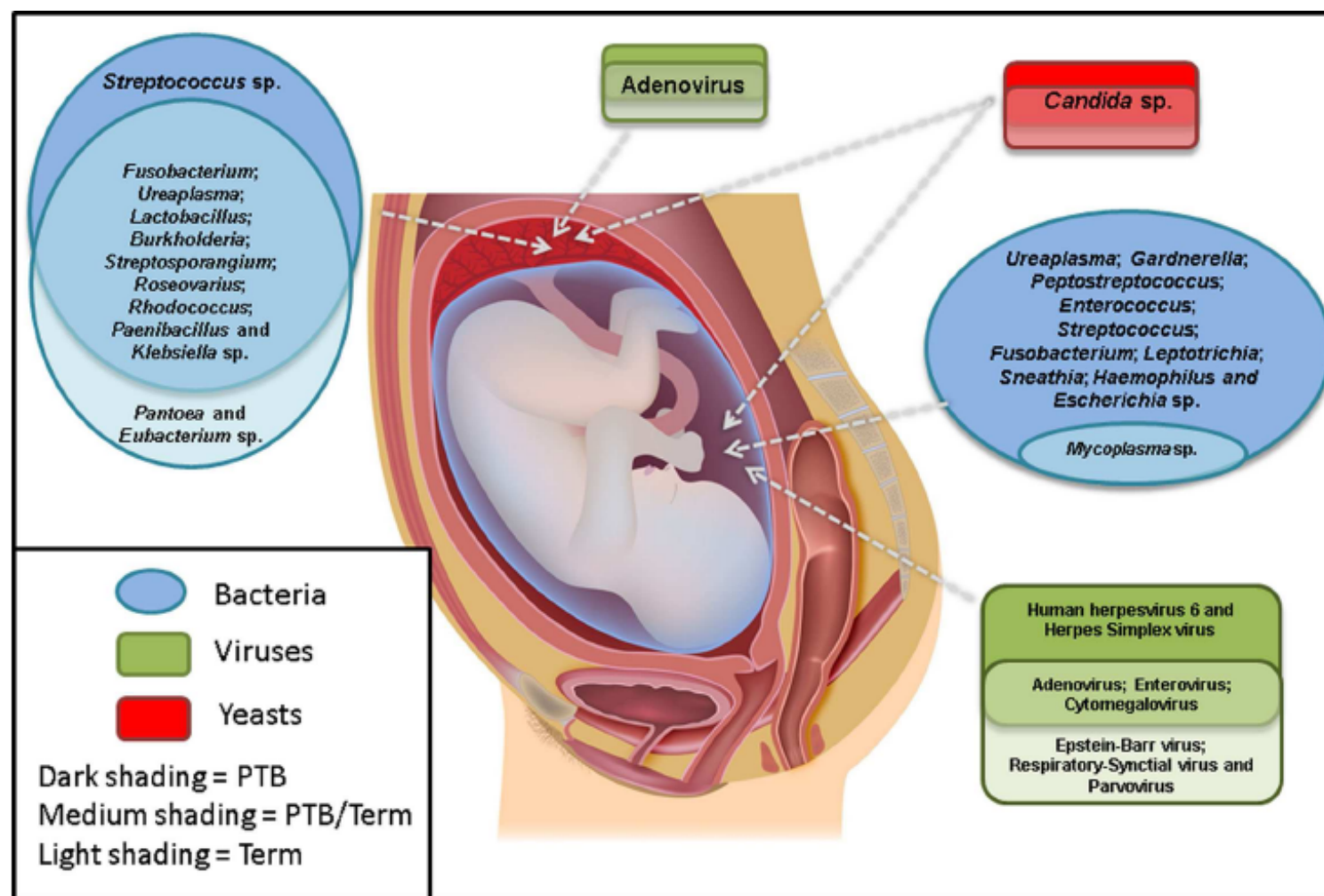
The Placenta Harbors a Unique Microbiome

Kjersti Aagaard,^{1,2,3*} Jun Ma,^{1,2} Kathleen M. Antony,¹ Radhika Ganu,¹ Joseph Petrosino,⁴ James Versalovic⁵



Exploring preterm birth as a polymicrobial disease: an overview of the uterine microbiome

Matthew S. Payne* and Sara Bayatibojakhi





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Stunning diversity of gut bacteria uncovered by new approach to gene sequencing devised at Stanford

The many microbes living in our intestines are far more diverse than once suspected, a new genomic technique reveals.

DEC 14
2015

A collaboration between computer scientists and geneticists at Stanford has produced a novel technique for mapping the diversity of bacteria living in the human gut.

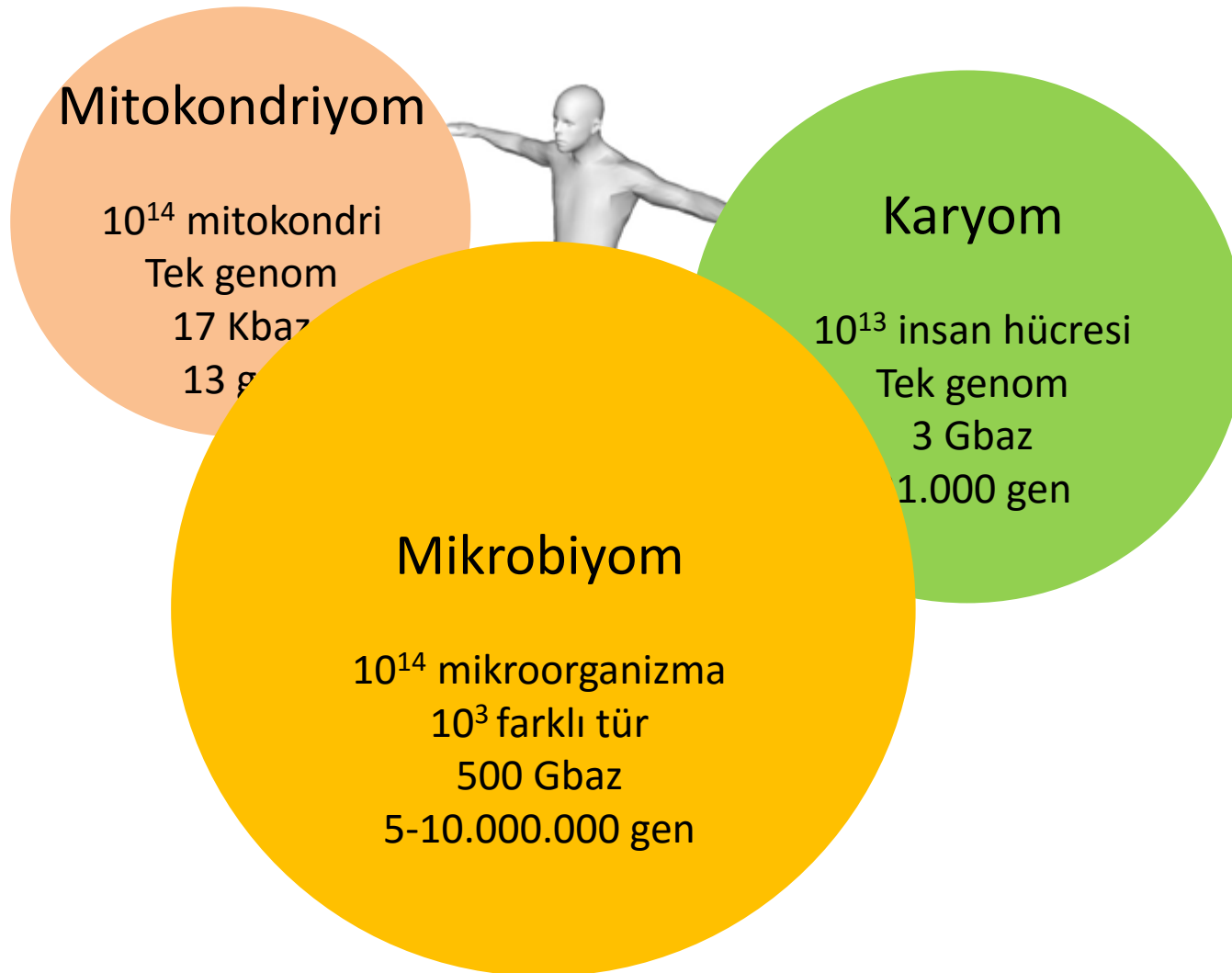
The new approach revealed a far more diverse community than the researchers had anticipated. “The bacteria are genetically much more heterogeneous than we thought,” said [Michael Snyder](#), PhD, professor and chair of genetics.

Any two humans typically differ by about 1 in 1,000 DNA bases, whereas bacteria of the same species may differ by as many as 250 in 1,000,

Synthetic long-read sequencing reveals intraspecies diversity in the human microbiome. Kuleshov V, Jiang C, Zhou W, Jahanbani F, Batzoglou S, Snyder M. Nature Biotechnology. 14 December 2015. 10.1038/nbt.316.

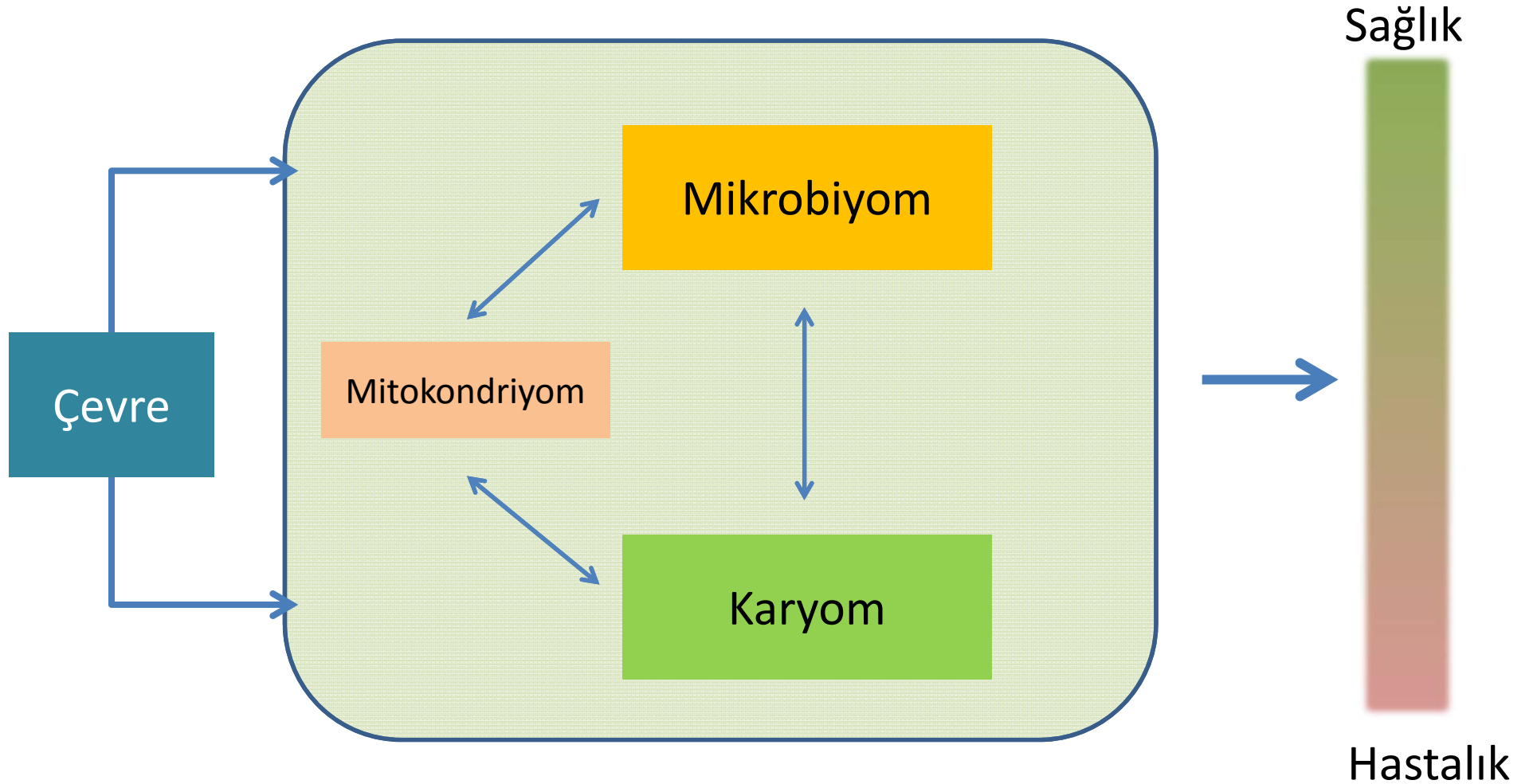


Öteki genomlarımız?



Simbiyotik etkileşimler

Meta-organizma



Simbiyoz

- Benzer olmayan iki organizmanın birlikte yaşaması
 - Anton de Bary 1878
- İki organizma arasında *kalıtsal değişim potansiyeli* taşıyan etkileşimler
 - Francis Patrick Ryan 2016

Kalıtımı deęiřtirmenin tek yolu mutasyon deęildir.

Deęiřim mekanizması	Genetik dizide deęiřim	Deęiřimin doęası	Seçilimin etkili olduęu düzey	Çevresel etkilenim
Mutasyon	Evet	Rastlantısal Birikici	Gen Organizma	Hayır (?)
Epigenetik	Hayır	Rastlantısal deęil Birikici	Epigenetik kalıtım sistemleri	Evet
Simbiyogenez	Evet	Rastlantısal deęil Hızlı	Holobiyont düzeyi	Hayır
Hibridogenez	Evet	Rastlantısal deęil Hızlı	Hibrit genom düzeyi	Hayır

RESEARCH

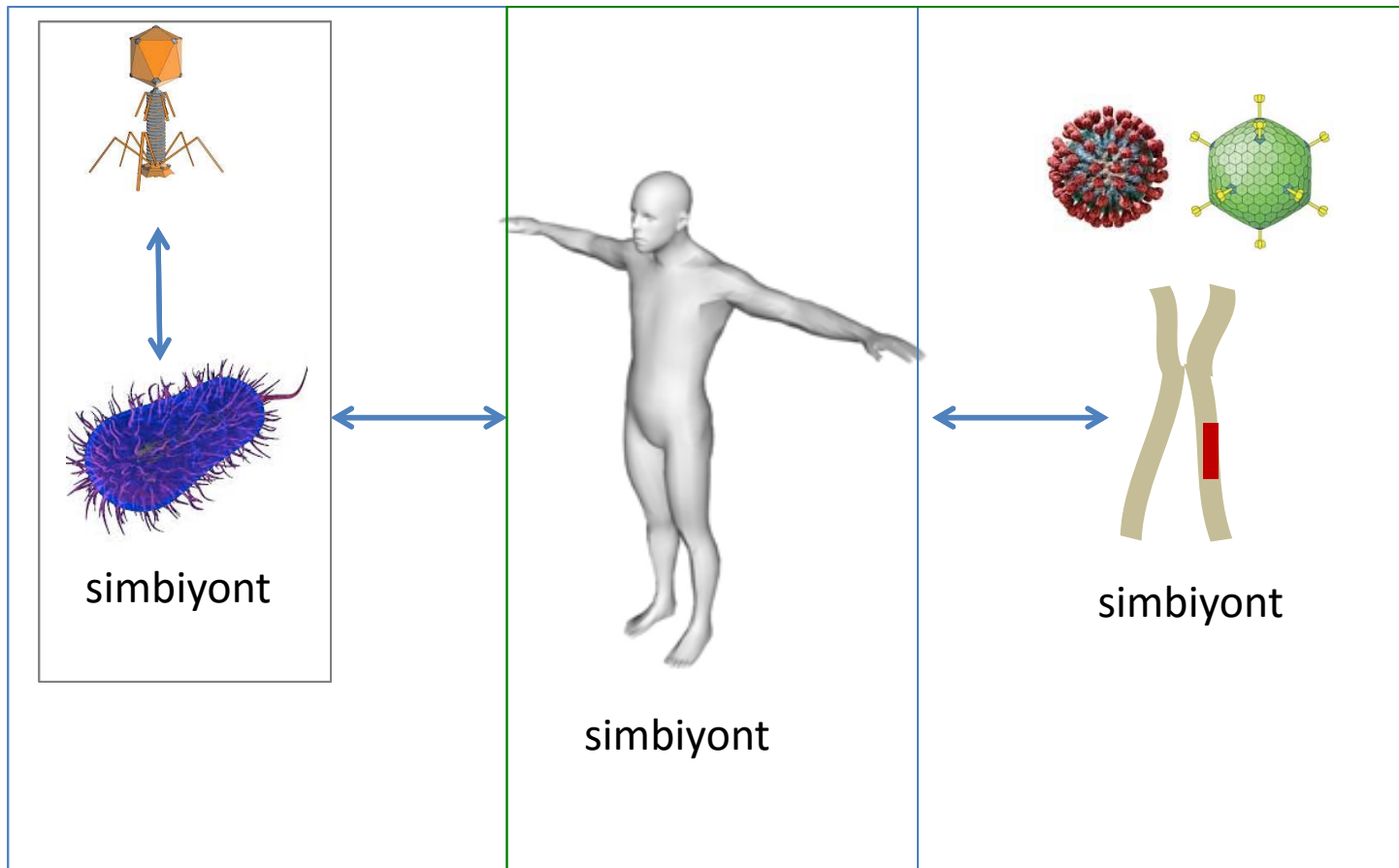
Open Access

Expression of multiple horizontally acquired genes is a hallmark of both vertebrate and invertebrate genomes

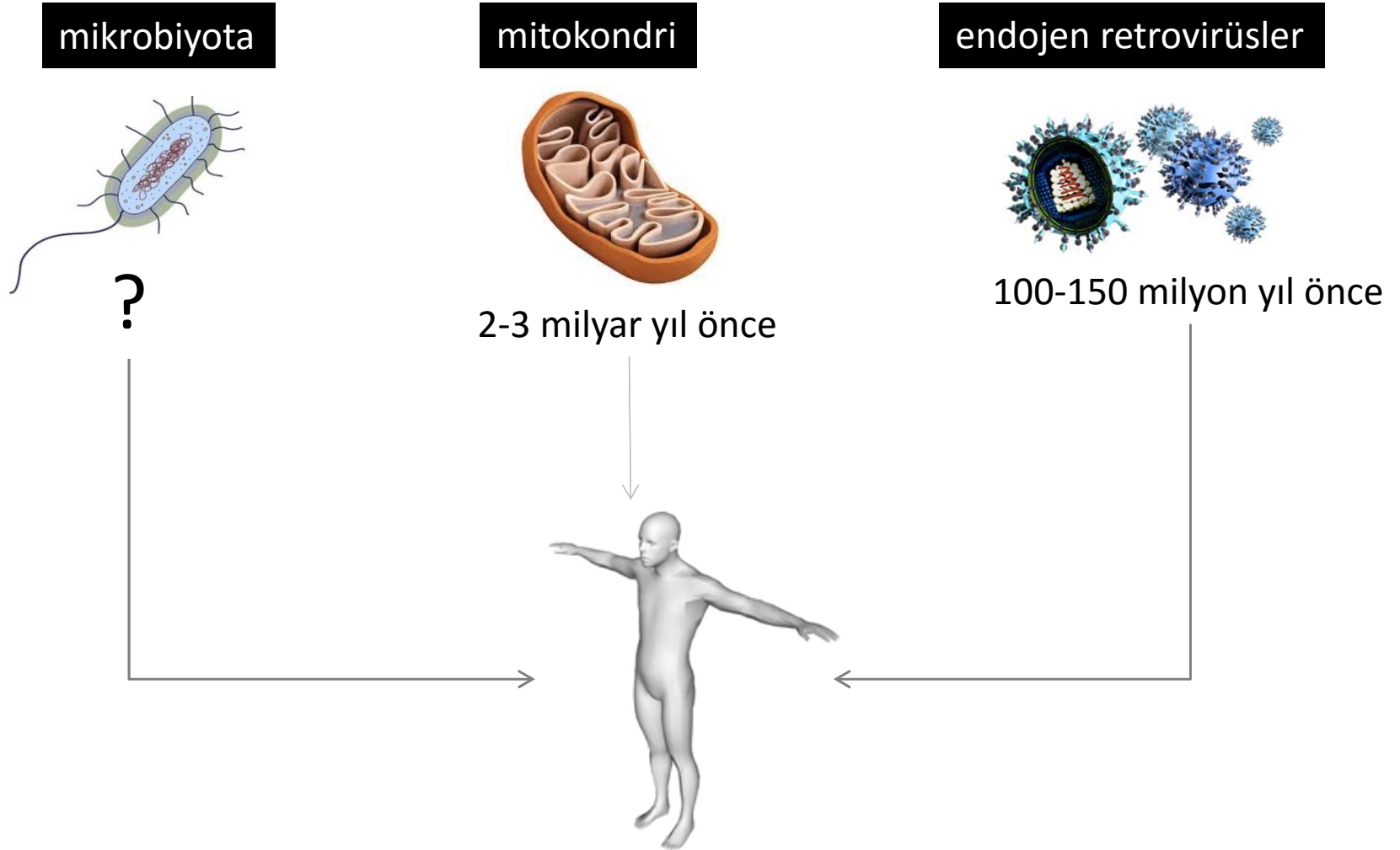
Alastair Crisp^{1†}, Chiara Boschetti^{1†}, Malcolm Perry^{1,2,3}, Alan Tunnacliffe^{1*} and Gos Micklem^{2,3*}

Simbiyont ve Holobiyont

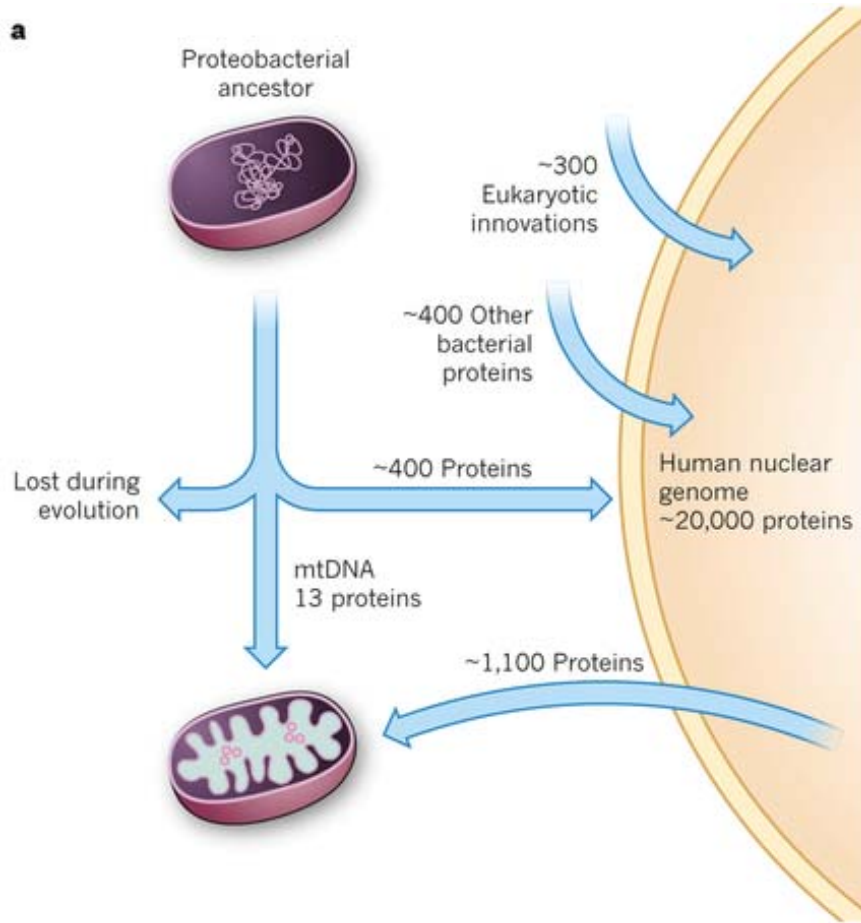
holobiyont



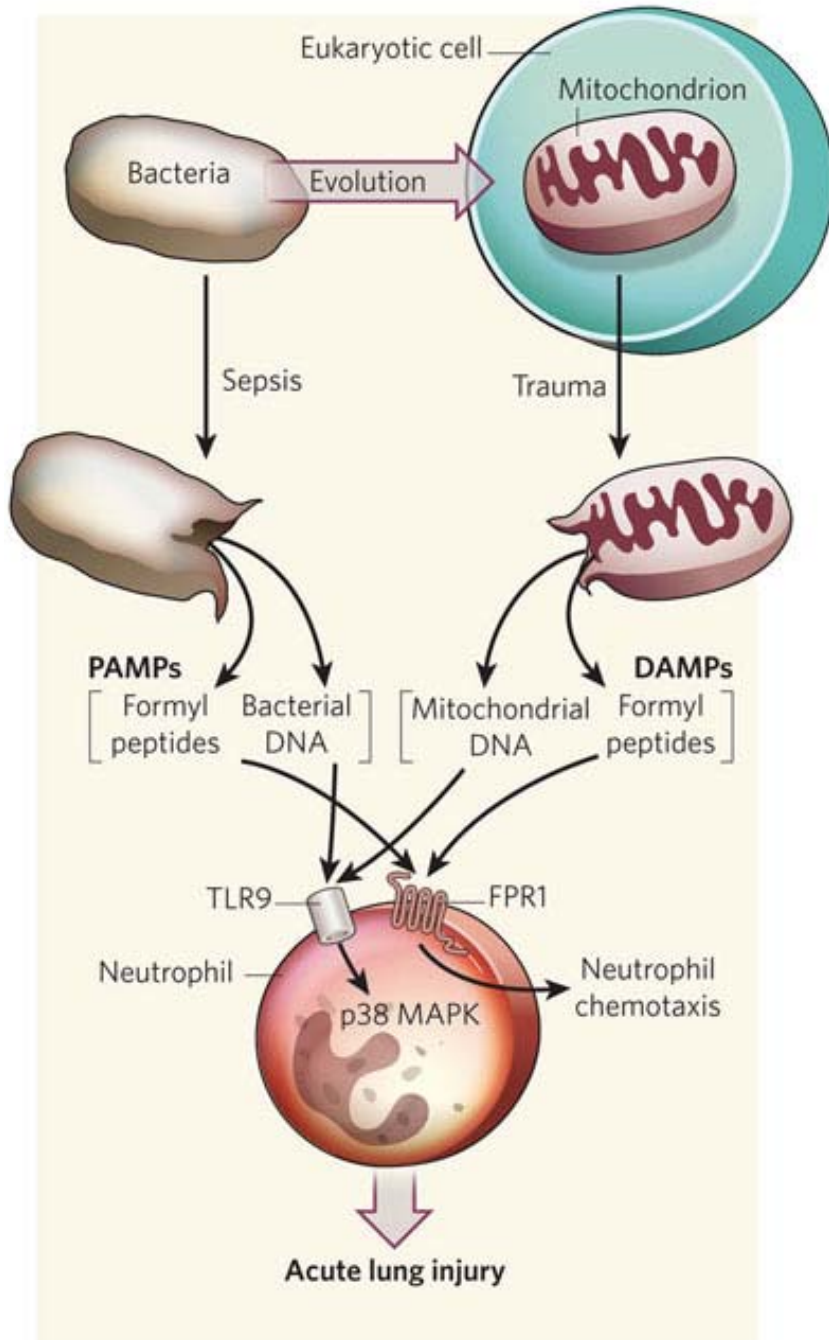
İnsanın tarihinde üç önemli *holobiyontik* olay



Mitokondrinin öyküsü

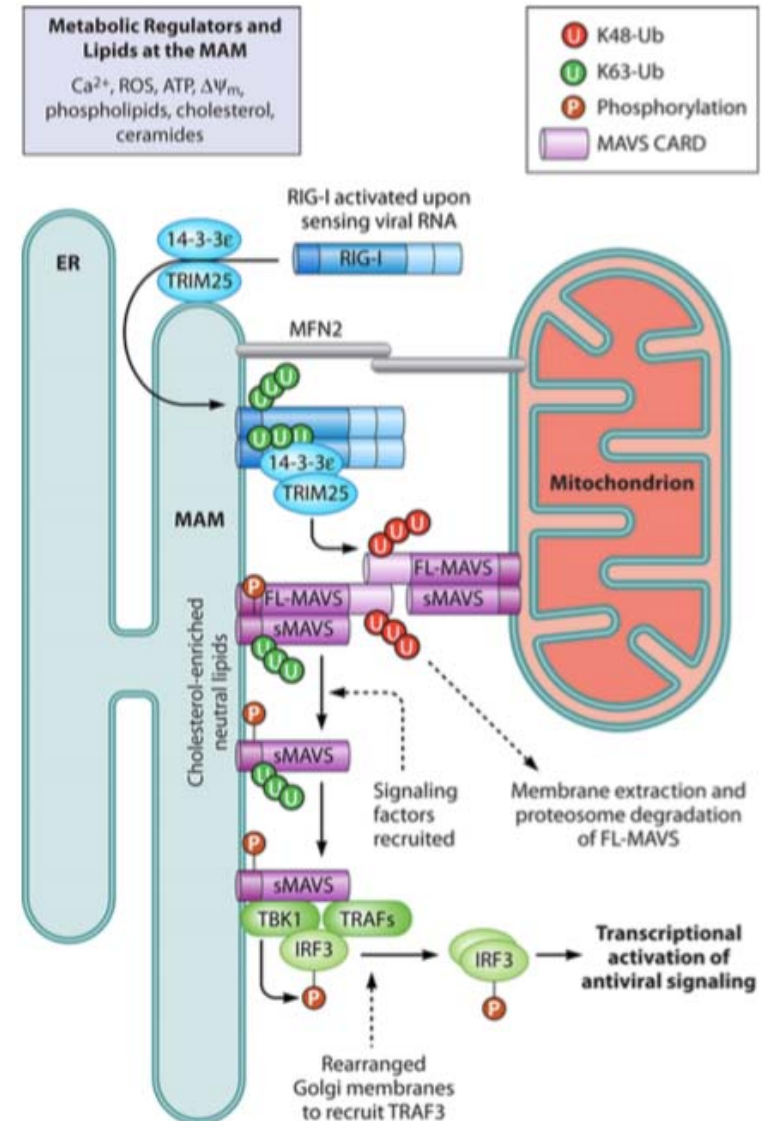
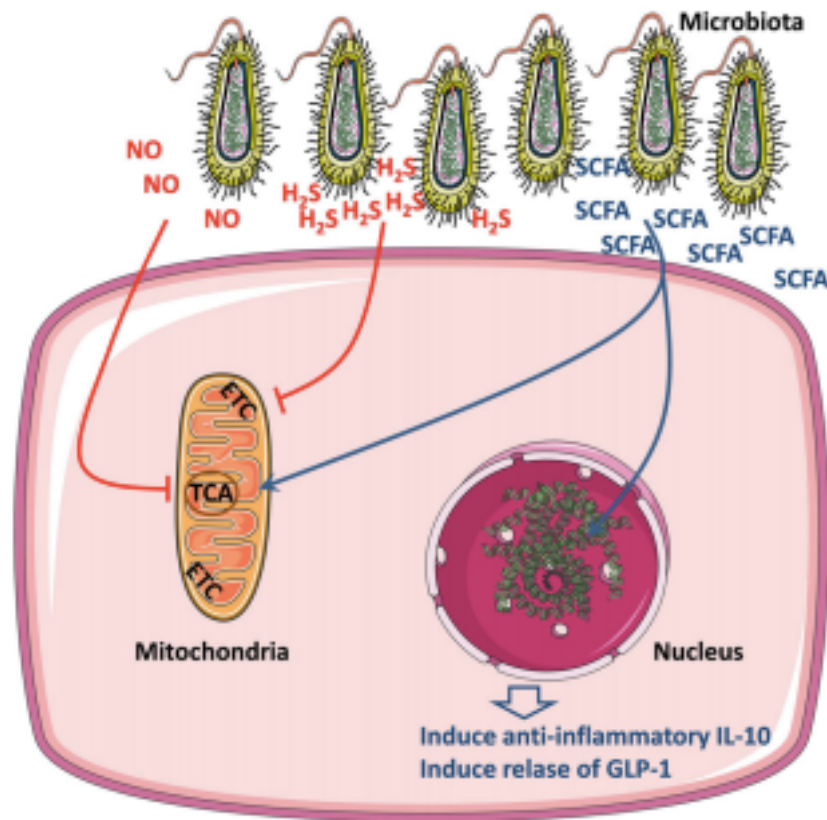


- Endosimbiyoz kuramı (2-3 milyar yıl önce)
- Mozaik yapı
 - Çembersel DNA
 - prokaryotik ribozom
 - Faj kökenli DNA polimeraz



- Doğal bağışık yanıtların başlatılması
 - PAMP (mikroplar)
 - DAMP (mitokondri)

Mikroplar *mitokondri* ile etkileşir



ANTIBIOTICS

Bactericidal Antibiotics Induce Mitochondrial Dysfunction and Oxidative Damage in Mammalian Cells

Sameer Kalghatgi,^{1*} Catherine S. Spina,^{1,2,3*} James C. Costello,¹ Marc Liesa,³
J. Ruben Morones-Ramirez,¹ Shimyn Slomovic,¹ Anthony Molina,^{3,4}
Orlan S. Shirihai,³ James J. Collins^{1,2,3†}

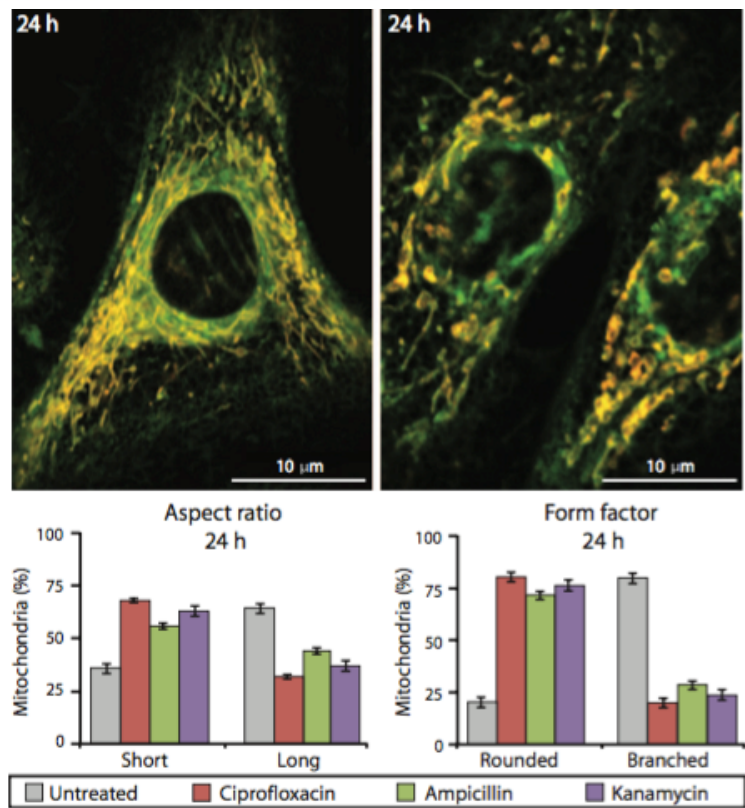


Fig. 3. Mitochondria in bactericidal antibiotic-treated cells show an abnormal, profligate state. Mitochondrial morphology was measured

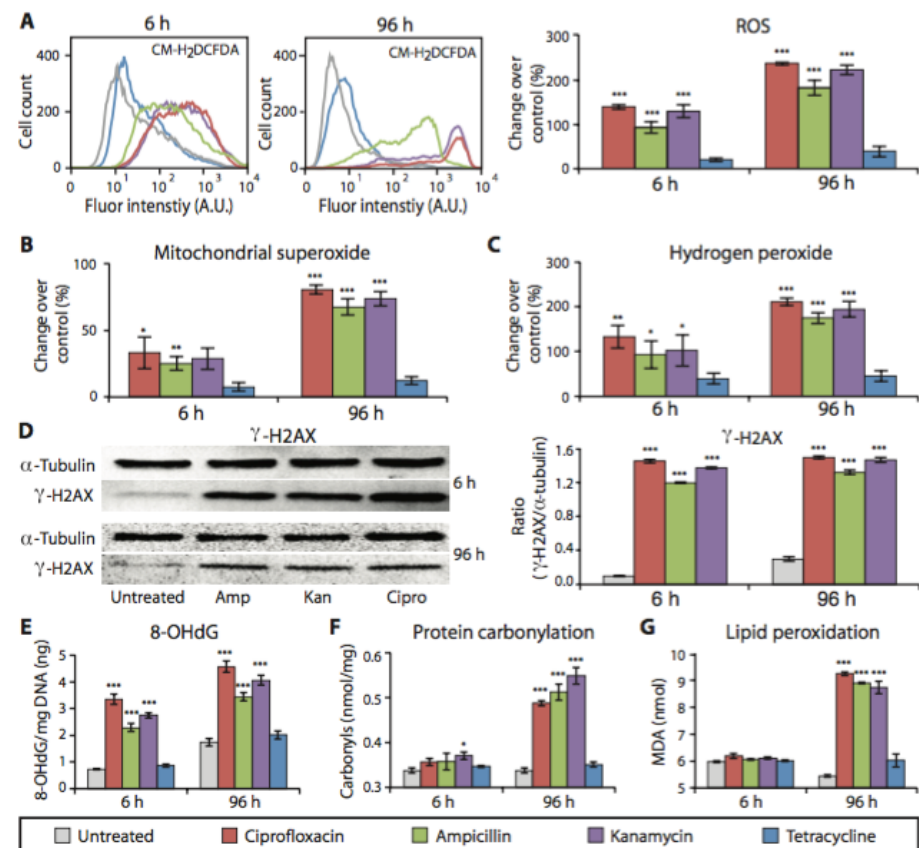
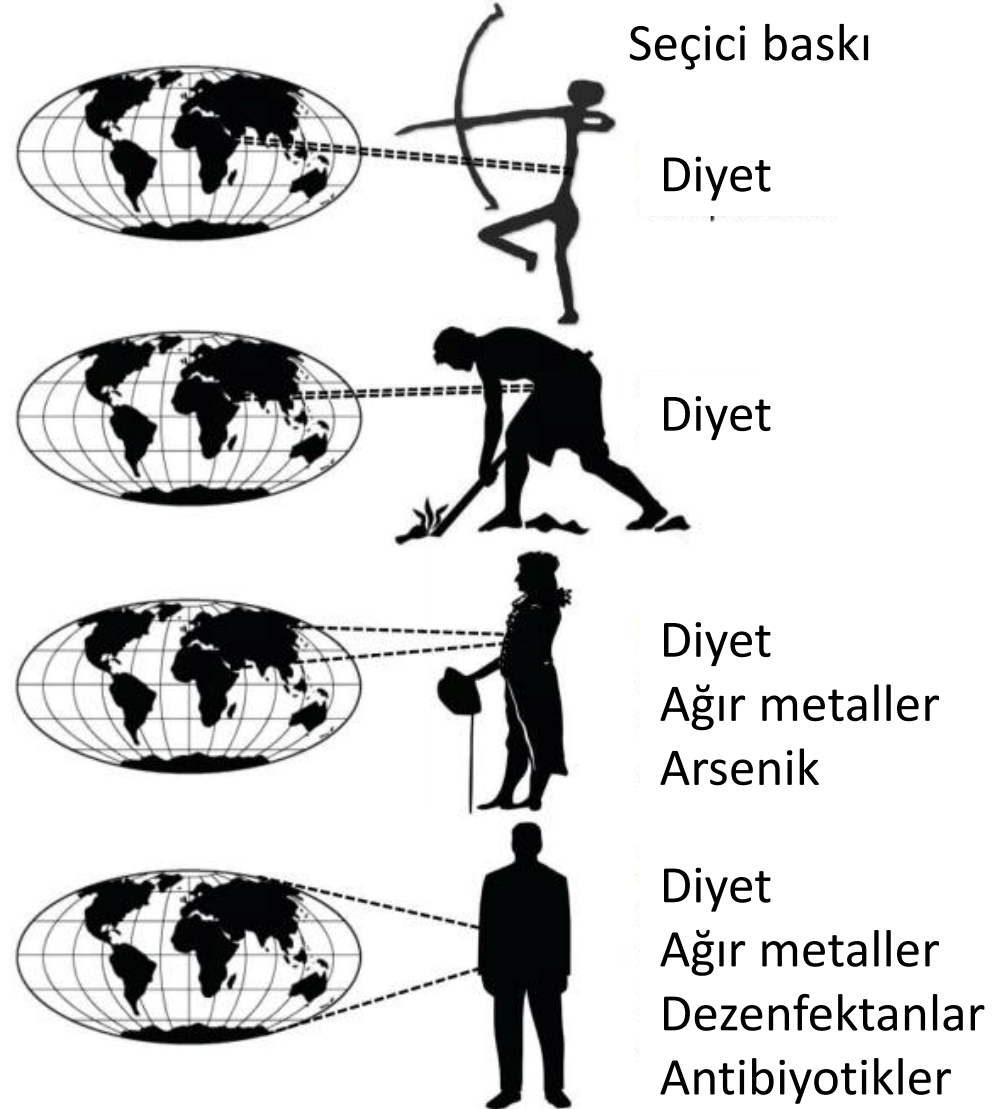


Fig. 1. Bactericidal antibiotics cause oxidative damage to mammalian cells. ROS and oxidative

Mikrobiyota üzerindeki seçici baskılar



Tn21'in evrimi

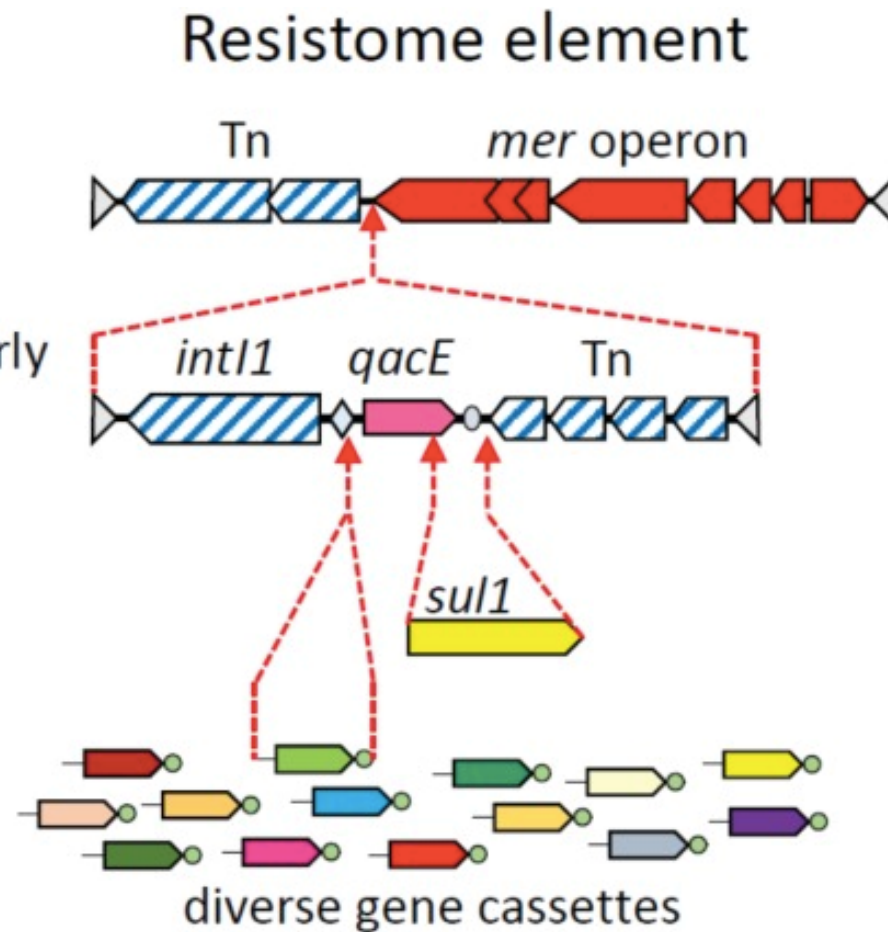
Selective Agent

Mercury pre-1900

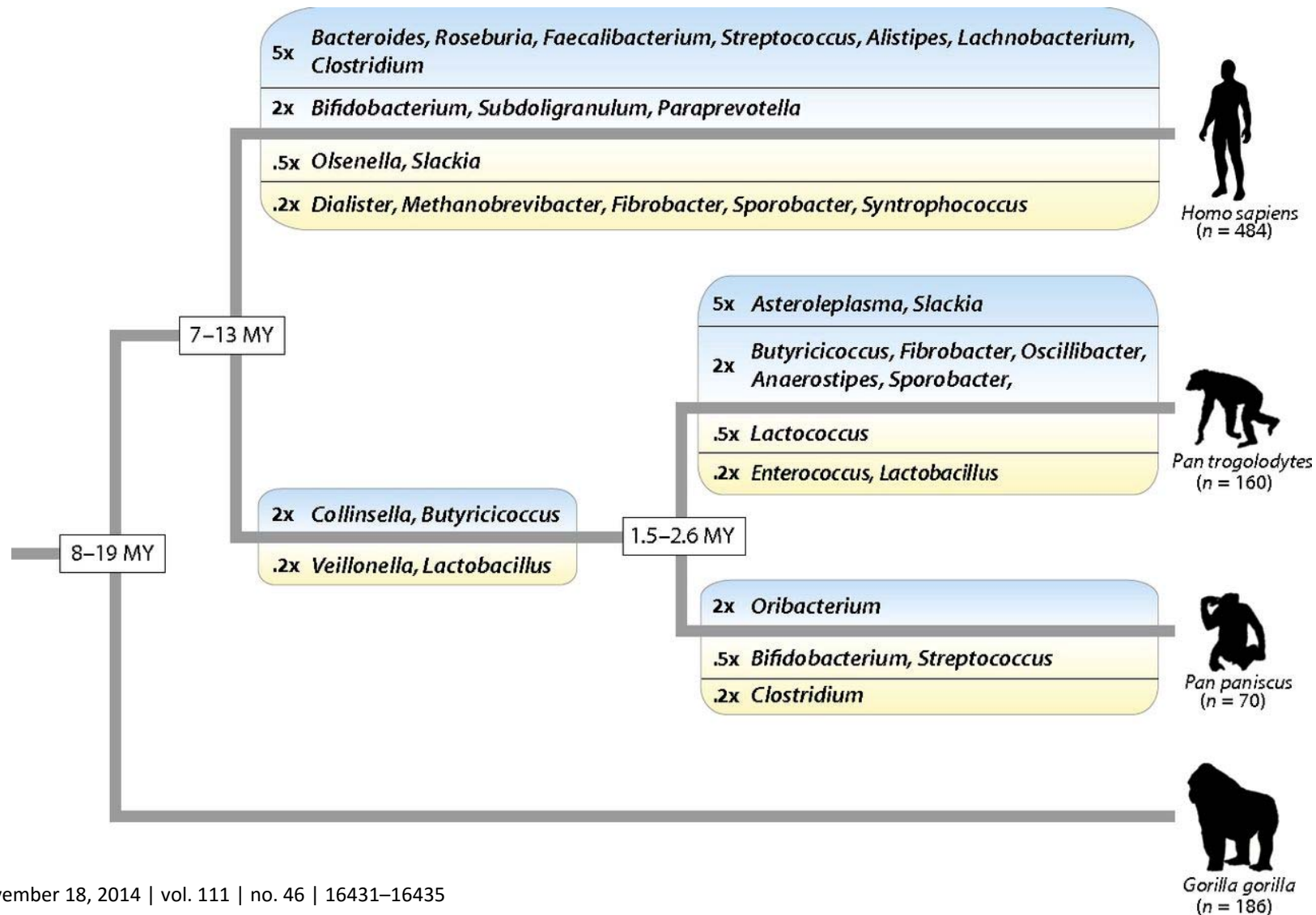
Quaternary ammonium early 1930s

Sulphonamide late 1930s

Diverse antibiotics 1950s to present



Atasal çeşitliliği kaybediyoruz...



MICROBIAL ECOLOGY

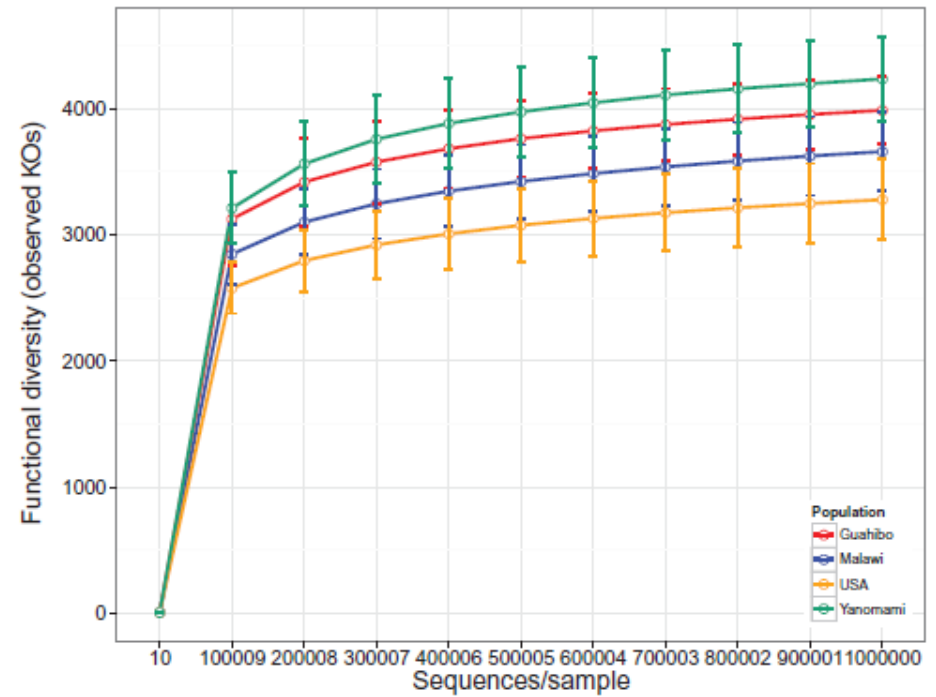
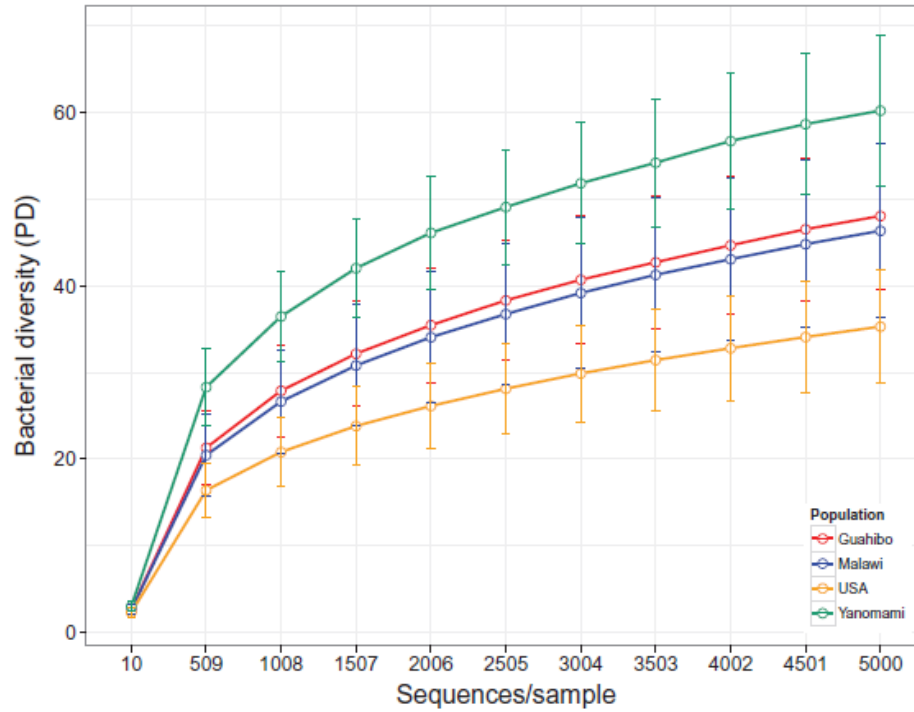
The microbiome of uncontacted Amerindians

Clemente et al. Sci. Adv. 2015;1:e1500183 17 April 2015



Yanomami'lerin şaşırtıcı zenginliği

bilinen en yüksek filogenetik ve işlevsel çeşitlilik



Mikrobiyomdaki antibiyotik direnç genleri

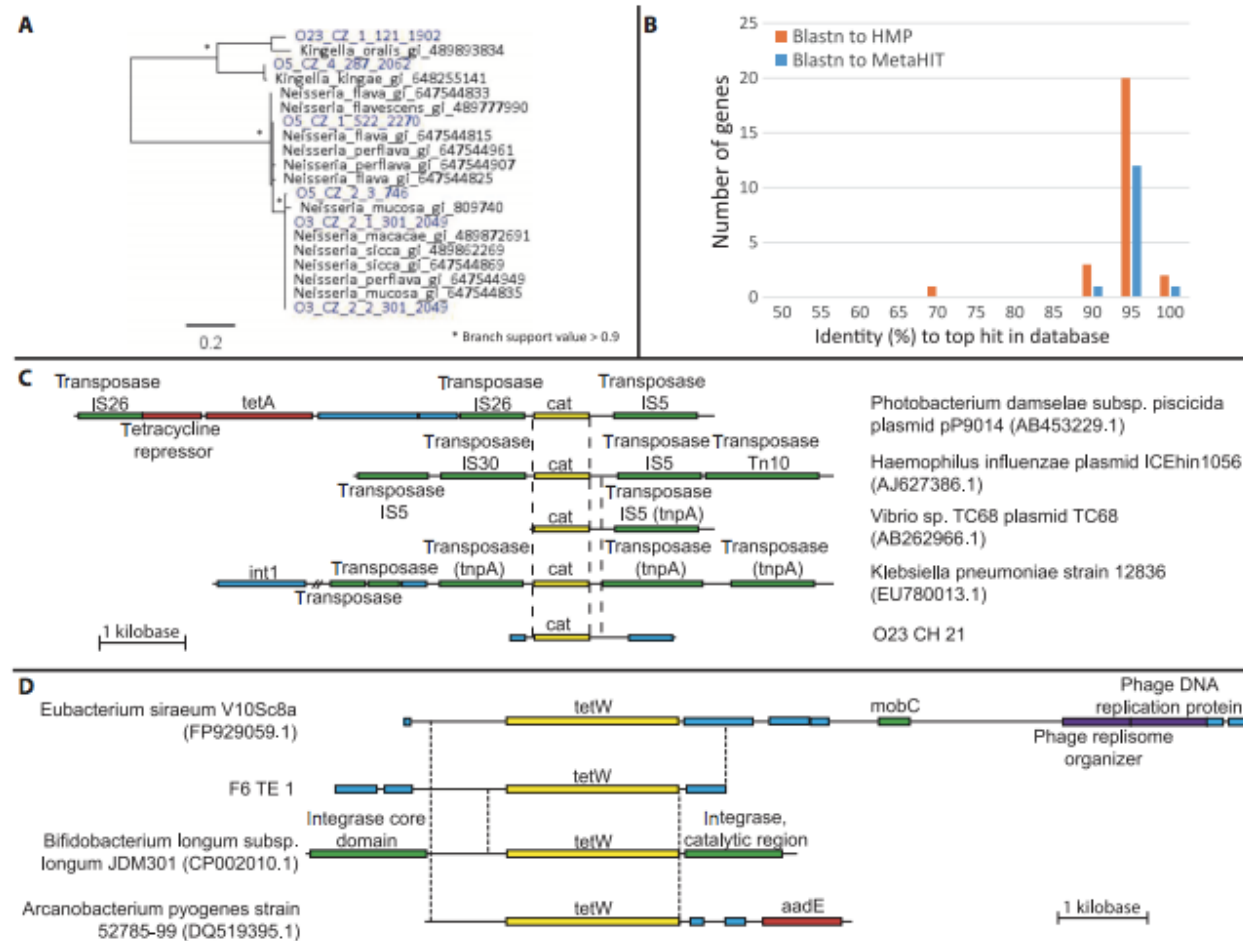


Fig. 3. Representative AR genes captured through functional metagenomic selection of Amerindian oral and fecal microbiota. (A) Maximum likelihood (ML) tree of ceftazidime-resistant PBPs from Amerindian oral microbiota (blue) and their top blastx hits in NCBI nr (black). (B) Identity (%) of the 28 AR genes to their top hits in HMP and MetaHIT (blastn). Fourteen aligned to MetaHIT, all isolated from fecal microbiota. (C) Chloramphenicol

acetyltransferase (*cat*) from O23_CH_21 and homologs in NCBI nt (nucleotide database). Dashed lines indicate 99% identical sequences. Dashes indicate omitted sequence (8487..25716). (D) *tetW* from F6_TE_1 and homologs in NCBI nt. Dashed lines indicate 98 to 99% identical sequences. Sequences are to scale. Yellow, AR gene; red, other resistance genes; green, mobile genetic elements; purple, bacteriophage genes; blue, other.

Antibiyotiklerin tarihi ya da antibiyotikler neden var?

- **Milyarlarca yıldır var** (Microbiol. Mol. Biol. Rev. 2010; 74, 417-433, Trends Microbiol. 2012; 20, 157–159.)
- Doğal ortamda kısıtlı kaynaklara erişim açısından üreticisine seçici avantaj sağlayabilir?
- Hücreler arası sinyal iletiminde rolü vardır? (PNAS 2006; 103: 19484-19489)
 - Örnek: Biyofilm oluşumu

Toprak: *biyoaktif moleküllerin kaynağı*

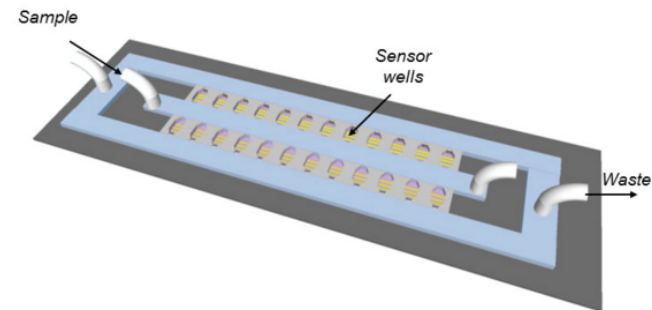
A new antibiotic kills pathogens without detectable resistance

Losee L. Ling^{1*}, Tanja Schneider^{2,3*}, Aaron J. Peoples¹, Amy L. Spoering¹, Ina Engels^{2,3}, Brian P. Conlon⁴, Anna Mueller^{2,3}, Till F. Schäberle^{3,5}, Dallas E. Hughes¹, Slava Epstein⁶, Michael Jones⁷, Linos Lazarides⁷, Victoria A. Steadman⁷, Douglas R. Cohen¹, Cintia R. Felix¹, K. Ashley Fetterman¹, William P. Millett¹, Anthony G. Nitti¹, Ashley M. Zullo¹, Chao Chen⁴ & Kim Lewis⁴

Antibiotic resistance is spreading faster than the introduction of new compounds into clinical practice, causing a public health crisis. Most antibiotics were produced by screening soil microorganisms, but this limited resource of cultivable bacteria was overmined by the 1960s. Synthetic approaches to produce antibiotics have been unable to replace this platform. Uncultured bacteria make up approximately 99% of all species in external environments, and are an untapped source of new antibiotics. We developed several methods to grow uncultured organisms by cultivation *in situ* or by using specific growth factors. Here we report a new antibiotic that we term teixobactin, discovered in a screen of uncultured bacteria. Teixobactin inhibits cell wall synthesis by binding to a highly conserved motif of lipid II (precursor of peptidoglycan) and lipid III (precursor of cell wall teichoic acid). We did not obtain any mutants of *Staphylococcus aureus* or *Mycobacterium tuberculosis* resistant to teixobactin. The properties of this compound suggest a path towards developing antibiotics that are likely to avoid development of resistance.



iCHIP



Direnç genlerinin (DG) kökeni

- Direnç genlerinin tarihi de **çok eskilere** dayanır.
 - “Serin β -laktamazlar” 2 milyar yıldan uzun süredir var (Drug Resist Updates 2004; 7: 111-123)
 - Bering bölgesinde 30,000 yıllık donmuş sedimentlerde β -laktam, tetrasiklin ve glikopeptit antibiyotiklere karşı direnç genleri (Nature 2011;477: 457-466)
 - OXA β -laktamazlar plazmitler üzerinde milyonlarca yıldır taşınıyor (J. Mol. Evol. 2002; 55, 314–321)

Direnç genleri *neden* var?

- Üretici (producer) hipotezi
 - Antibiyotik üreten mikroorganizmalar kendilerini korumak için direnç geliştirir (PNAS 1973; 70:2276-2280)
- Direnç neden olan genler orijinal konağında tümüyle farklı bir işleve sahip?
 - *Providencia stuartii*'deki 2-N'-asetiltransferaz normal işlevi peptidoglikan modifikasyonu ancak aminoglikozitleri de parçalıyor (Front. Biosci. J. Virtual Libr. 4, D132 – D140).

Context matters — the complex interplay between resistome genotypes and resistance phenotypes

Gautam Dantas^{1,2} and Morten OA Sommer^{3,4}

Current Opinion in Microbiology 2012, 15:577–582

Definitions

Antibiotic resistance: A phenotype, which is related to the ability of an organism to grow in the presence of an antibiotic.

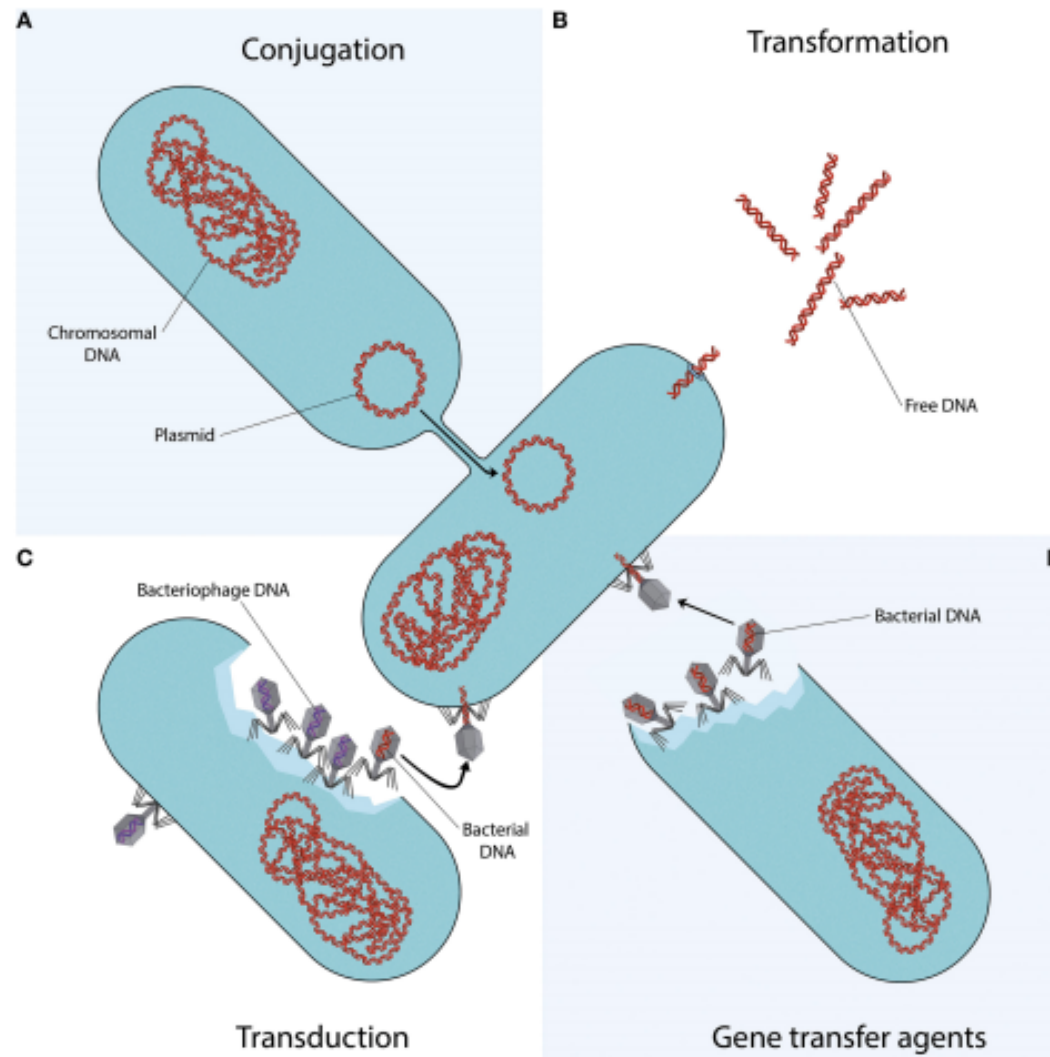
Antibiotic resistome: A collection of genes, that is capable of conferring resistance towards antibiotics when expressed in a susceptible organism.

Silent resistance gene: A gene, which does not confer resistance to its native host, yet is capable of conferring resistance when expressed in other hosts

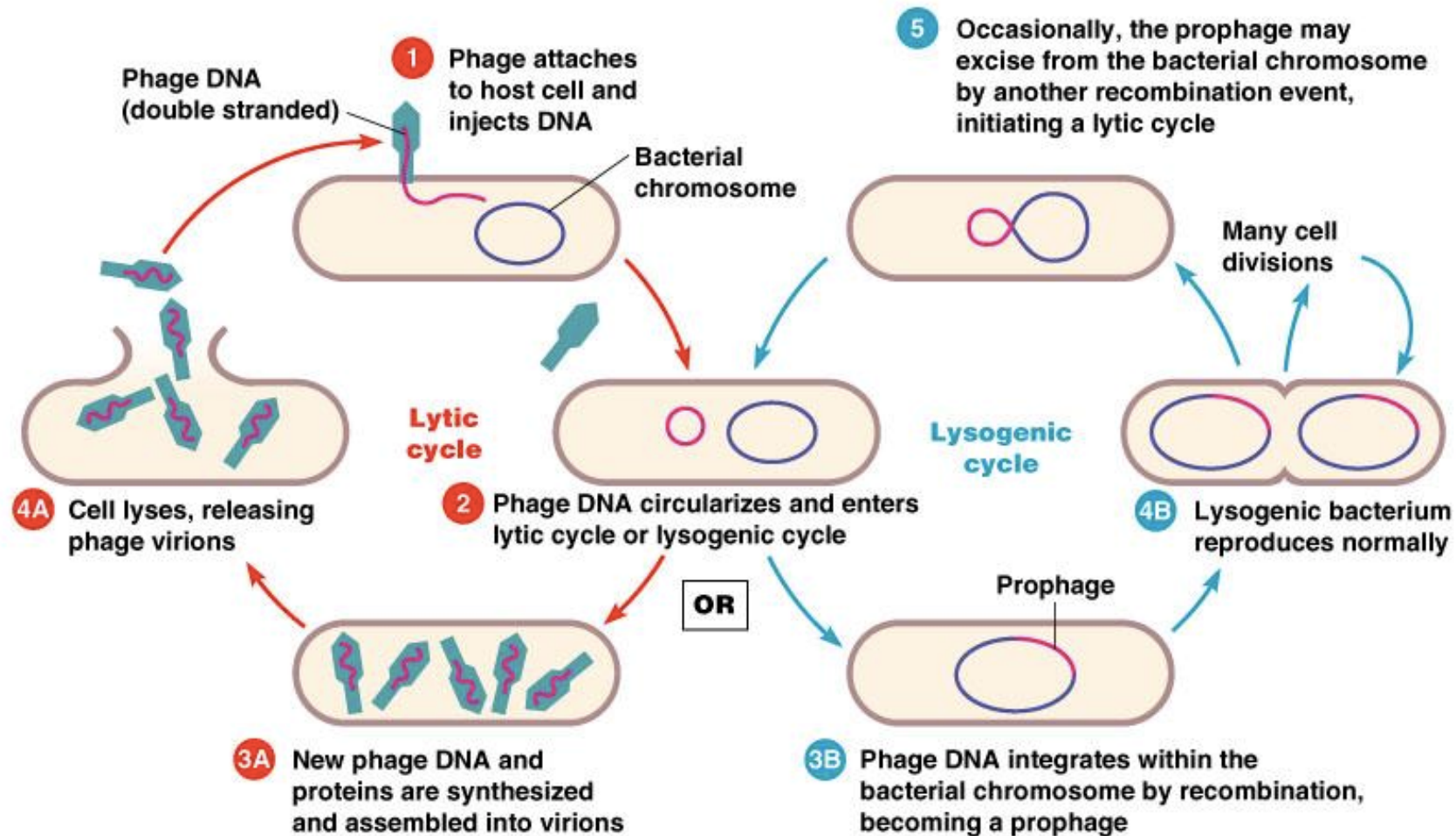


Yatay gen aktarımı

Yatay gen aktarımı



Barsak viromundaki fajların çoğu ılımlı fajlardır.



Faj-mikrobiyota etkileşimleri

- Bakteri popülasyon büyüklüğünü/dağılımını kontrol eder.
- Konakçılarının çevresel koşullara uyumunu arttırır/sağlar.
- Antibiyotik direnç genlerinin biriktiricileridir.

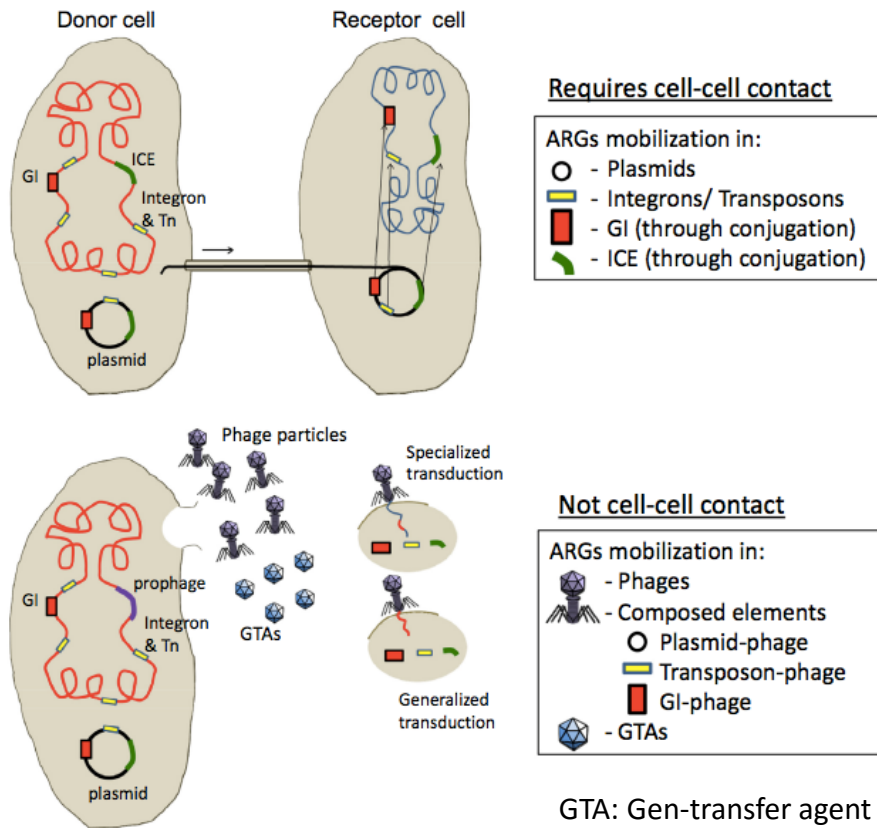
Konakçılarının çevresel koşullara uyumunu arttırır/sağlar.

- Karbohidrat ve aminoasit metabolizmasında görev alan çok sayıda gen kodlarlar.
 - Örnek: musin ile etkileşen BACON domeyni
- Kriptik profajlar bakterilerin olumsuz koşullara dayanmalarını sağlar.
 - Örnek: antibiyotik, ozmotik, oksidatif stres, vb

Antibiyotik direnç genleri, fajlar ve faj-ilişkili elemanlar

M. Brown-Jaque et al./Plasmid 79 (2015) 1–7

3



- Plazmid-faj

- *P. aeruginosa* – AP 1 ve AP 12

- imipenem/aztreonam/seftazidim direnci

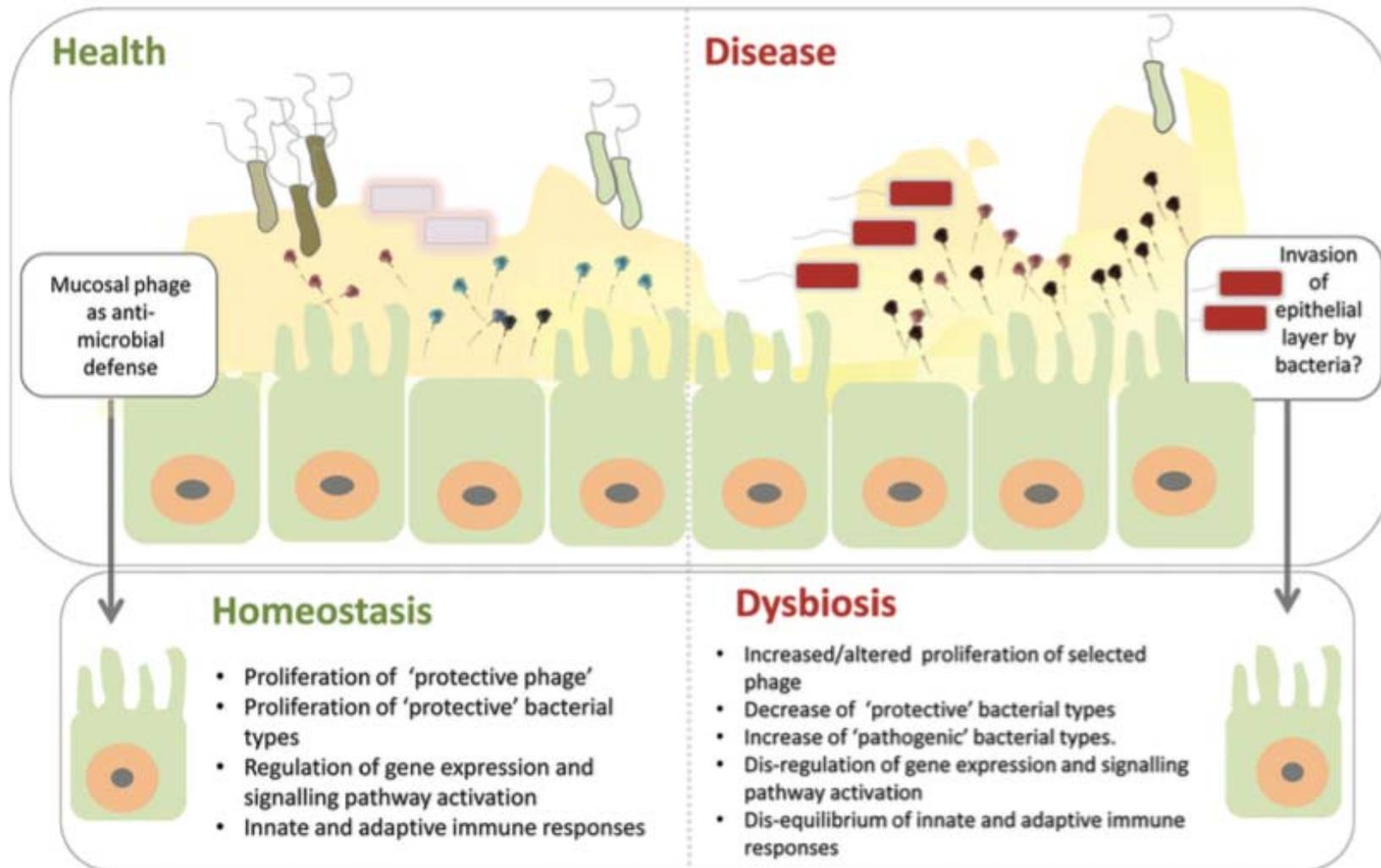
- Genomik ada-faj

- *S. aureus* fajı - SSCmec

- Transpozon-faj

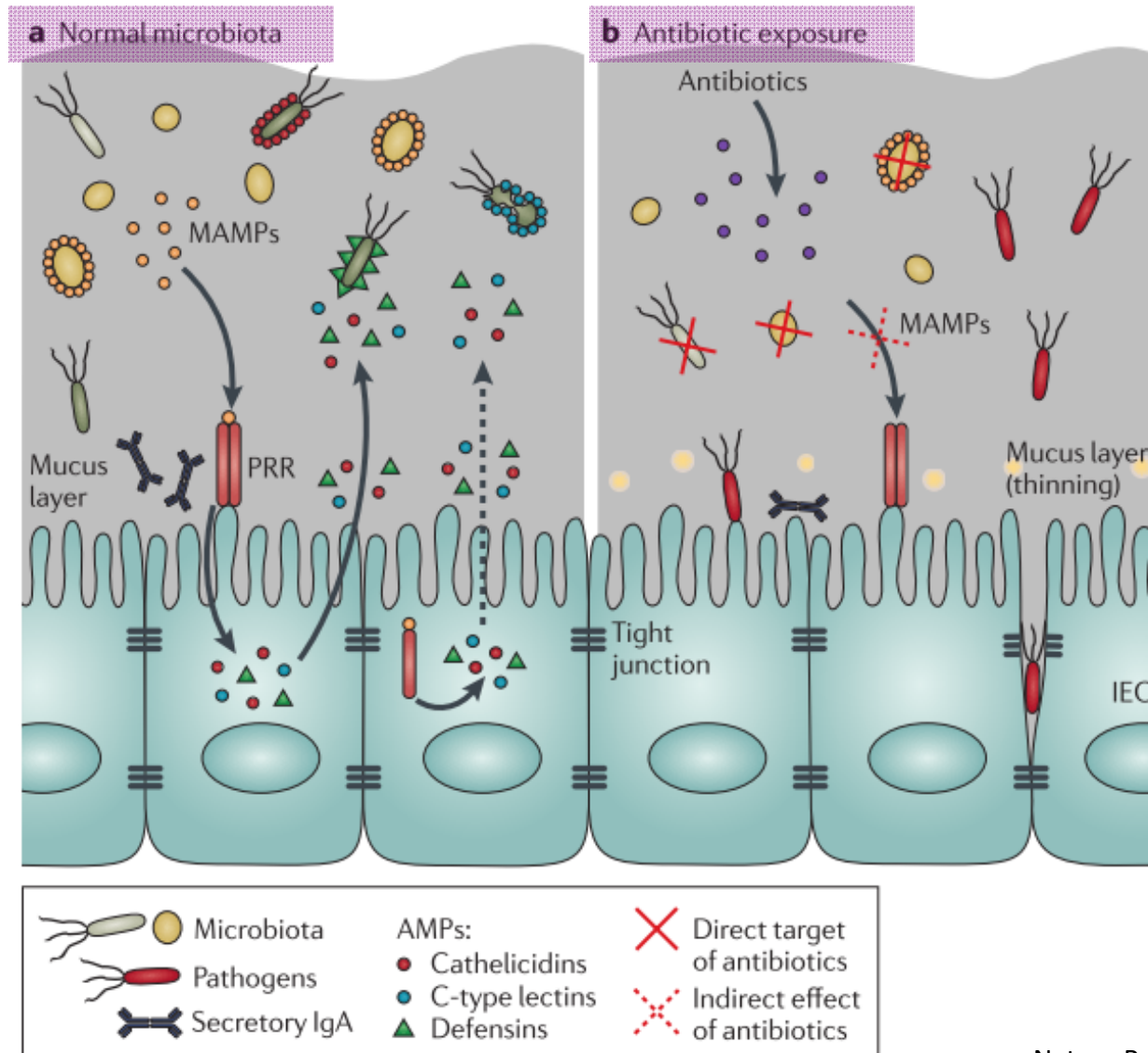
- *A. actinomycetemcomitans* da bulunan ve tetrasiklin direnci kodlayan transpozon

Homeostaz-disbiyoz ve fajlar

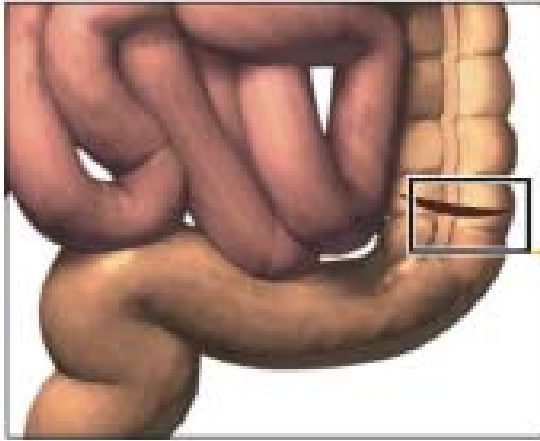


Shifting the balance: antibiotic effects on host–microbiota mutualism

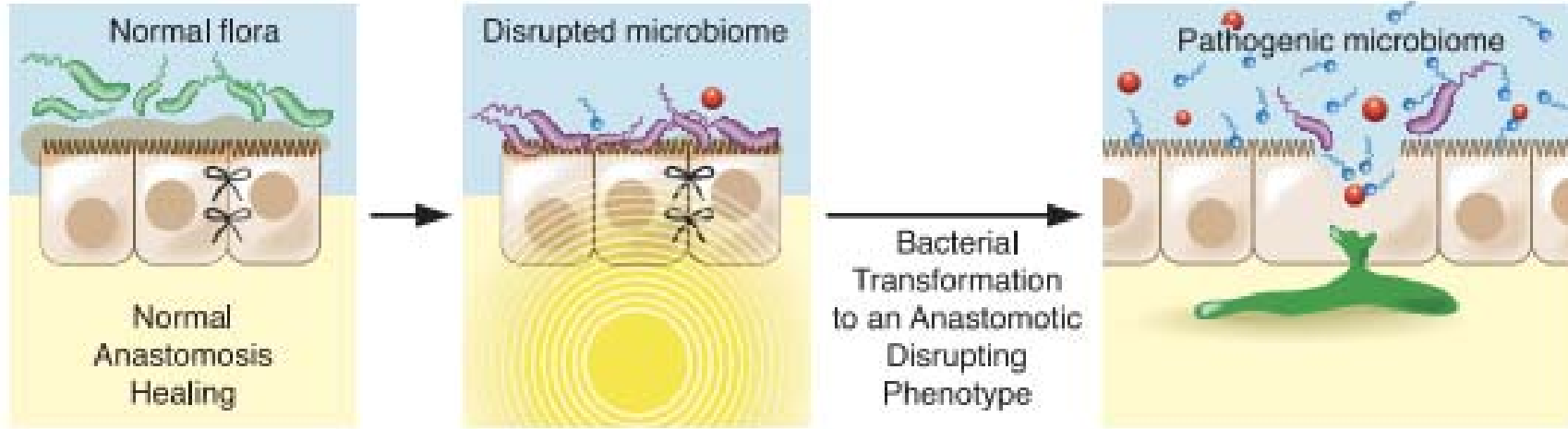
Benjamin P. Willing^{*§}, Shannon L. Russell^{**§} and B. Brett Finlay^{*†}



Bağlam önemli!



- Operasyon sırasında barsak oksijene maruz kalıyor
- Post-op hasta aç bırakılıyor
- Bakteriler fosfat gibi besin maddelerinden yoksun kalıyor
- Kollajen indirgeyen enzimler aktive oluyor



Curing an anastomotic leak.

Yeni yollar...

The image is a screenshot of the DaVolterra website. The header is dark blue with the DaVolterra logo on the left and navigation links (Home, Contact, social media icons, Search) on the right. Below the header is a white navigation bar with links: ABOUT US, THE CHALLENGES, PIPELINE, PARTNERSHIPS, NEWS & EVENTS, CAREERS. The main content area has a light green sidebar on the left with a 'PIPELINE' section containing links for Overview, DAV132 (with sub-links: Concept, Mechanism of action, Development status, About Clostridium difficile, Publications), and DAV133. The main content area features a title 'DAV132 - Preventing occurrence and recurrence of Clostridium difficile infection' and a horizontal timeline diagram. The timeline has five stages: Discovery, Preclinical, Phase I, Phase II, and Phase III. A blue arrow labeled 'DAV132' spans from the start of the Discovery stage to the end of the Phase II stage. Below the timeline, the word 'Concept' is visible.

DaVolterra

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PIPELINE

Overview

DAV132

- Concept
- Mechanism of action
- Development status
- About Clostridium difficile
- Publications

DAV133

DAV132 - Preventing occurrence and recurrence of Clostridium difficile infection

Discovery | Preclinical | Phase I | Phase II | Phase III

Preventing occurrence and recurrence of C. difficile infections

DAV132

Concept

Table 2. Pathogen Directed Agents Under Development

CDC classification	Target Pathogen	Compound	Sponsor	Type of molecule	Development Stage	Direct or Adjunctive Therapy	Single pathogen specificity	Target/mechanism of action	Novel class
Urgent Threat	Carbapenemase-Resistant Enterobacteriaceae (CRE)	Carbavance	The Medicines Company (with funding from BARDA)	Combination of meropenem & novel boron based β -lactamase inhibitor, RPX7009	Phase 3, Tier B	Direct & Adjunctive	No	Cell wall biosynthesis (inhibition of PBPs and class A carbapenemases)	Yes
		Plazomicin (ACHN-490)	Achaogen (with funding from BARDA)	Novel aminoglycoside	Phase 3, Tier B	Direct	No	Protein synthesis (ribosome)	No
	Metallo- β -lactamase-expressing Enterobacteriaceae	ATM-AV1	Allergan & AstraZeneca (with funding from BARDA & the IMI)	Combination of aztreonam & avibactam	Phase 2/3, Tier C	Direct & Adjunctive	No	Cell wall biosynthesis (inhibition of PBP3 in strains that express class B β -lactamases)	No
		<i>Clostridium difficile</i>	Bezlotoxumab	Merck	Anti-toxin B monoclonal antibody	Registration	Adjunctive	Yes	Toxin B neutralization
	<i>Neisseria gonorrhoeae</i>	SER-109	Seres Therapeutics	Encapsulated Firmacure Eubacterial Spores	Phase 2/3, Tier C	Adjunctive	No	Microbiome (repopulate with beneficial bacteria)	Yes
		CRS3123 (REP3123)	Crestone (with funding from NIAID)	Thienopyridinone	Phase 1	Direct	No	Protein synthesis (Met tRNA synthetase)	Yes
		Avidocin	Avidbiotics (with funding from NIAID)	Engineered bacteriocin	Preclinical	Direct	Yes	Membrane disruption	Yes
		Solithromycin	Cempra	Fluoroketolide	Phase 3, Tier B	Direct	No	Protein synthesis (ribosome)	No
		Zoliflodacin (ETX0914)	Entasis (with funding from NIAID)	Spiropyrimidinetrione	Phase 2	Direct	No	GyrB subunit of DNA topoisomerases	Yes
		Gepotidacin (GSK2140944)	GlaxoSmithKline with funding from BARDA)	Acenaphthene (NBTI)	Phase 2	Direct	No	GyrA subunit of DNA topoisomerases	Yes
Serious Threat	<i>Pseudomonas aeruginosa</i>	P300847	PTC Therapeutics	Novel aminoglycoside, ACHN-490	Preclinical	Direct	Yes	Undisclosed	Yes
		POL7080 (RG7929)	Polyphor	Macrocyclic (peptidomimetic)	Phase 2	Direct	Yes	Membrane disruption (LptD)	Yes
		MEDI3902	MedImmune	Bispecific, opsonic monoclonal antibody	Phase 2	Adjunctive	Yes	Psl (adhesion),PcrV (virulence), opsonophagocytic	Yes
		AR101	Aridis (with funding from NIAID)	Anti-LPS monoclonal antibody	Phase 2	Adjunctive	Yes	Serotype O1 strains	Yes
		Ampliphage	AmphiPhi Biosciences (with funding from Cystic Fibrosis Foundation)	Bacteriophage cocktail	Preclinical	Direct	Yes	Membrane disruption	Yes
	Methicillin-resistant <i>Staphylococcus aureus</i> (MRSA)	M64	Spero Therapeutics	Benzamide- benzimidazole	Preclinical	Adjunctive	Yes	Virulence inhibitor (MvfR)	Yes
		Anticalin	Pieris/Sanofi	Tetraspecific engineered lipocalin	Preclinical	Adjunctive	Yes	Siderophore production	Yes
		MEDI4893	MedImmune	Anti-alpha toxin monoclonal antibody	Phase 2	Adjunctive	Yes	Alpha toxin neutralization	Yes
		AR301	Aridis (with funding from NIAID)	Anti-alpha toxin monoclonal antibody	Phase 2	Adjunctive	Yes	Alpha toxin neutralization	Yes
		SASPECT PT1.2	Phico Therapeutics (with funding from Wellcome Trust)	"Nano-delivered" DNA binding protein	Phase 2	Direct	Yes	DNA replication	Yes
	Debio 1450 (AFN-1252)	DebioPharm	Aryl acrylamide	Phase 2	Direct	Yes	Fatty acid biosynthesis (FabI)	Yes	
	CG40059	Crystal Genomics	Alkoxypyridinone	Phase 2	Direct	Yes	Fatty acid biosynthesis (FabI)	Yes	
	ASN100	Arsanis (with funding from FFG)	Combination of two anti-toxin monoclonal antibodies	Preclinical	Adjunctive	Yes	Neutralization of six cytotoxins	Yes	

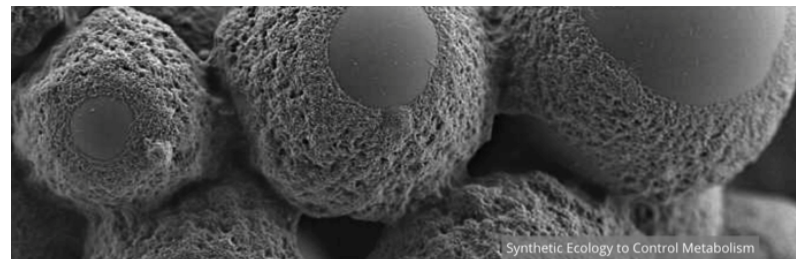
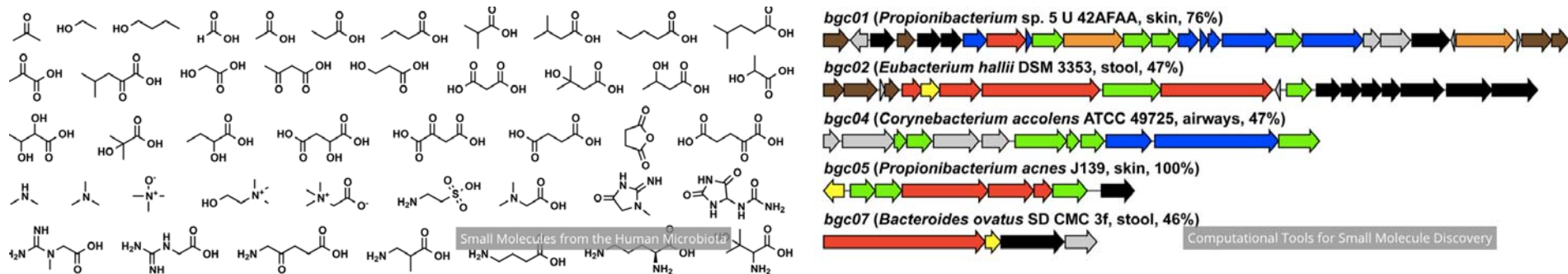
Barsak mikrobiyotası yeni *biyoaktif moleküllerin* kaynağı olabilir.

- Tiyopeptit antibiyotikler, polifenoller, gallik asit ve pirogallol, vb

The New York Academy of Sciences. Advances in Human Microbiome Science: Intestinal Diseases. Academy eBriefings. 2015. Available at: www.nyas.org/Microbiome2015-eB

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Son söz

