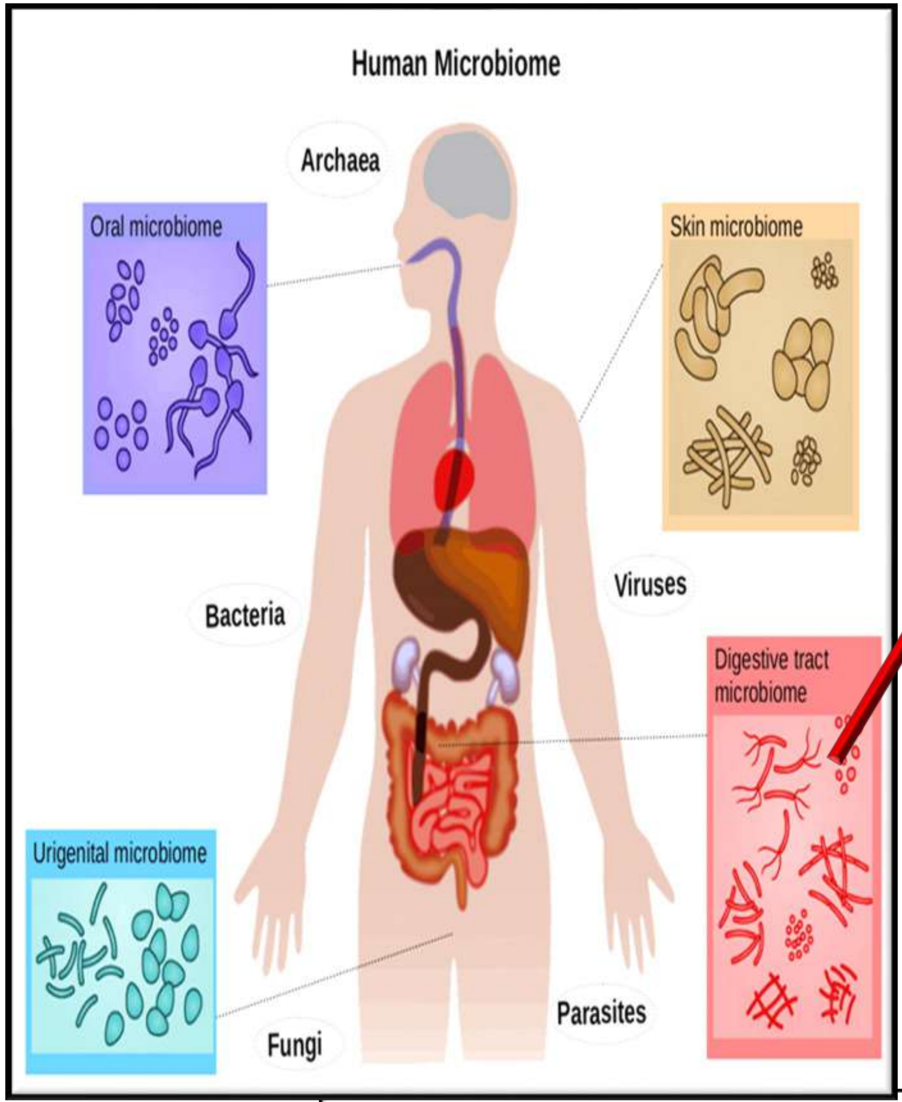
Sağlıkta ve Hastalıkta Virobiyom

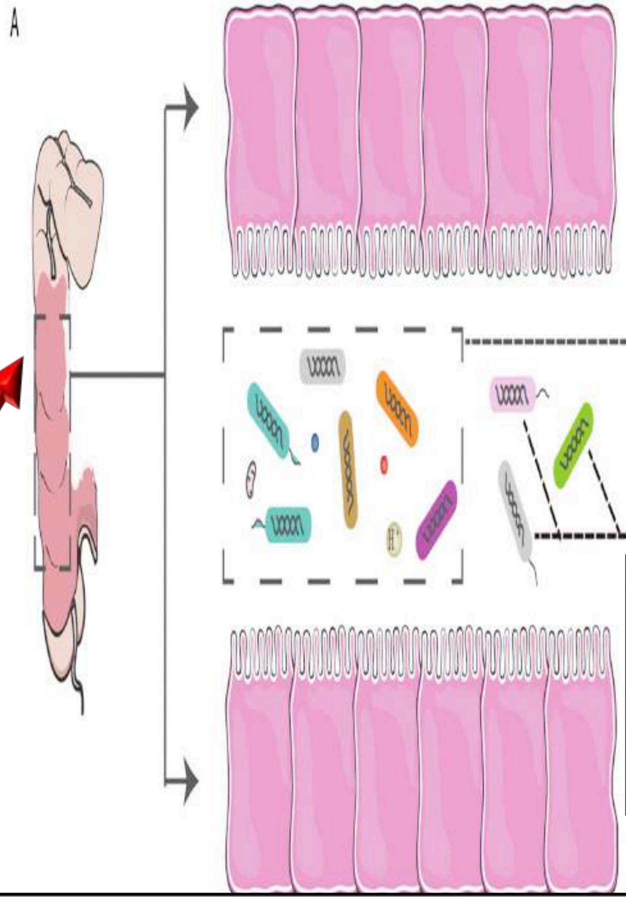
Image 15/21 from *1000 Handshakes*, a bioartistic microbiome mapping project.
François-Joseph Lapointe, Université de Montréal, CC BY

www.nytimes.com/2020/03/24/science/viruses

Dr. Murat YAMAN

"***Mikrobiyom***" geniş mikrobiyal toplulukları (bakteriler, virüsler, arkeler, mantarlar ve protozoalar), genomları ve çevre koşulları dahil tüm yaşam alanlarını





Mikrobiyom → Virobiyom

Mikrobiyota → Virobiyota

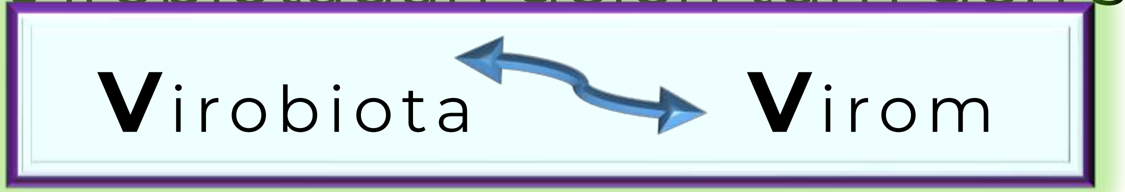
Tanımlı bir ortamdan gelen mikroorganizma toplulukları

A guide to human microbiome research: study design, sample collection, and bioinformatics analysis, Xu-Bo Qian, Tong Chen, Yi-Ping Xu, et al 2021

Virobiyom; Mikrobiyomun viral fraksiyonu

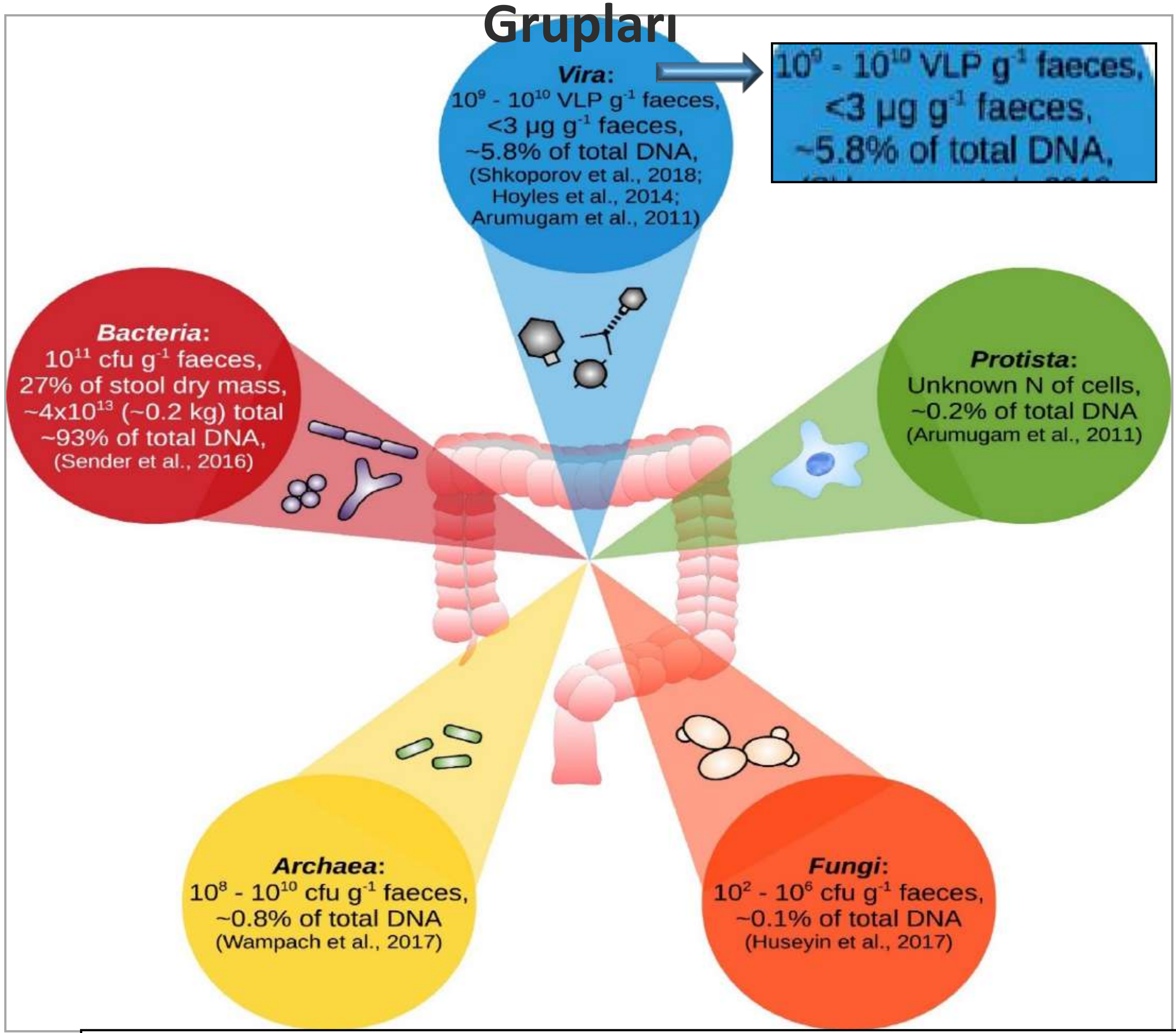
"**V**irobiota" terimi bir konakçı içindeki virüs topluluğunu

«**V**irom" **V**irobiotadan gelen tüm gen setini ifade etse de

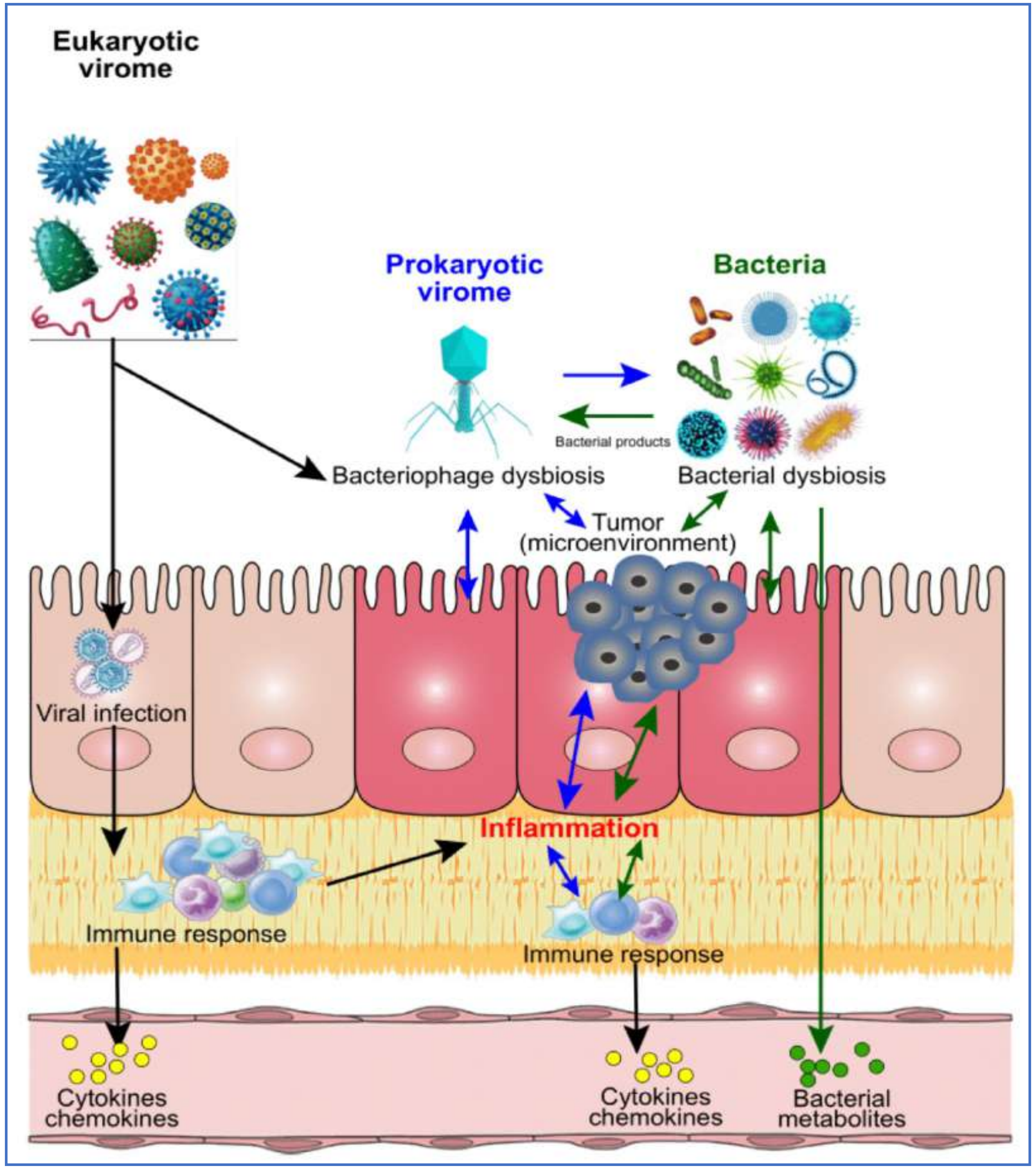


Virobiota **V**irom

Bağırsak Mikrobiyomunun Taksonomik Grupları



Virom & Mikrobiyom Etkileşimi



Bacteriophages of the Human Gut: The "Known Unknown" of the Microbiome Shkoporov, Andrey N. et al. Cell Host & Microbe, Volume 25, Issue 2, 195 - 209

nature reviews microbiology

nature > nature reviews microbiology > review articles > article

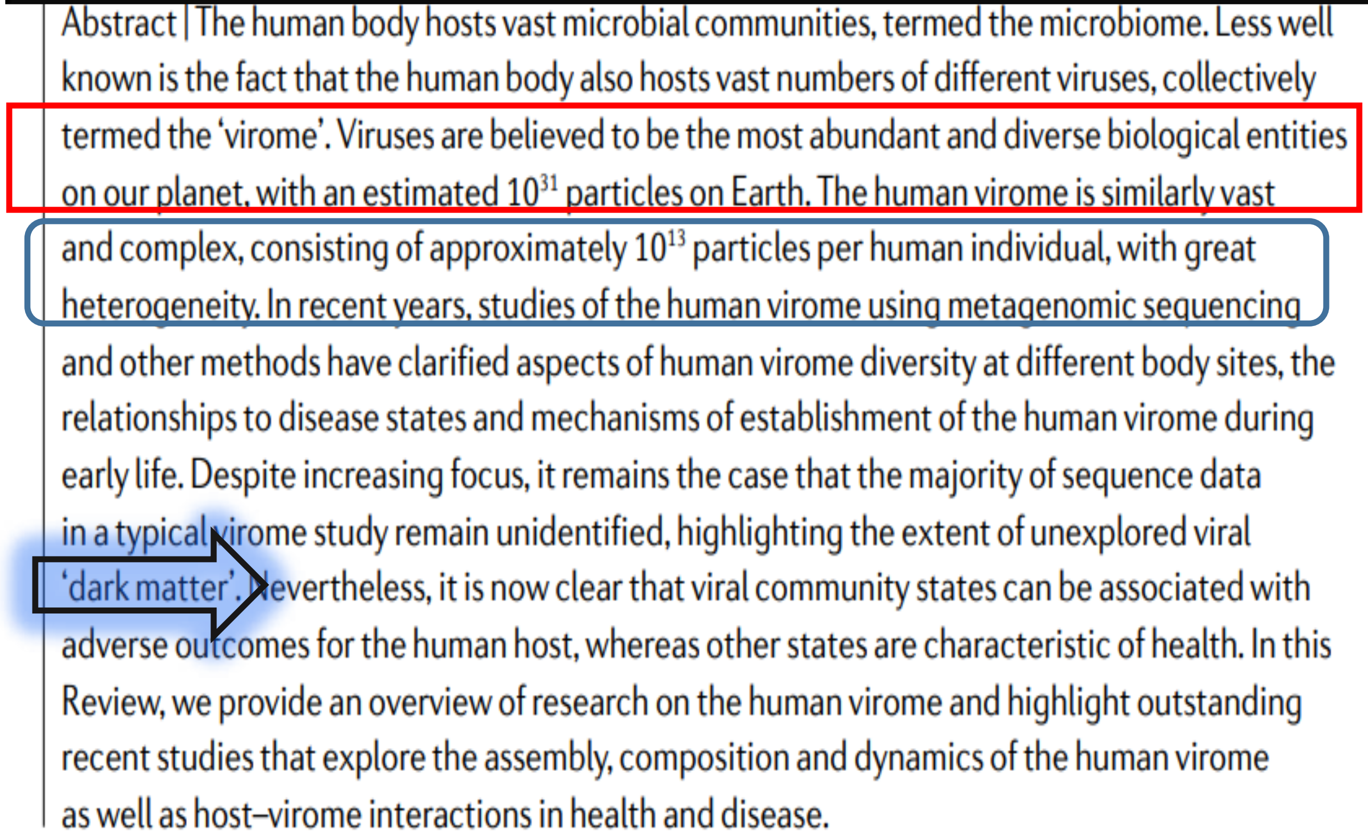
Review Article | Published: 30 March 2021

The human virome: assembly, composition and host interactions

Guanxiang Liang & Frederic D. Bushman

Nature Reviews Microbiology **19**, 514–527 (2021) | Cite this article

60k Accesses | **281** Citations | **322** Altmetric | Metrics



Abstract | The human body hosts vast microbial communities, termed the microbiome. Less well known is the fact that the human body also hosts vast numbers of different viruses, collectively termed the 'virome'. Viruses are believed to be the most abundant and diverse biological entities on our planet, with an estimated 10^{31} particles on Earth. The human virome is similarly vast and complex, consisting of approximately 10^{13} particles per human individual, with great heterogeneity. In recent years, studies of the human virome using metagenomic sequencing and other methods have clarified aspects of human virome diversity at different body sites, the relationships to disease states and mechanisms of establishment of the human virome during early life. Despite increasing focus, it remains the case that the majority of sequence data in a typical virome study remain unidentified, highlighting the extent of unexplored viral 'dark matter'. Nevertheless, it is now clear that viral community states can be associated with adverse outcomes for the human host, whereas other states are characteristic of health. In this Review, we provide an overview of research on the human virome and highlight outstanding recent studies that explore the assembly, composition and dynamics of the human virome as well as host–virome interactions in health and disease.

Virüslerin dünyamızda, çok sayıda ve çeşitte biyolojik varlıklar olduğuna inanılmakta ve Dünya'da tahmini 10^{31} VLP

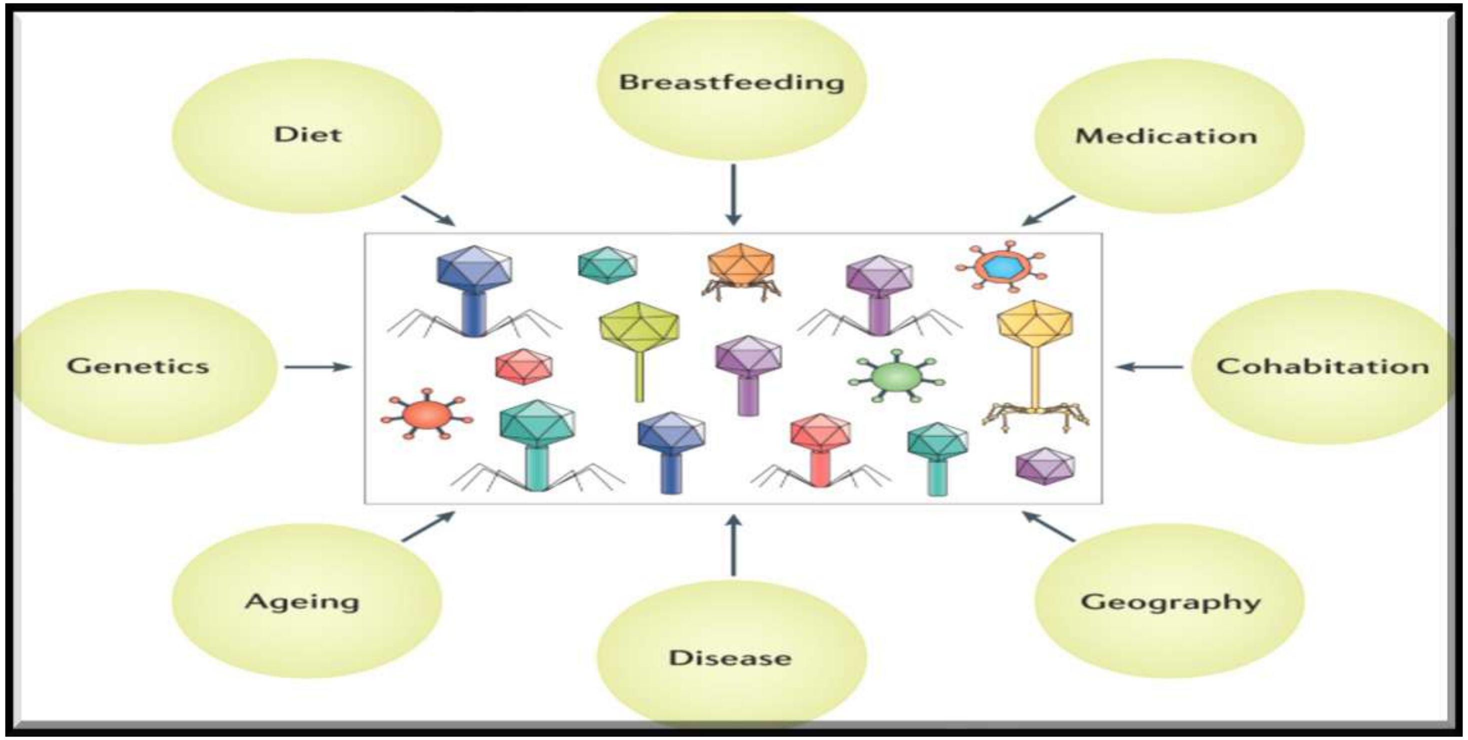
İnsan **V**iromunda ~10^{13} VLP

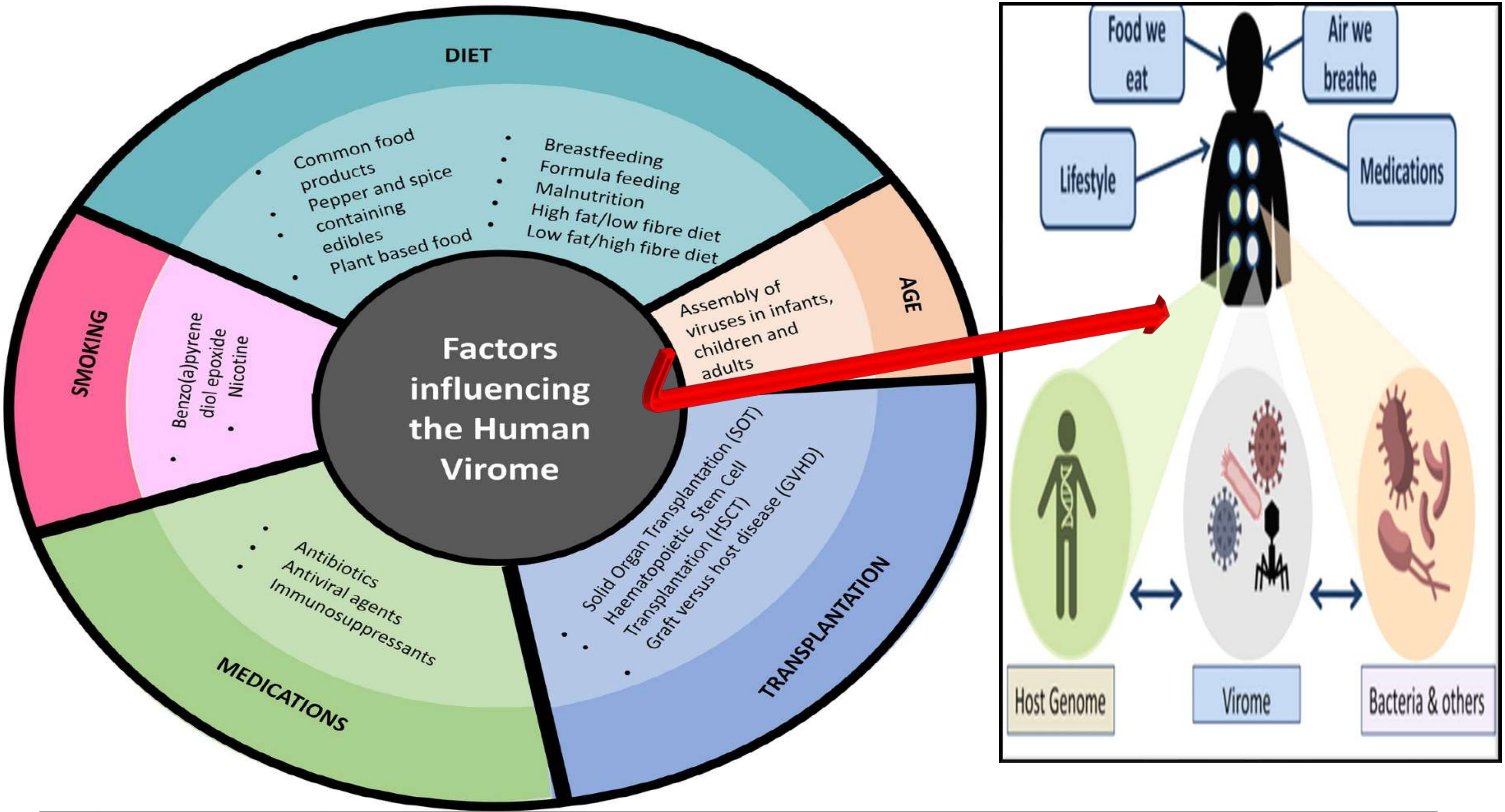
Keşfedilmemiş **V**iral **'karanlık madde'**

Virom çalışmasındaki dizi verilerinin çoğu tanımlanmamış

Virüsler, Yaşamın Olduğu Tüm Alanları Enfekte Edebilirler

İnsan Viromunun Belirleyicileri?





Factors influencing the Human Virome

DIET
- Common food products
- Pepper and spice containing edibles
- Plant based food
- Breastfeeding
- Formula feeding
- Malnutrition
- High fat/low fibre diet
- Low fat/high fibre diet

AGE
- Assembly of viruses in infants, children and adults

SMOKING
- Benzo(a)pyrene diol epoxide
- Nicotine

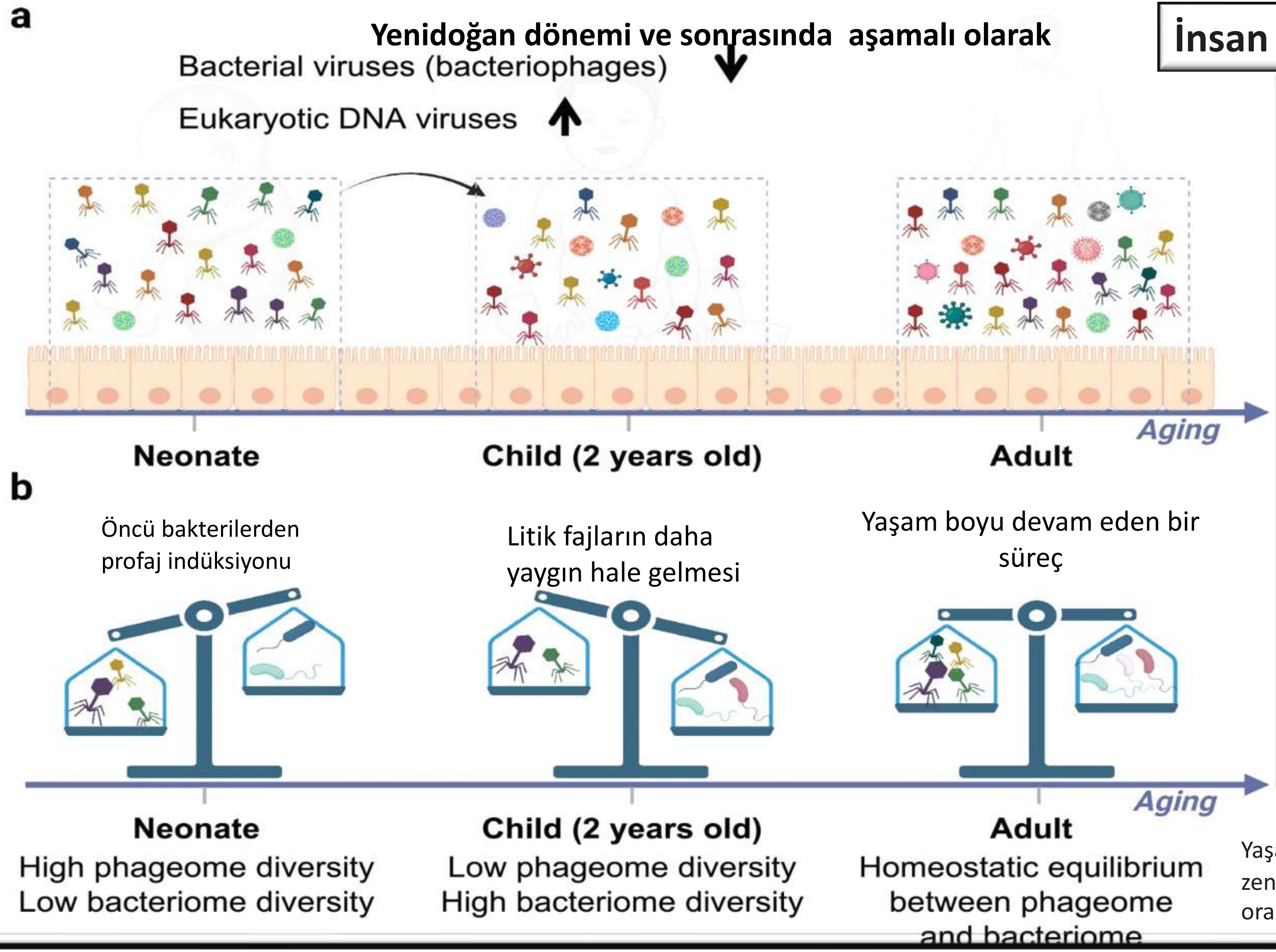
MEDICATIONS
- Antibiotics
- Antiviral agents
- Immunosuppressants

TRANSPLANTATION
- Solid Organ Transplantation (SOT)
- Haematopoietic Stem Cell Transplantation (HSCT)
- Graft versus host disease (GVHD)

Bhagchandani, T., Nikita, Verma, A. *et al.* Exploring the Human Virome: Composition, Dynamics, and Implications for Health and Disease. *Curr Microbiol* **81**, 16 (2024). https://doi.org/10.1007/s00284-023-03537-0

Viromumuzu Nasıl Ediniriz?

Yenidoğan dönemi ve sonrasında aşamalı olarak



Öncü bakterilerden profaj indüksiyonu

Litik fajların daha yaygın hale gelmesi

Yaşam boyu devam eden bir süreç

İnsan Bağırsağı Viromunun Bileşimi

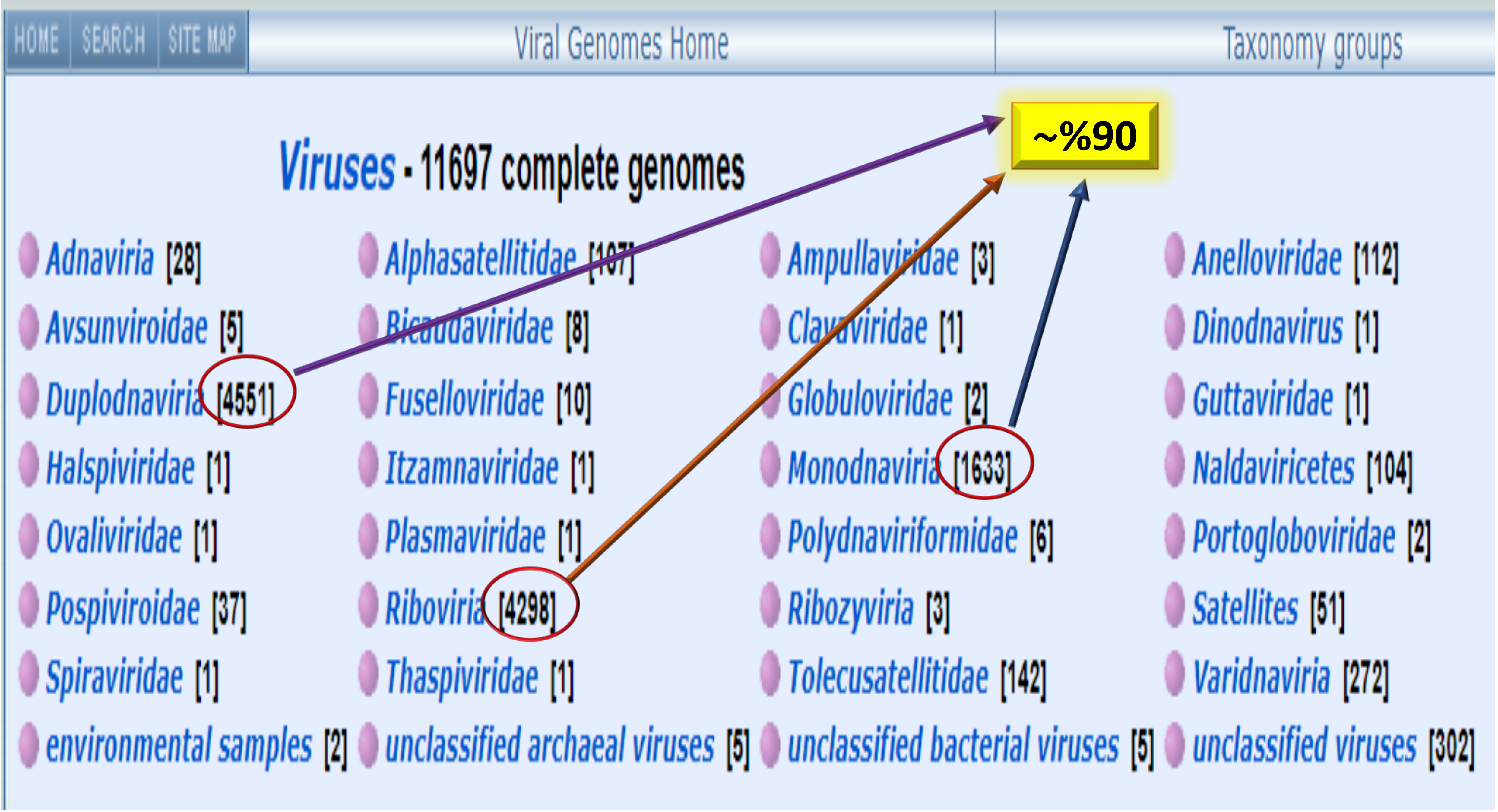
Adult-like gut virome

Bacterial viruses
(bacteriophages, > 90%)
dsDNA phages:
Caudovirales
ssDNA phages:
Microviridae
Eukaryotic DNA viruses (< 10%)
Anelloviruses
Herpesviruses
Adenoviruses
Eukaryotic RNA viruses
Plant viruses
Sapoviruses
Rotaviruses
Coronaviruses

Yaşa bağlı olarak a) Bağırsak viromunun bileşimi, zenginliği ve çeşitliliği b) Bakteriyofaj/bakteri bolluğu oranı değişir.

Zhirui Cao, Naoki Sugimura, Elke Burgermeister, Matthias P. Ebert, Tao Zuo, Ping Lan,The gut virome: A new microbiome component in health and disease, eBioMedicine, Volume 81, 2022,104113.

- Yakın zamanlarda keşfedilen yeni virüsler, veritabanları….
- Güncel Ulusal Biyoteknoloji Bilgi Merkezi (NCBI) Genom veritabanı, 11.697 viral genom dizisi içermekte



Viruses - 11697 complete genomes

Adnaviria [28]
Alphasatellitidae [107]
Ampullaviridae [3]
Anelloviridae [112]
Avsunviroidae [5]
Bicaudaviridae [8]
Clavaviridae [1]
Dinodnavirus [1]
Duplodnaviria [4551]
Fuselloviridae [10]
Globuloviridae [2]
Guttaviridae [1]
Halspiviridae [1]
Itzamnaviridae [1]
Monodnaviria [1633]
Naldaviricetes [104]
Ovaliviridae [1]
Plasmaviridae [1]
Polydnaviriformidae [6]
Portogloboviridae [2]
Pospiviroidae [37]
Riboviria [4298]
Ribozyviria [3]
Satellites [51]
Spiraviridae [1]
Thaspiviridae [1]
Tolecusatellitidae [142]
Varidnaviria [272]
environmental samples [2]
unclassified archaeal viruses [5]
unclassified bacterial viruses [5]
unclassified viruses [302]

(https://www.ncbi.nlm.nih.gov/genomes/GenomesGroup.cgi?taxid)

VİRÜS TAKSONOMİSİ

Virüs sınıflandırması; virüslerin yapı (morfoloji), nükleik asit tipi, çoğalma şekli, konakçı ve neden oldukları hastalıklar…

Günümüzde iki ana sınıflandırma

1–Baltimore

Virüslerin NA, ds/ss, polarite (mRNA sentezi) ve replikasyon stratejileri

2- ICTV

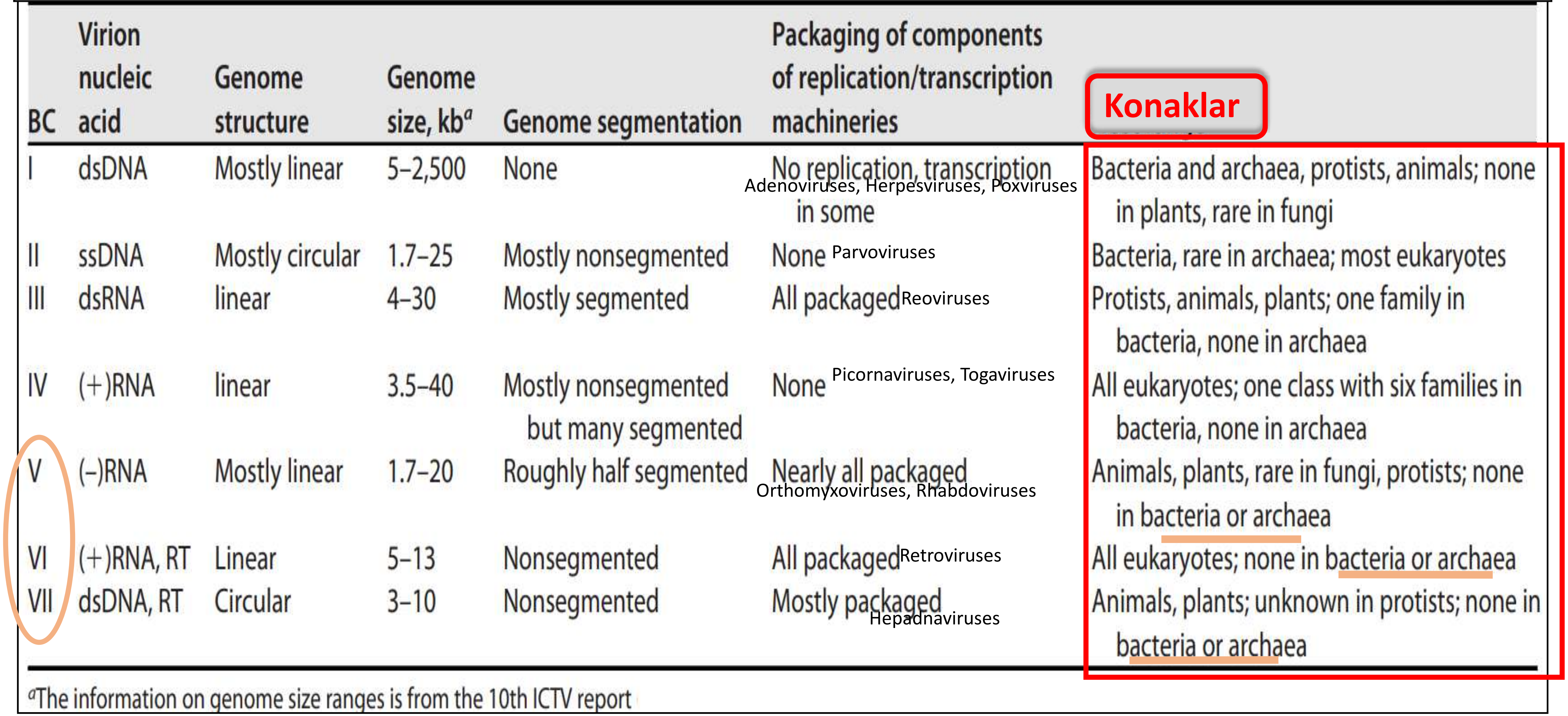
I. Partikül Özellikleri

II. Genom Organizasyonu ve Replikasyon

III. Antijenik Özellikler

…..virüs dünyasının (virosfer) megataksonomisi …

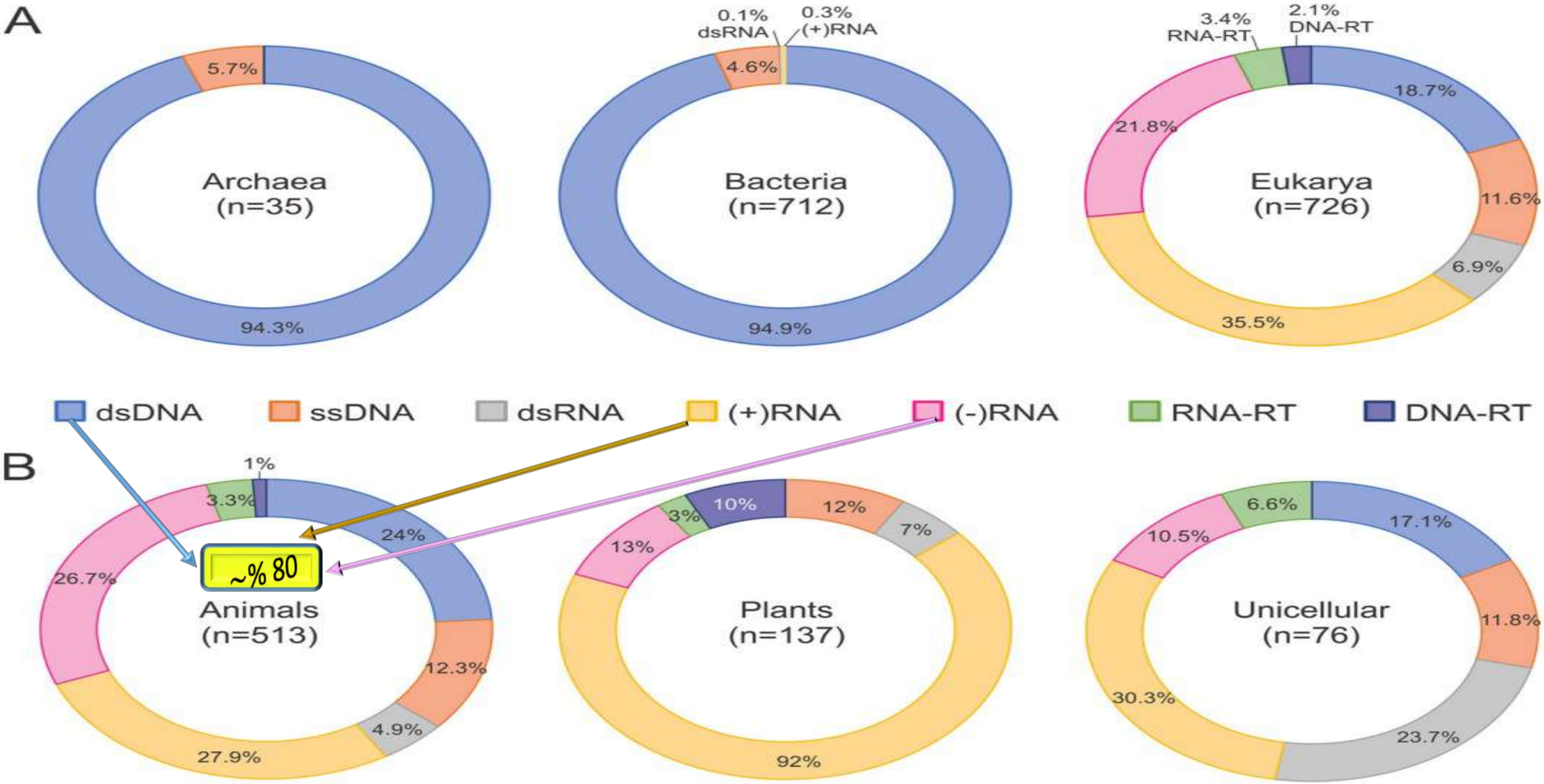
Baltimore Virüs Sınıfları ve Temel Moleküler/ Biyolojik Özellikleri



BC	Virion nucleic acid	Genome structure	Genome size, kb[a]	Genome segmentation	Packaging of components of replication/transcription machineries	Konaklar
I	dsDNA	Mostly linear	5–2,500	None	No replication, transcription in some Adenoviruses, Herpesviruses, Poxviruses	Bacteria and archaea, protists, animals; none in plants, rare in fungi
II	ssDNA	Mostly circular	1.7–25	Mostly nonsegmented	None Parvoviruses	Bacteria, rare in archaea; most eukaryotes
III	dsRNA	linear	4–30	Mostly segmented	All packaged Reoviruses	Protists, animals, plants; one family in bacteria, none in archaea
IV	(+)RNA	linear	3.5–40	Mostly nonsegmented but many segmented	None Picornaviruses, Togaviruses	All eukaryotes; one class with six families in bacteria, none in archaea
V	(–)RNA	Mostly linear	1.7–20	Roughly half segmented	Nearly all packaged Orthomyxoviruses, Rhabdoviruses	Animals, plants, rare in fungi, protists; none in bacteria or archaea
VI	(+)RNA, RT	Linear	5–13	Nonsegmented	All packaged Retroviruses	All eukaryotes; none in bacteria or archaea
VII	dsDNA, RT	Circular	3–10	Nonsegmented	Mostly packaged Hepadnaviruses	Animals, plants; unknown in protists; none in bacteria or archaea

[a] The information on genome size ranges is from the 10th ICTV report

Baltimore Virüs Sınıfı & Konakçı Aralığı Dağılımı



Nobs, Stephanie-Jane et al. “Eukarya the chimera: eukaryotes, a secondary innovation of the two domains of life?.” *Trends in microbiology* vol. 30,5 (2022): 421-431. doi:10.1016/j.tim.2021.11.003

International Committee on Taxonomy of Viruses: ICTV

Official Taxonomic Resources

ICTV Taxonomy Browser

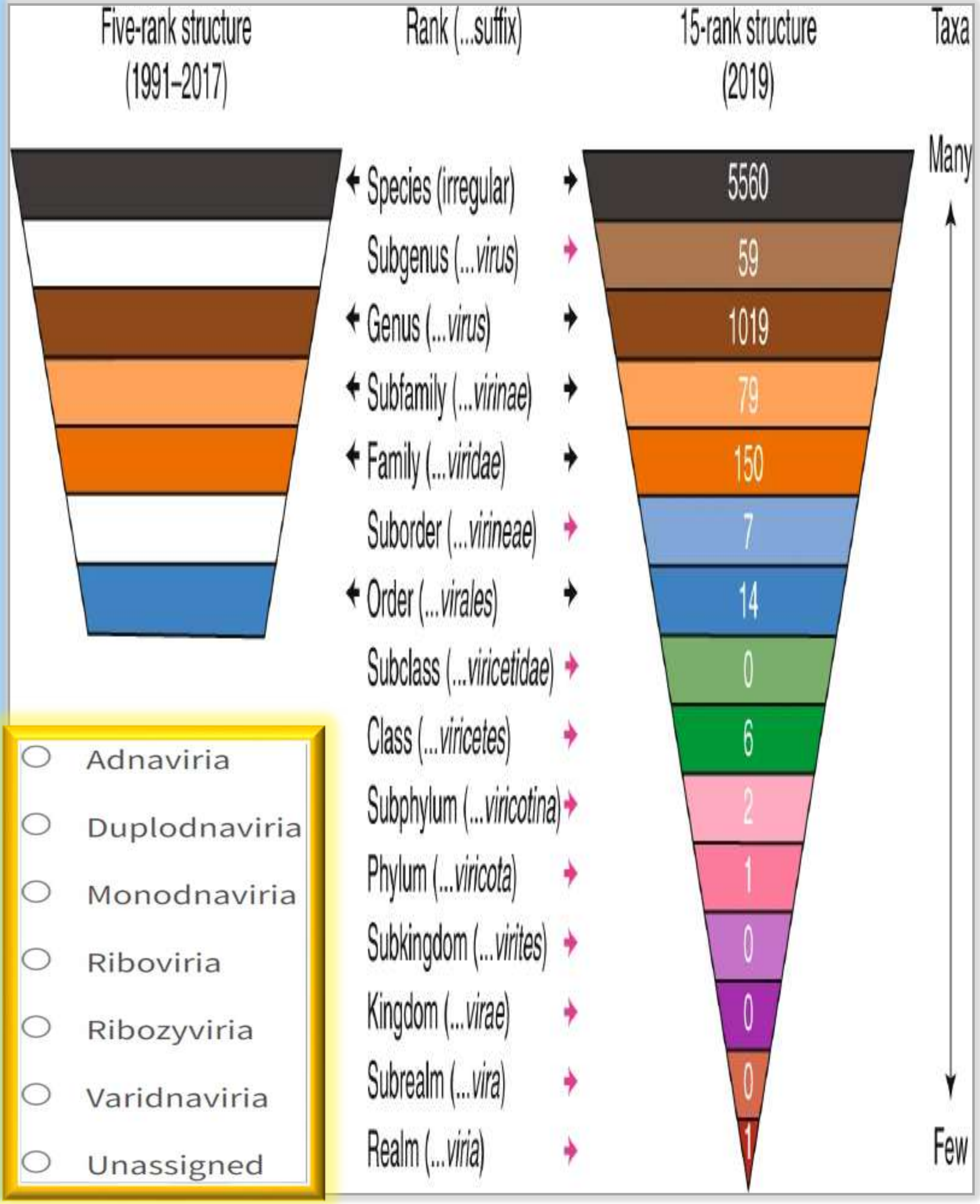
Search and browse the virus taxonomy

Master Species List

MSL: Spreadsheet of all current species

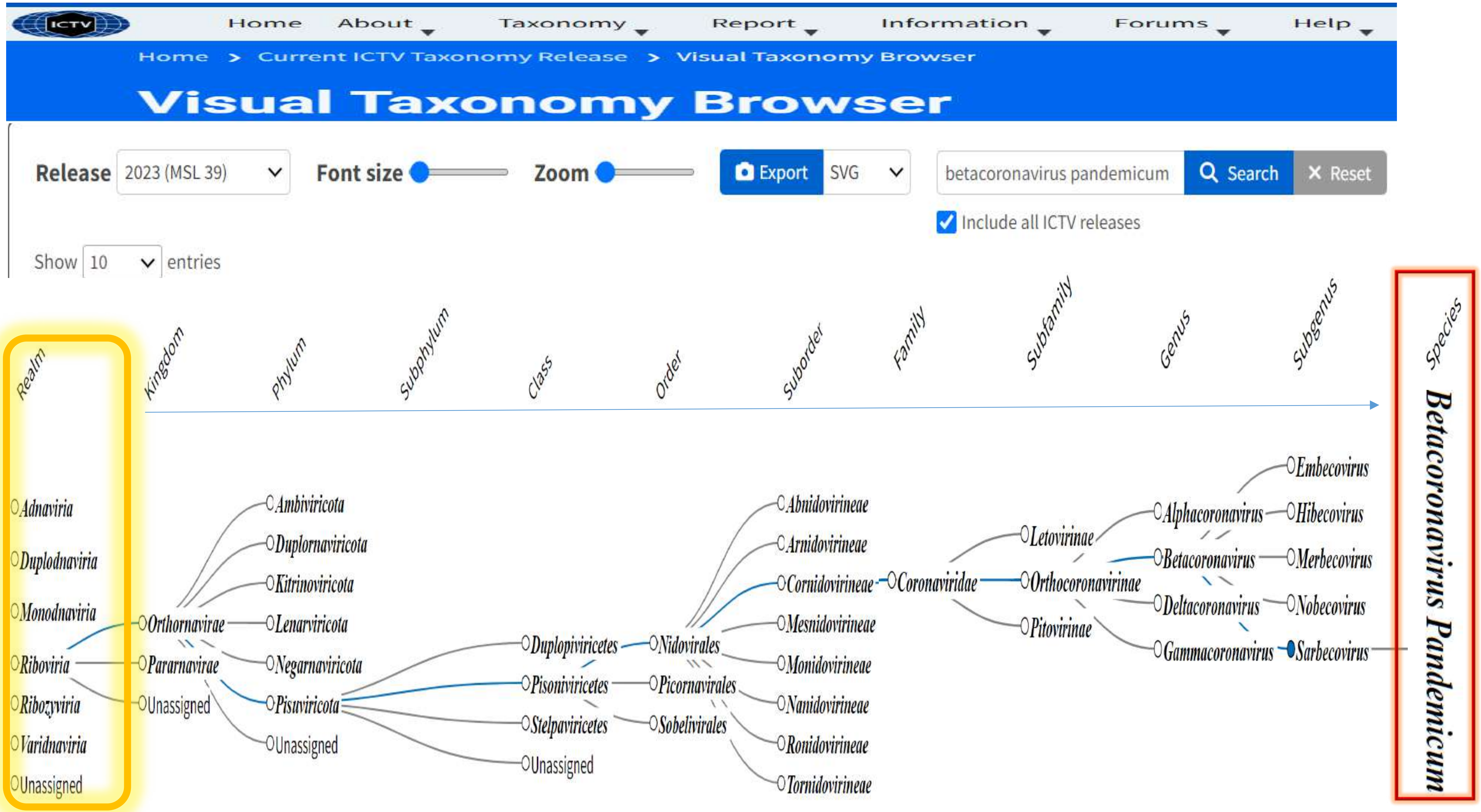
Virus Metadata Resource

VMR: Virus exemplars for every species



○ Adnaviria
○ Duplodnaviria
○ Monodnaviria
○ Riboviria
○ Ribozyviria
○ Varidnaviria
○ Unassigned

https://www.nature.com/articles/s41564-020-0709-x/figures/1



Visual Taxonomy Browser

Release 2023 (MSL 39)

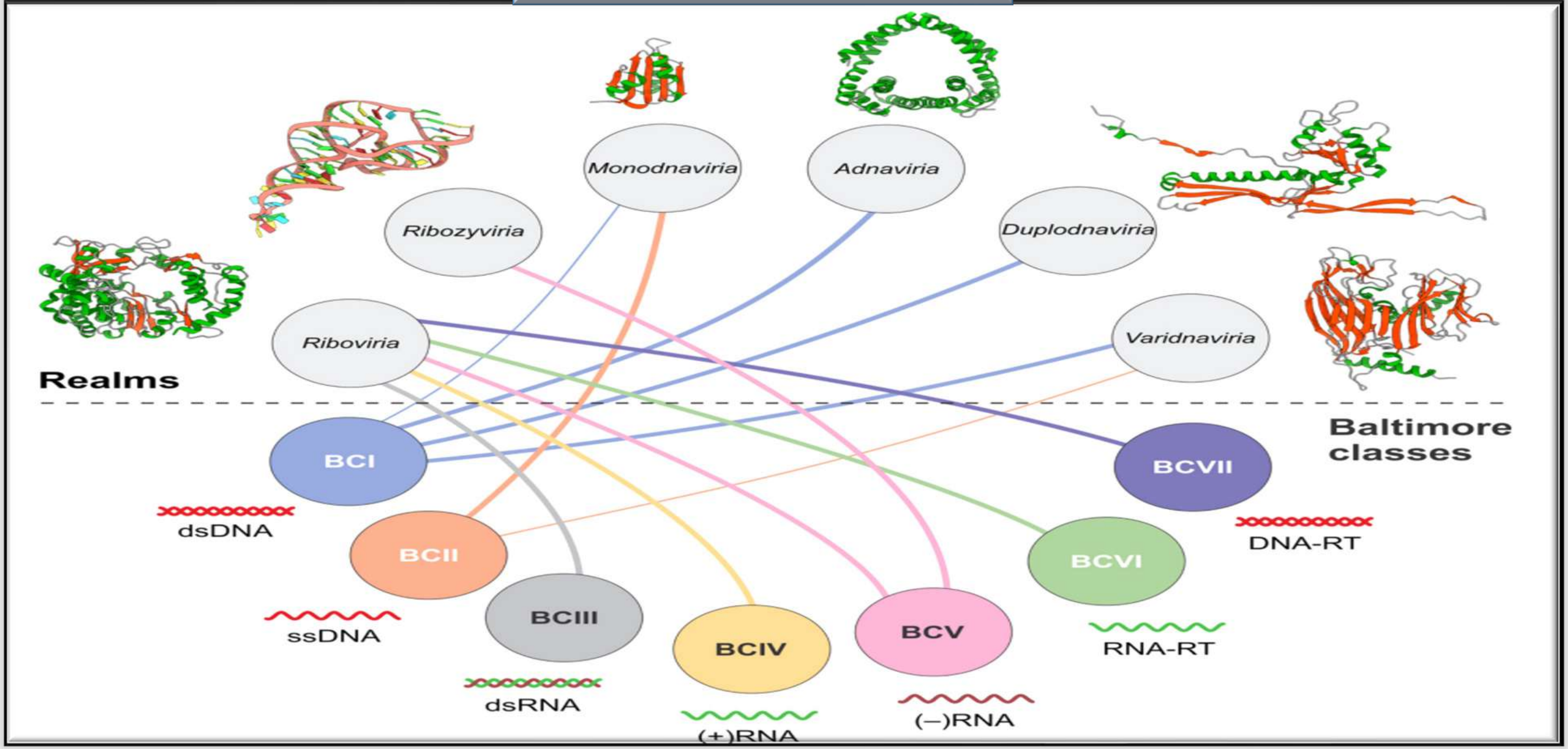
betacoronavirus pandemicum

☑ Include all ICTV releases

Show 10 entries

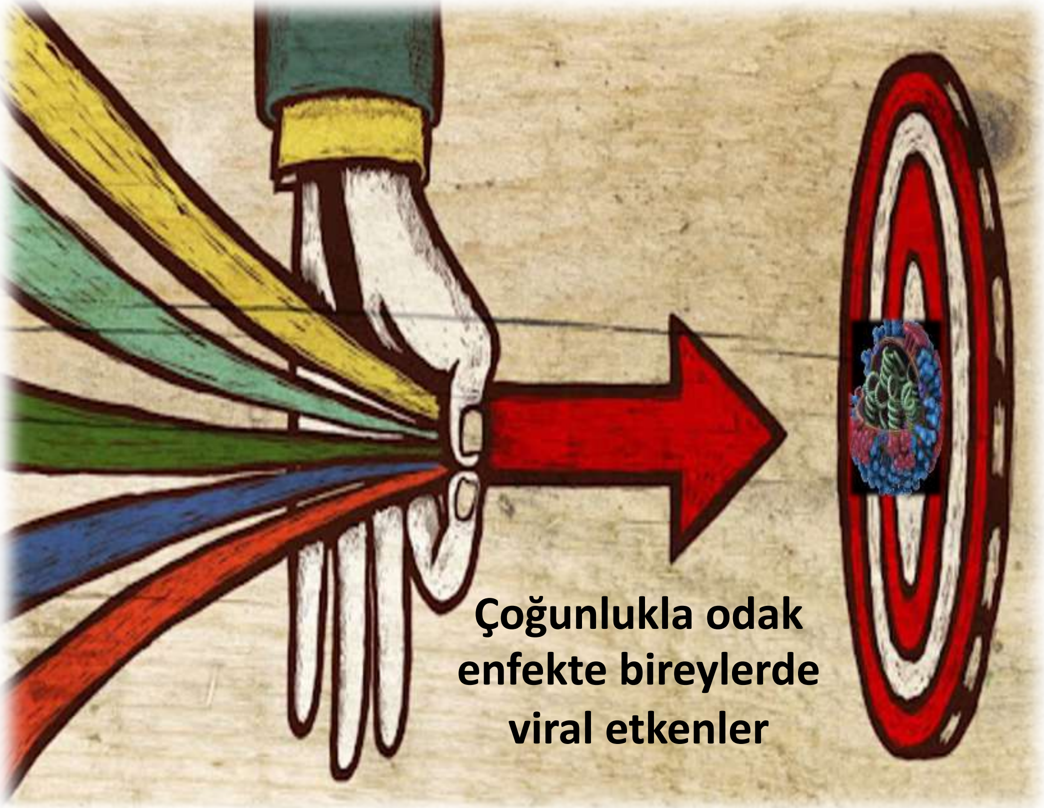
Betacoronavirus Pandemicum

Baltimore & ICTV



Cadwell, K. ve Wang, D. (2021). *Editöryal özet: Sağlık ve hastalıkta virom. Virolojide Güncel Görüş, 49, 139–141.* doi:10.1016/j.coviro.2021.06.0

İçimizde Yaşayan
Virüsler Hakkında
Sınırlı Bilgi



Çoğunlukla odak enfekte bireylerde viral etkenler

Adapte olmuş virüsler çoğunlukla klinik olarak sessiz, karşı seçilimden kaçınmak için konakçılarıyla dengede ….. viral kalıcılık

İnsan Viromunu Tanımlamanın Zorlukları?

Kronik virüs infeksiyonları

Az sıklıkta

- Immunsupressif Hasta

- Bakteriler (16S r) aksine, virüsler korunan ortak bir gen-evrensel bir viral dizi Ø

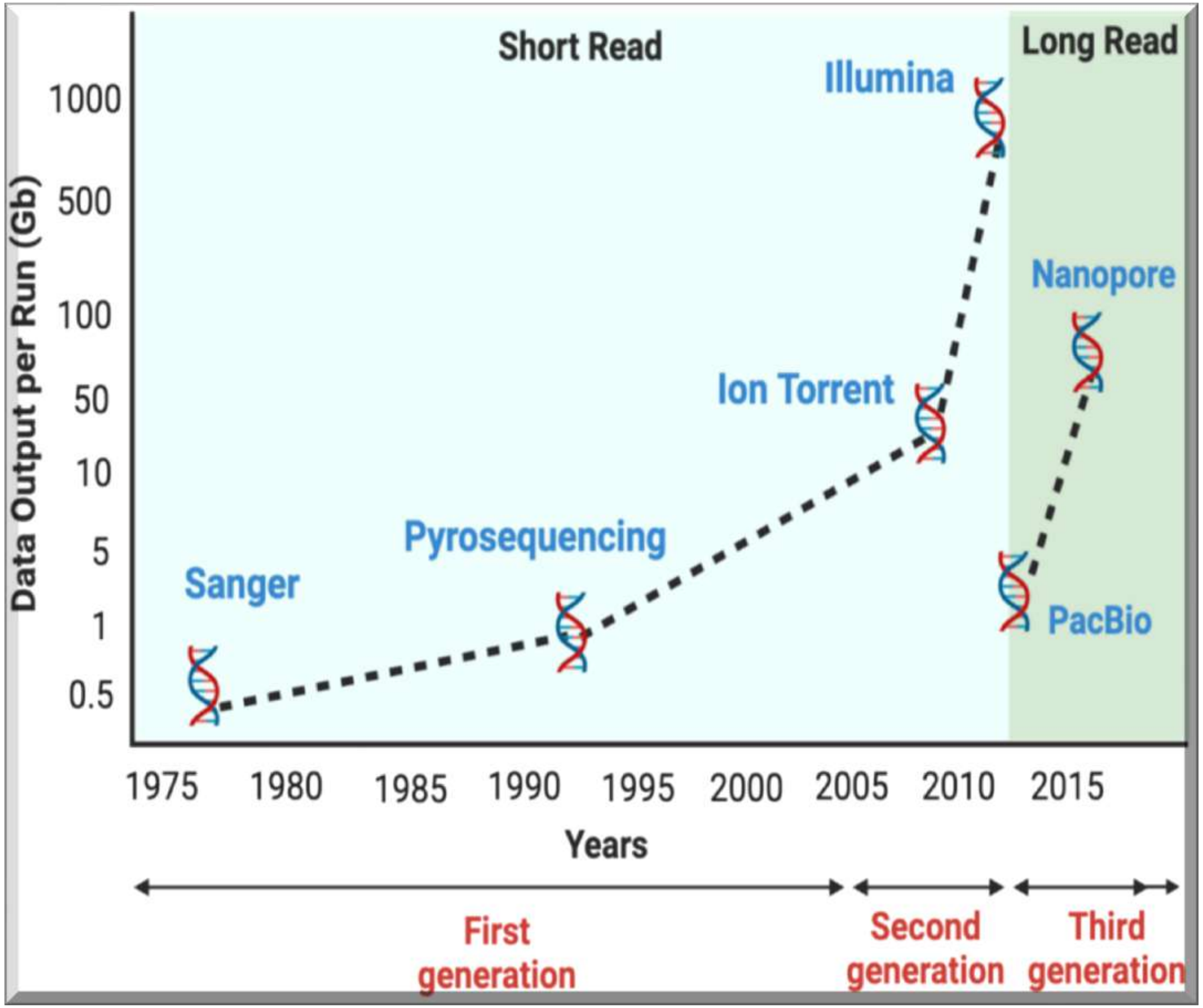
İnsan viromu veritabanı/kategorize zorluk ‘karanlık madde’ (%13 — %95)

- Faj & konakçıları arasında ilinti kurmada zorluklar (CRISPR-cas?)

- Düşük biyokütleli örnekler viral titre ve DNA kont. (çevresel DNA ±)

Çözüm: Deneysel örneklerle birlikte birden fazla negatif C. analizi ve veritabanlarına negatif kontrol verileri +

Dizileme Teknolojilerinin Evrimi

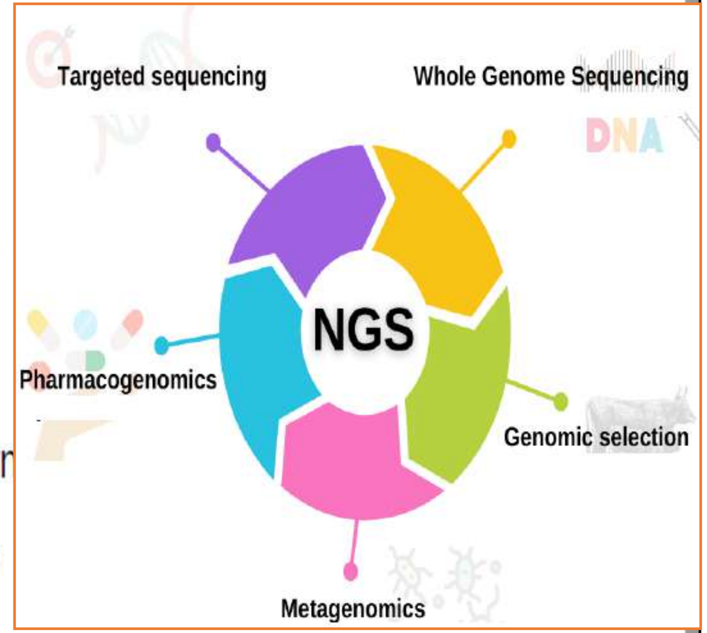


Birinci Nesil

- Sanger Dizilemesi

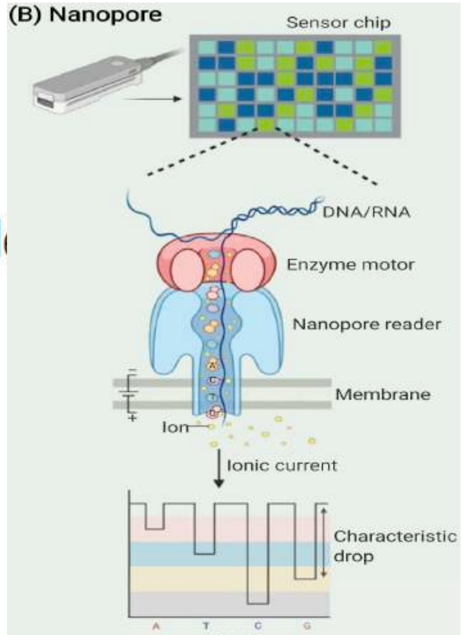
İkinci Nesil Dizileme

- Pirosekanslama
- Geri Dönüşümlü Term
- Ligasyonla Dizileme



Üçüncü Nesil Dizileme

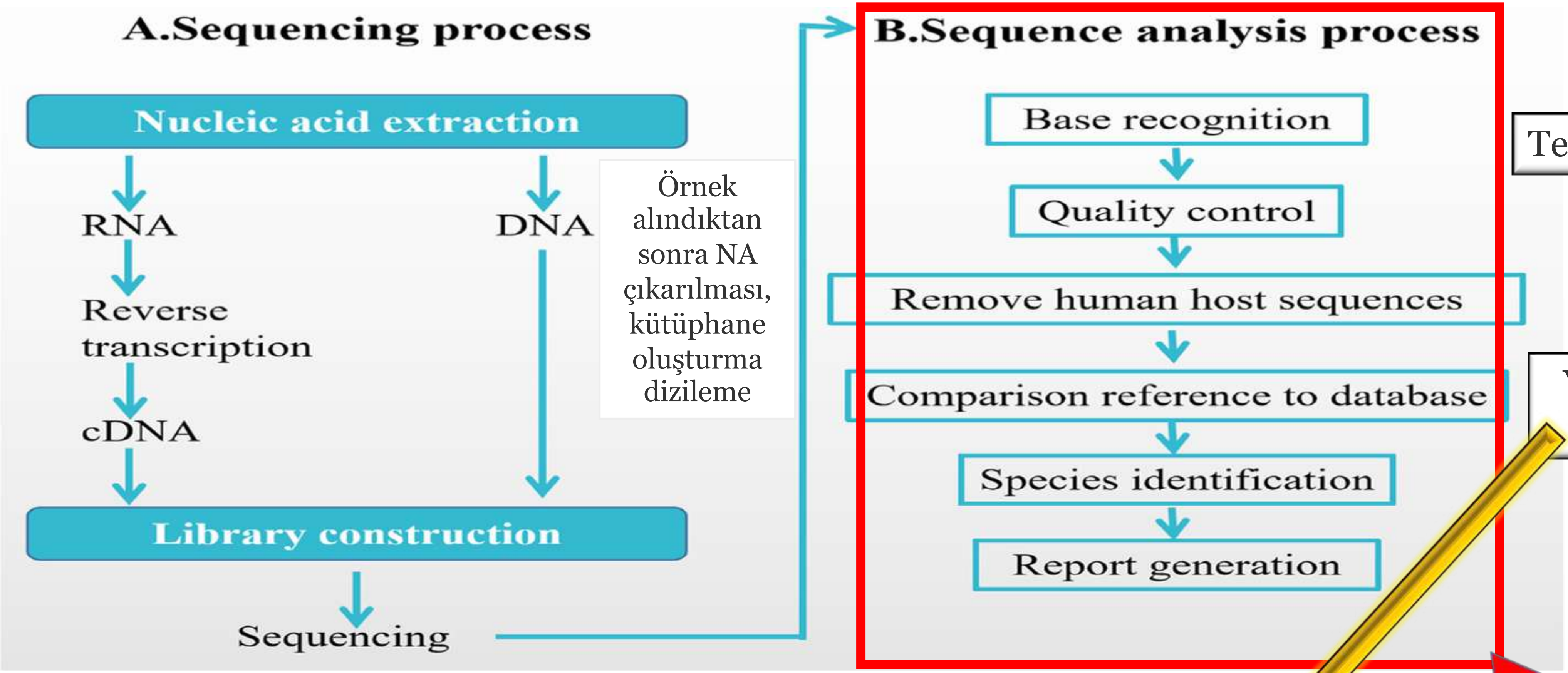
- Tek Molekül Floresan Dizilemesi
- Tek Molekül Gerçek Zamanlı Dizil
- Yarıiletken Dizileme
- Nanopore Dizileme



Dördüncü Nesil Dizileme

Genomik analizin doğrudan hücre içerisinde yapılmasını amaçlar.

Yeni Nesil Dizileme Analizi Akış Şeması



Örnek alındıktan sonra NA çıkarılması, kütüphane oluşturma dizileme

Temel tanımlama

Verilerin referans veritabanına +


Genome

Search by taxonomic name or ID, Assembly name, BioProject, BioSample, WGS or Nucleotide accession

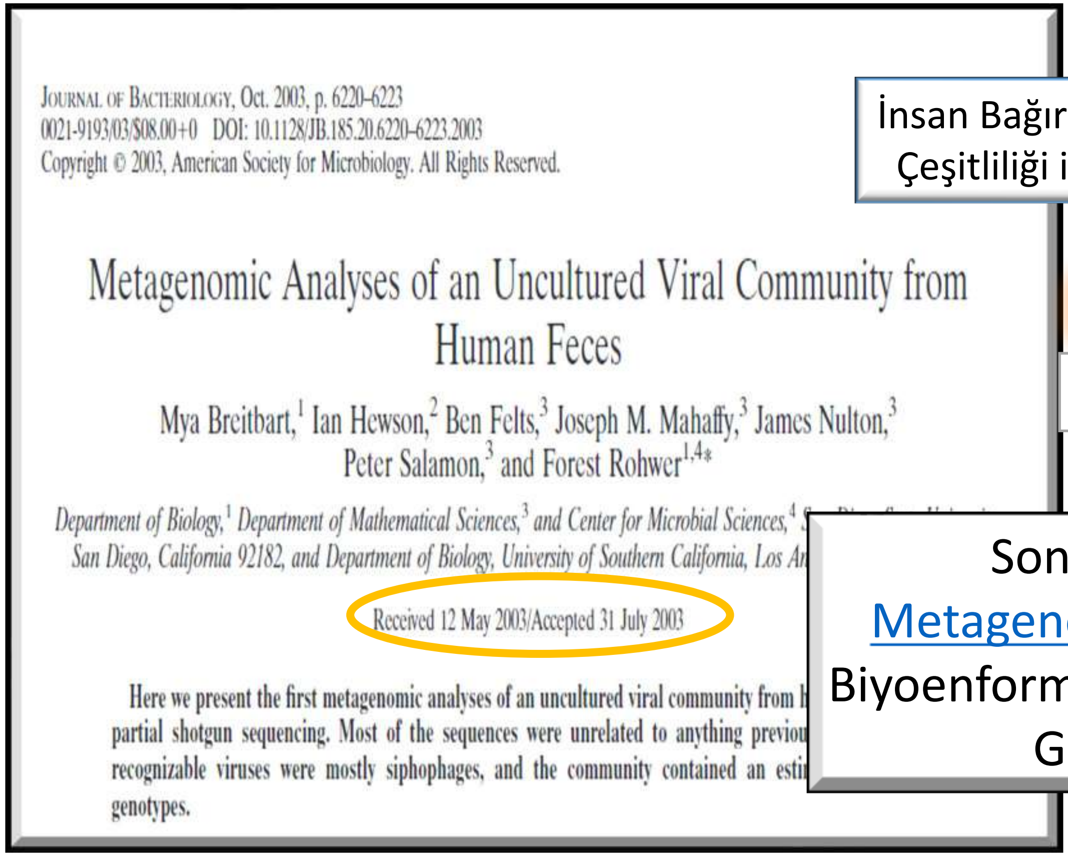
Search term

Try examples: Homo sapiens GCF_000001405.40 PRJNA489243 SAMN15960293 WFKY01 GRCh38.p14 NC_000913.3

ftp://ftp.ncbi.nlm.nih.gov/genomes

Biyoinformatik Analiz
(Kuru Laboratuvar)

Biyoenformatik metagenomik kayıtlar kullanarak keşfedilmemiş virüslerin tespiti



Journal of Bacteriology, Oct. 2003, p. 6220–6223
0021-9193/03/$08.00+0 DOI: 10.1128/JB.185.20.6220–6223.2003

Metagenomic Analyses of an Uncultured Viral Community from Human Feces

Mya Breitbart,[1] Ian Hewson,[2] Ben Felts,[3] Joseph M. Mahaffy,[3] James Nulton,[3]
Peter Salamon,[3] and Forest Rohwer[1,4]*

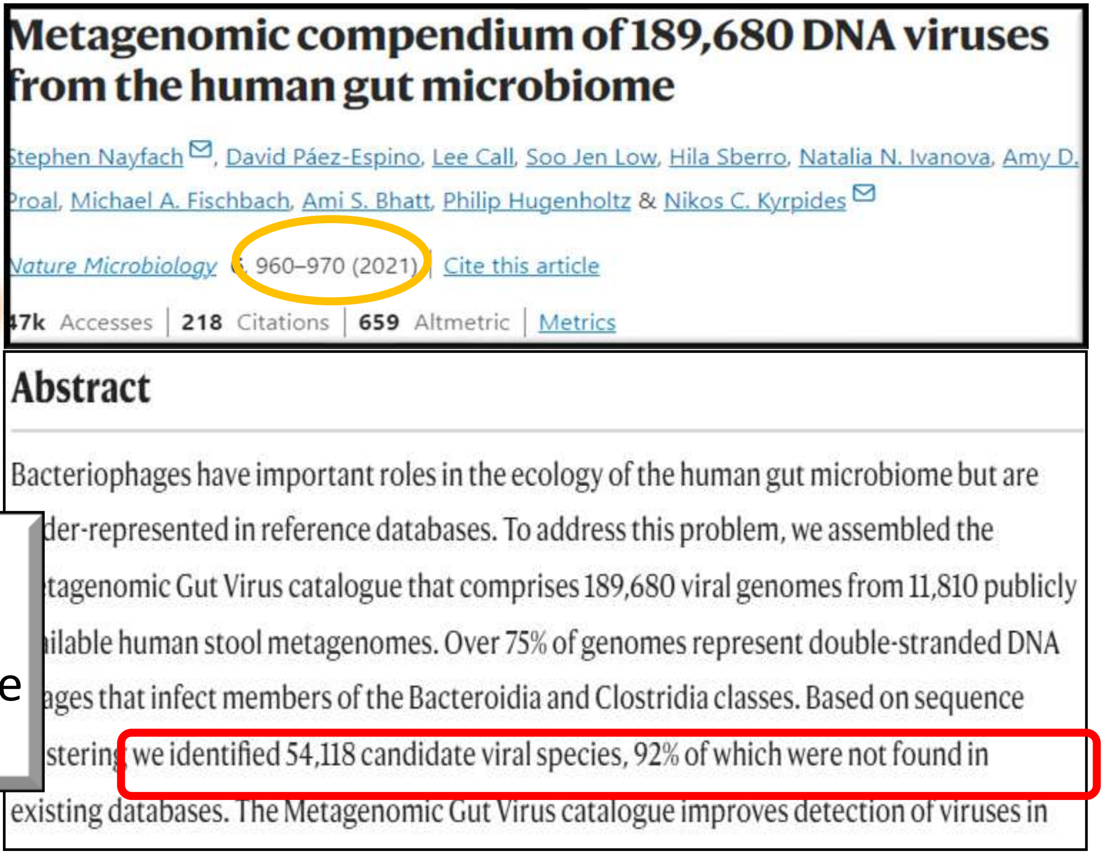
Department of Biology,[1] Department of Mathematical Sciences,[3] and Center for Microbial Sciences,[4]
San Diego, California 92182, and Department of Biology, University of Southern California, Los An

Received 12 May 2003/Accepted 31 July 2003

Here we present the first metagenomic analyses of an uncultured viral community from h
partial shotgun sequencing. Most of the sequences were unrelated to anything previou
recognizable viruses were mostly siphophages, and the community contained an esti
genotypes.

İnsan Bağırsak Viromunun
Çeşitliliği ilk Kez 2003'te

~ 20 yıl sonra



Metagenomic compendium of 189,680 DNA viruses from the human gut microbiome

Stephen Nayfach, David Páez-Espino, Lee Call, Soo Jen Low, Hila Sberro, Natalia N. Ivanova, Amy D.
roal, Michael A. Fischbach, Ami S. Bhatt, Philip Hugenholtz & Nikos C. Kyrpides

Nature Microbiology 6, 960–970 (2021) | Cite this article

7k Accesses | 218 Citations | 659 Altmetric | Metrics

Abstract

Bacteriophages have important roles in the ecology of the human gut microbiome but are
der-represented in reference databases. To address this problem, we assembled the
tagenomic Gut Virus catalogue that comprises 189,680 viral genomes from 11,810 publicly
ilable human stool metagenomes. Over 75% of genomes represent double-stranded DNA
ages that infect members of the Bacteroidia and Clostridia classes. Based on sequence
stering we identified 54,118 candidate viral species, 92% of which were not found in
existing databases. The Metagenomic Gut Virus catalogue improves detection of viruses in

Son 20 Yılda
Metagenomik Dizileme
Biyoenformatik Analizlerde
Gelişme

Open Access Article

VOGDB—Database of Virus Orthologous Groups

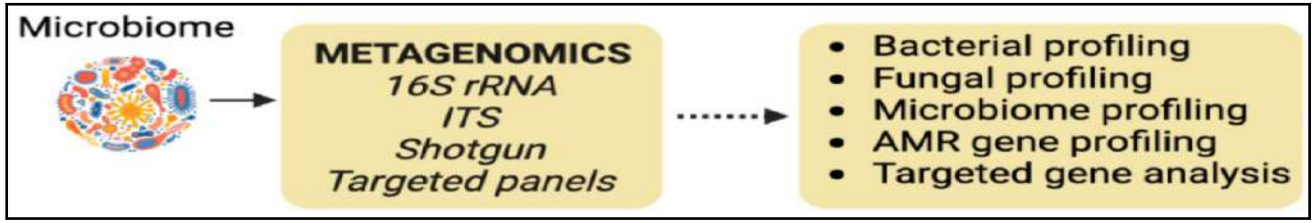
by Lovro Trgovec-Greif[1,2], Hans-Jörg Hellinger[2,3], Jean Mainguy[4], Alexander Pfundner[1,2], Dmitrij Frishman[5], Michael Kiening[5], Nicole Suzanne Webster[6,7,8], Patrick William Laffy[6], Michael Feichtinger[1] and Thomas Rattei[1,*]

Viruses **2024**, *16*(8), 1191; https://doi.org/10.3390/v16081191

Submission received: 1 July 2024 / Revised: 21 July 2024 / Accepted: 23 July 2024 / Published: 25 July 2024

- VOGDB (database of virus orthologous groups), virüs protein aileleri ve virüs protein yapısal kıvrımlarının analiz edildiği çok katmanlı bir veritabanı
- Katmanlar, daha yüksek dizi farklılaşmasında yansıtılan artan evrimsel mesafeye sahip proteinleri toplamak için tasarlanmış

Metagenomik Veriler & Heterojen Mikrobiyal Topluluklar



- Bacterial profiling
- Fungal profiling
- Microbiome profiling
- AMR gene profiling
- Targeted gene analysis

Kim var?

Başka Kim Var?

"Ne yapıyorlar« ???

The New York Times

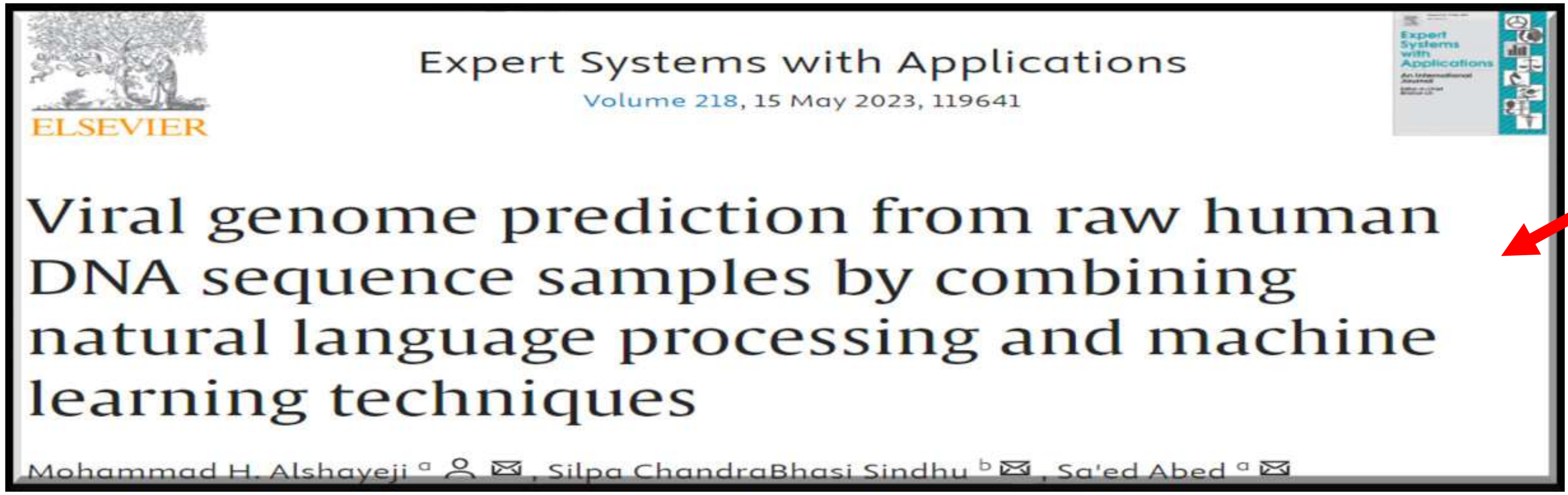
> But in recent years, virologists have changed the way they hunt. Now they look for bits of genetic material in samples — water, mud, blood — and use sophisticated computer programs to recognize viral genes.

https://www.nytimes.com/2020/03/24/science/viruses-coranavirus-biology.html

İşlev, Metabolik süreçler…

→ Metagenomik yöntemler, ileri yanıtlama…

İnsan Virom Analizi & Bilgisayar Yazılımları



ELSEVIER

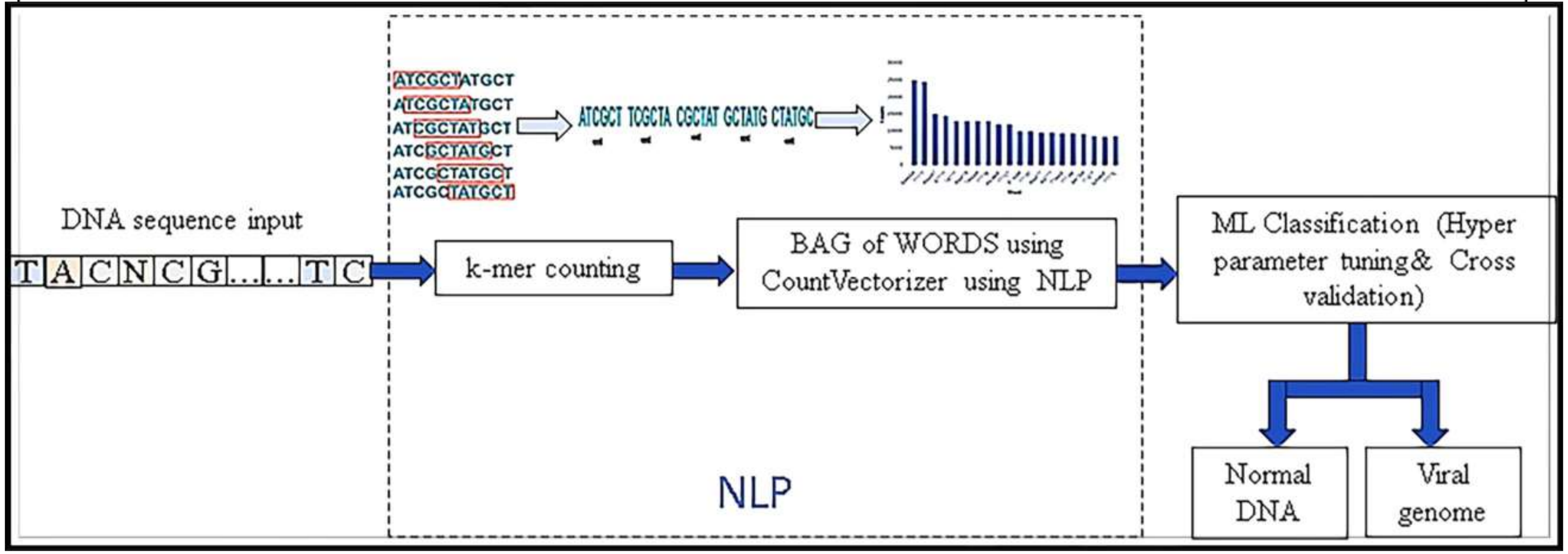
Expert Systems with Applications

Volume 218, 15 May 2023, 119641

Viral genome prediction from raw human DNA sequence samples by combining natural language processing and machine learning techniques

Mohammad H. Alshayeji [a], Silpa ChandraBhasi Sindhu [b], Sa'ed Abed [a]

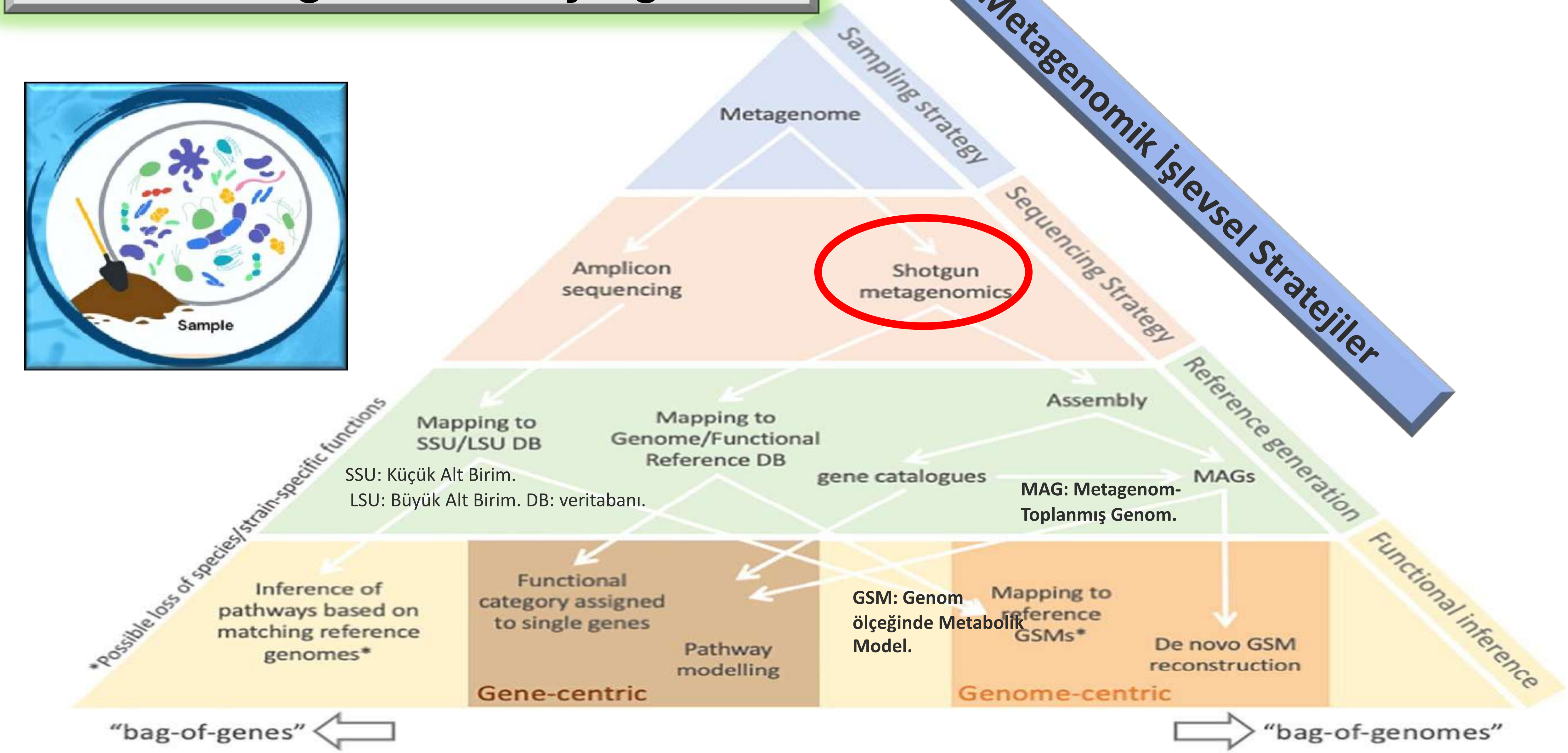
Ham insan DNA dizisi örneklerinden viral genom tahmini (Doğal dil işleme + makine öğrenim teknikleri)



- ❑ Viral ve viral olmayan dizileri ayırmak için vFams
- ❑ Virüs analizi için Viral MetaGenome Annotation Pipeline (VMGAP)
- ❑ Metagenomik Araştırma için Viral Bilişim Kaynağı (VIROME) ve Metavir 2, DisCVR
- ❑ SURPI (dizi tabanlı ultra hızlı patojen tanımlama) ve CZ ID (IDseq) gibi bulut tabanlı klinik metagenomik bilgi işlem iş akışları
- ❑ Tüm virüs genomik verileri Galaxy platformu (https://usegalaxy.eu/)

Metagenomik Çağ

Metagenomik İşlevsel Stratejiler



SSU: Küçük Alt Birim.
LSU: Büyük Alt Birim. DB: veritabanı.

MAG: Metagenom-Toplanmış Genom.

GSM: Genom ölçeğinde Metabolik Model.

From bag-of-genes to bag-of-genomes: metabolic modelling of communities in the era of metagenome-assembled genomes Frioux, Clémence et al. Computational and Structural Biotechnology Journal, Volume 18, 1722 - 1734

- ❑ Sağlıklı insanlarda, 'normal- patojenik viromlar’ arasındaki sınırlar net değil

- ▪ Metagenomik yöntemlerin rutin Lab. süreçleri ; teslerin duyarlılığı, özgüllüğü ve tekrarlanabilirliği…???

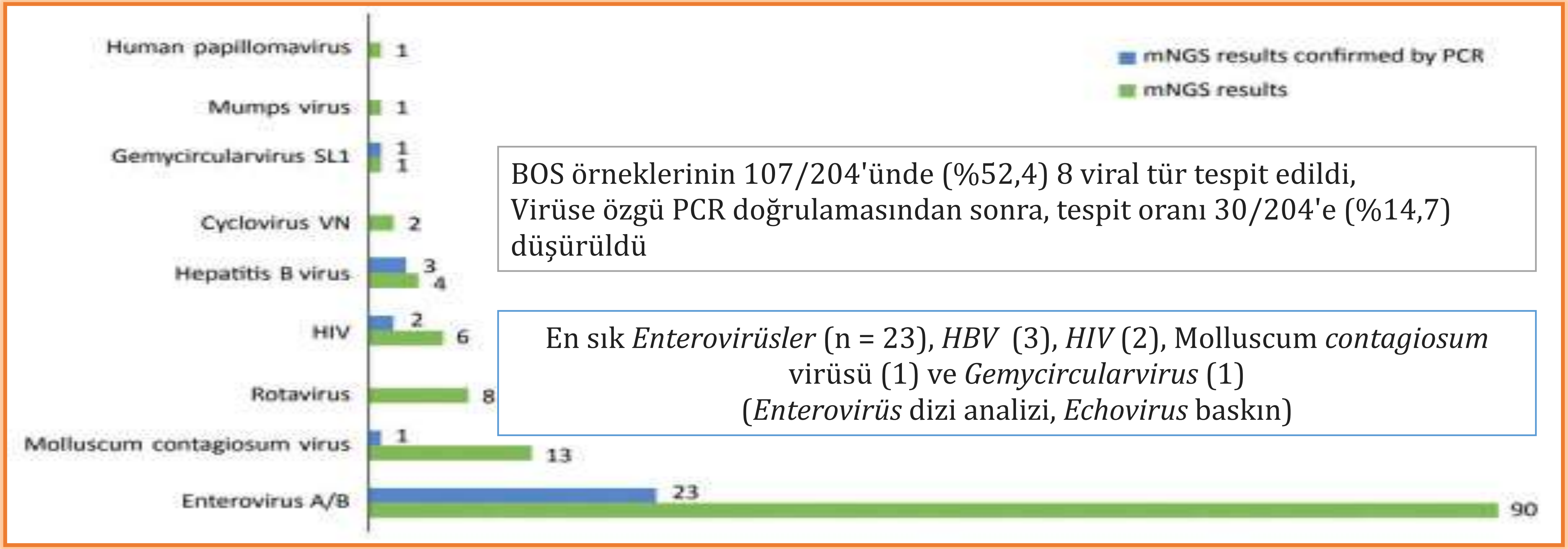
Emerg Infect Dis. 2021 Jan; 27(1): 205–213.
doi: 10.3201/eid2701.202723
PMCID: PMC7774551
PMID: 33350920

Viral Metagenomic Analysis of Cerebrospinal Fluid from Patients with Acute Central Nervous System Infections of Unknown Origin, Vietnam

Nguyen To Anh,✉ Le Nguyen Truc Nhu, Nguyen Thi Thu Hong, Tran My Phuc, Pham Thi Thanh Tam, Dang Thao Huong, Tran Tuan Anh, Xutao Deng, Ho Dang Trung Nghia, Tran Thua Nguyen, Nguyen Van Hung, Nguyen Dac Thuan, Pham Thi Hong Phuong, Nguyen Van Vinh Chau, Stephen Baker, Eric Delwart, Guy Thwaites, Le Van Tan,✉ and for the VIZIONS Consortium[1]

▸ Author information ▸ Copyright and License information PMC Disclaimer

Akut MSS enfeksiyonu olan hastalardan alınan 204 beyin omurilik sıvısı (BOS) örneğindeki virüs tespitinde metagenomik NGS

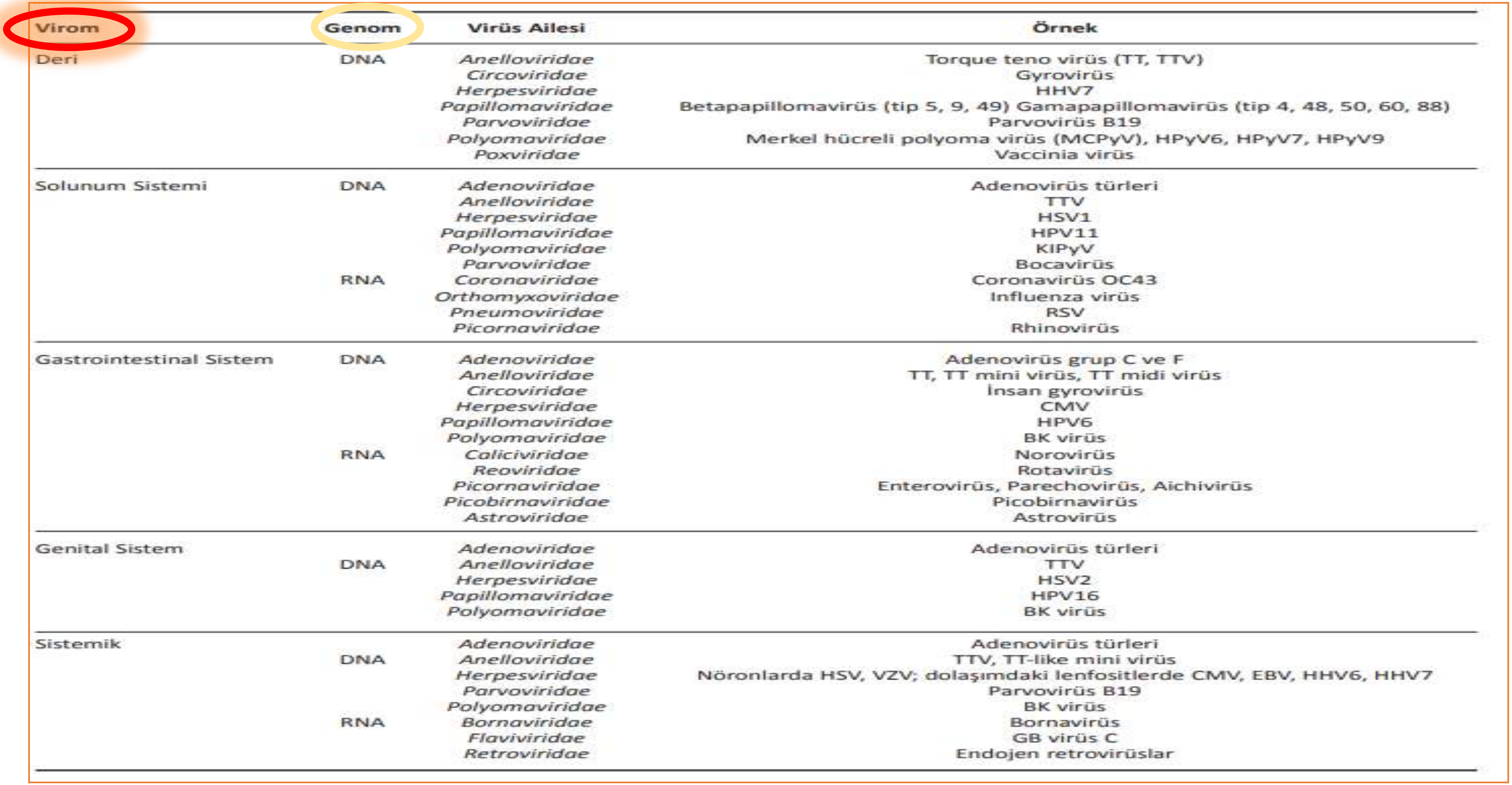


BOS örneklerinin 107/204'ünde (%52,4) 8 viral tür tespit edildi,
Virüse özgü PCR doğrulamasından sonra, tespit oranı 30/204'e (%14,7) düşürüldü

En sık *Enterovirüsler* (n = 23), *HBV* (3), *HIV* (2), Molluscum *contagiosum* virüsü (1) ve *Gemycircularvirus* (1)
(*Enterovirüs* dizi analizi, *Echovirus* baskın)

- ☐ Yakın zamanda çok sayıdaki derleme makalelerinde; insan vücudunun farklı bölgelerindeki çeşitli **V**iromlar ile insan konakçılar arasındaki etkileşimler sağlık ve hastalık yönüyle incelenmiş

- ☐ İnsan **V**iromu; vücudun her yerinde; deride, solunum, gastrointestinal, genital sistem ve sistemik dahil olmak üzere çeşitli örnek tiplerinde bulunabilir



Virom	Genom	Virüs Ailesi	Örnek
Deri	DNA	*Anelloviridae*	Torque teno virüs (TT, TTV)
		Circoviridae	Gyrovirüs
		Herpesviridae	HHV7
		Papillomaviridae	Betapapillomavirüs (tip 5, 9, 49) Gamapapillomavirüs (tip 4, 48, 50, 60, 88)
		Parvoviridae	Parvovirüs B19
		Polyomaviridae	Merkel hücreli polyoma virüs (MCPyV), HPyV6, HPyV7, HPyV9
		Poxviridae	Vaccinia virüs
Solunum Sistemi	DNA	*Adenoviridae*	Adenovirüs türleri
		Anelloviridae	TTV
		Herpesviridae	HSV1
		Papillomaviridae	HPV11
		Polyomaviridae	KIPyV
		Parvoviridae	Bocavirüs
	RNA	*Coronaviridae*	Coronavirüs OC43
		Orthomyxoviridae	Influenza virüs
		Pneumoviridae	RSV
		Picornaviridae	Rhinovirüs
Gastrointestinal Sistem	DNA	*Adenoviridae*	Adenovirüs grup C ve F
		Anelloviridae	TT, TT mini virüs, TT midi virüs
		Circoviridae	İnsan gyrovirüs
		Herpesviridae	CMV
		Papillomaviridae	HPV6
		Polyomaviridae	BK virüs
	RNA	*Caliciviridae*	Norovirüs
		Reoviridae	Rotavirüs
		Picornaviridae	Enterovirüs, Parechovirüs, Aichivirüs
		Picobirnaviridae	Picobirnavirüs
		Astroviridae	Astrovirüs
Genital Sistem		*Adenoviridae*	Adenovirüs türleri
	DNA	*Anelloviridae*	TTV
		Herpesviridae	HSV2
		Papillomaviridae	HPV16
		Polyomaviridae	BK virüs
Sistemik		*Adenoviridae*	Adenovirüs türleri
	DNA	*Anelloviridae*	TTV, TT-like mini virüs
		Herpesviridae	Nöronlarda HSV, VZV; dolaşımdaki lenfositlerde CMV, EBV, HHV6, HHV7
		Parvoviridae	Parvovirüs B19
		Polyomaviridae	BK virüs
	RNA	*Bornaviridae*	Bornavirüs
		Flaviviridae	GB virüs C
		Retroviridae	Endojen retrovirüslar

Sağlıklı Bireylerden Sıklıkla İzole Edilen Virüsler (Bozdayi, Gülendam & Fidan, Işıl. 2021)

Oral cavity

Eukaryotic viruses	Phages
Herpesviridae	*Siphoviridae*
Redondoviridae	*Podoviridae*
Anelloviridae	*Myoviridae*
Papillomaviridae	

~10^8 VLPs per millilitre of saliva

Lung

Eukaryotic viruses	Phages
Anelloviridae	*Siphoviridae*
Redondoviridae	*Podoviridae*
Adenoviridae	*Myoviridae*
Herpesviridae	*Microviridae*
Papillomaviridae	*Inoviridae*

Gastrointestinal tract

Eukaryotic viruses	Phages
Anelloviridae	*Siphoviridae*
Adenoviridae	*Podoviridae*
Caliciviridae	*Myoviridae*
Picornaviridae	*Microviridae*
Herpesviridae	*Inoviridae*
Circoviridae	
Virgaviridae	

~10^9 VLPs per gram of faeces

Vagina

Eukaryotic viruses	Phages
Anelloviridae	*Siphoviridae*
Herpesviridae	*Podoviridae*
	Myoviridae
	Microviridae

Nervous system

Eukaryotic viruses	Phages
Herpesviridae	*Siphoviridae*
	Podoviridae
	Myoviridae

~10^4 VLPs per millilitre of cerebrospinal fluid

Sağlıklı bireylerde rutin tespit mikrobiyomun bakteriyel üyelerine benzer şekilde konakçıyla simbiyotik ilişki ?

Daha fazla insan popülasyonu araştırıldıkça ve daha fazla viral tip keşfedildikçe vücut bölgesinde bilinenler, artacaktır.

Blood

Eukaryotic viruses	Phages
Anelloviridae	*Siphoviridae*
Herpesviridae	*Podoviridae*
Picornaviridae	*Myoviridae*
	Microviridae
	Inoviridae

~10^8 VLPs per millilitre of saliva

Skin

Eukaryotic viruses	Phages
Adenoviridae	*Siphoviridae*
Anelloviridae	*Podoviridae*
Circoviridae	*Myoviridae*
Herpesviridae	
Papillomaviridae	
Polyomaviridae	

Urinary system

Eukaryotic viruses	Phages
Papillomaviridae	*Siphoviridae*
Polyomaviridae	*Podoviridae*
Herpesviridae	*Myoviridae*

~10^7 VLPs per millilitre of urine

Semen

Eukaryotic viruses	Phages
Anelloviridae	Unknown
Papillomaviridae	
Herpesviridae	

Liang, Guanxiang, and Frederic D Bushman. “The human virome: assembly, composition and host interactions.” *Nature reviews. Microbiology* vol. 19,8 (2021): 514-527. doi:10.1038/s41579-021-00536-5

Virom & İnsan Hastalıkları Etkileşimleri

❑ Gastrointestinal sistemin **V**irom içeriğindeki değişimler;

- ✓ **O**toimmün
- ✓ **M**etabolik
- ✓ **O**nkolojik ve
- ✓ **İ**nfeksiyon hastalıklarının patogenezinde

Viromdaki Değişimler, Otoimmün Hastalıkların Potansiyel Tetikleyicisi ?

> Proc Natl Acad Sci U S A. 2017 Jul 25;114(30):E6166-E6175. doi: 10.1073/pnas.1706359114. Epub 2017 Jul 10.

Intestinal virome changes precede autoimmunity in type I diabetes-susceptible children

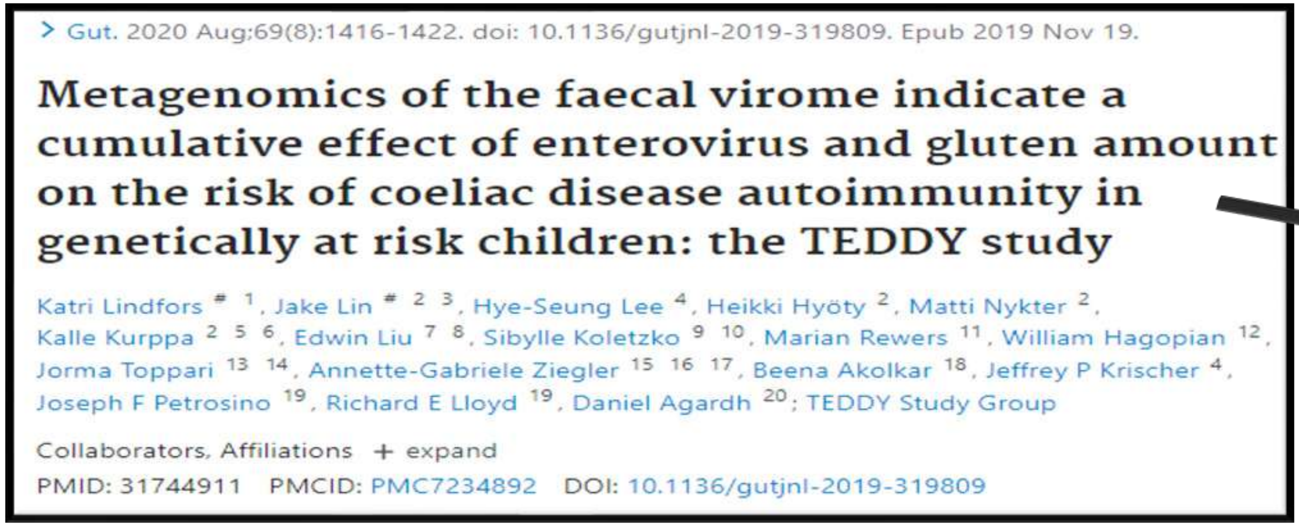
Guoyan Zhao [1], Tommi Vatanen [2, 3], Lindsay Droit [4], Arnold Park [4], Aleksandar D Kostic [2], Tiffany W Poon [2], Hera Vlamakis [2], Heli Siljander [5, 6], Taina Härkönen [5, 6], Anu-Maaria Hämäläinen [7], Aleksandr Peet [8, 9], Vallo Tillmann [8, 9], Jorma Ilonen [10], David Wang [4, 11], Mikael Knip [5, 6, 12, 13], Ramnik J Xavier [2, 14], Herbert W Virgin [1]

Affiliations + expand

PMID: 28696303 PMCID: PMC5544325 DOI: 10.1073/pnas.1706359114

○ Viral popülasyonlardaki değişiklikler Pediatrik tip 1 DM gelişimiyle ilişkili

- ***C**ircoviridae* ile ilişkili dizilerden anlamlı artış



> Gut. 2020 Aug;69(8):1416-1422. doi: 10.1136/gutjnl-2019-319809. Epub 2019 Nov 19.

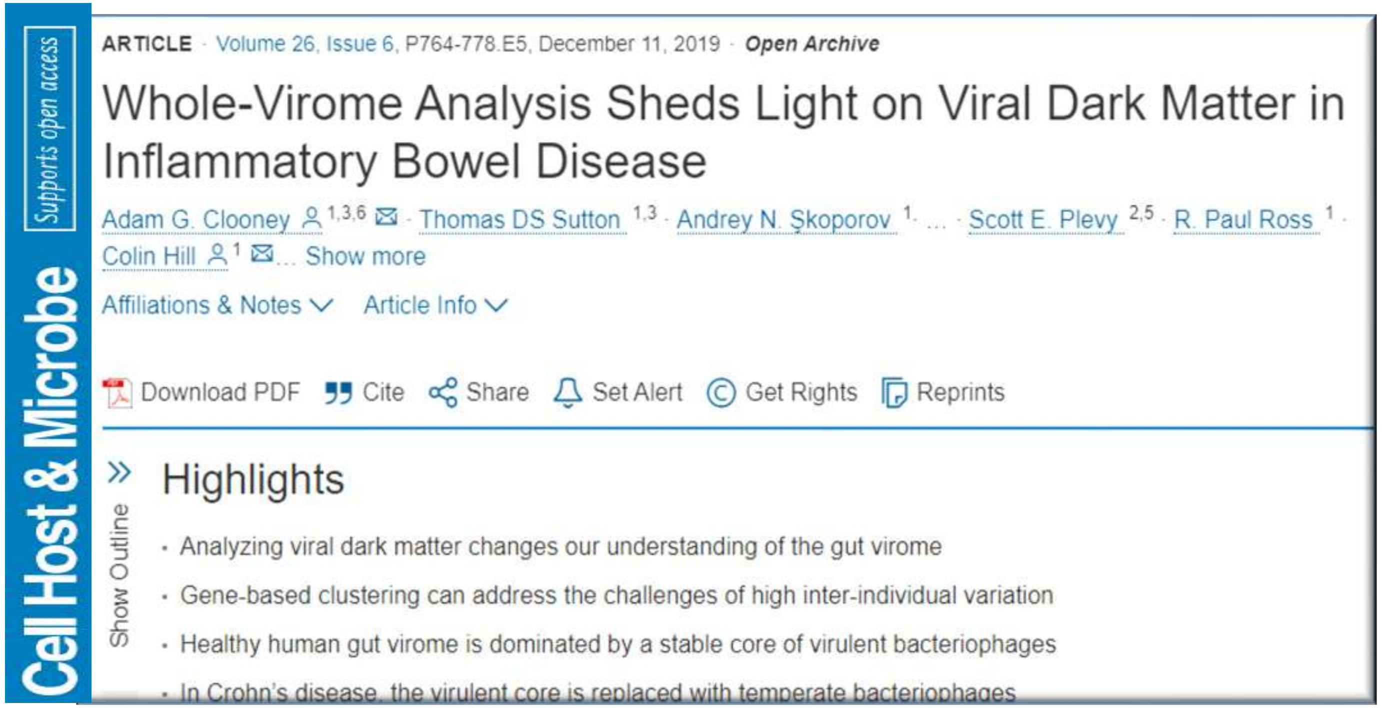
Metagenomics of the faecal virome indicate a cumulative effect of enterovirus and gluten amount on the risk of coeliac disease autoimmunity in genetically at risk children: the TEDDY study

Katri Lindfors [#, 1], Jake Lin [#, 2, 3], Hye-Seung Lee [4], Heikki Hyöty [2], Matti Nykter [2], Kalle Kurppa [2, 5, 6], Edwin Liu [7, 8], Sibylle Koletzko [9, 10], Marian Rewers [11], William Hagopian [12], Jorma Toppari [13, 14], Annette-Gabriele Ziegler [15, 16, 17], Beena Akolkar [18], Jeffrey P Krischer [4], Joseph F Petrosino [19], Richard E Lloyd [19], Daniel Agardh [20]; TEDDY Study Group

Collaborators, Affiliations + expand

PMID: 31744911 PMCID: PMC7234892 DOI: 10.1136/gutjnl-2019-319809

○ Bir metagenomik çalışmada, 1-2 yaş arasında *Enterovirüse* sık maruz kalan çocukların Çölyak hastalığı riski daha yüksek



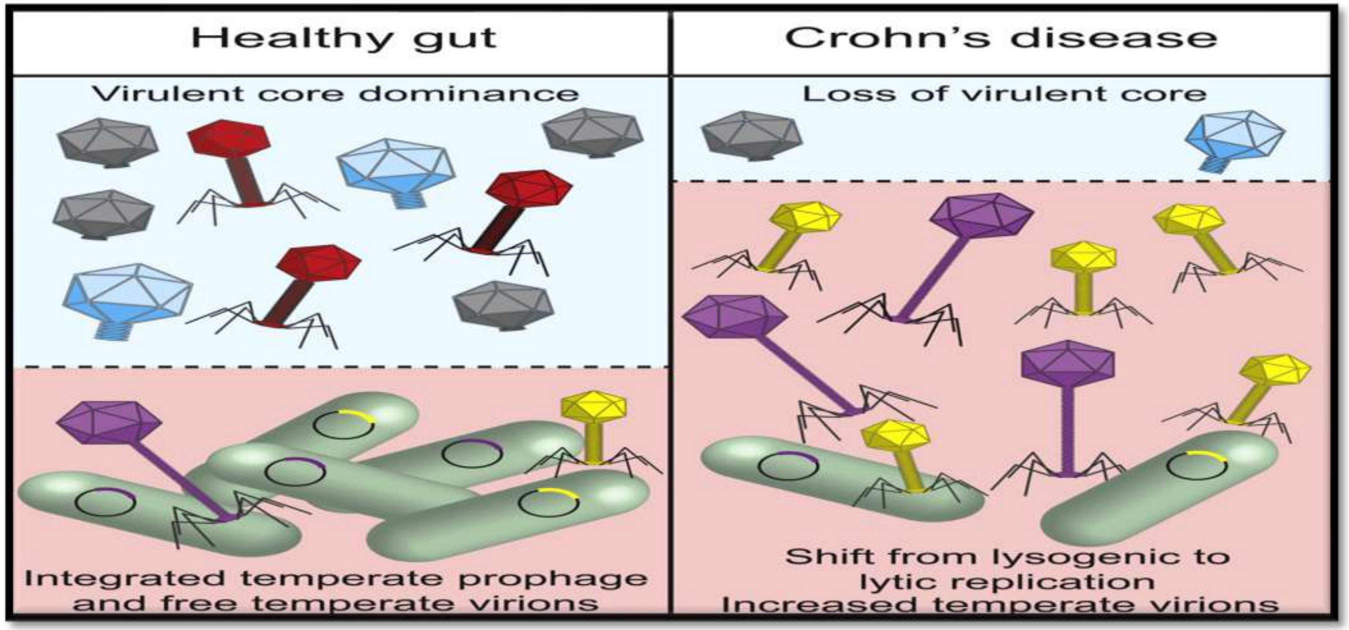
ARTICLE · Volume 26, Issue 6, P764-778.E5, December 11, 2019 · *Open Archive*

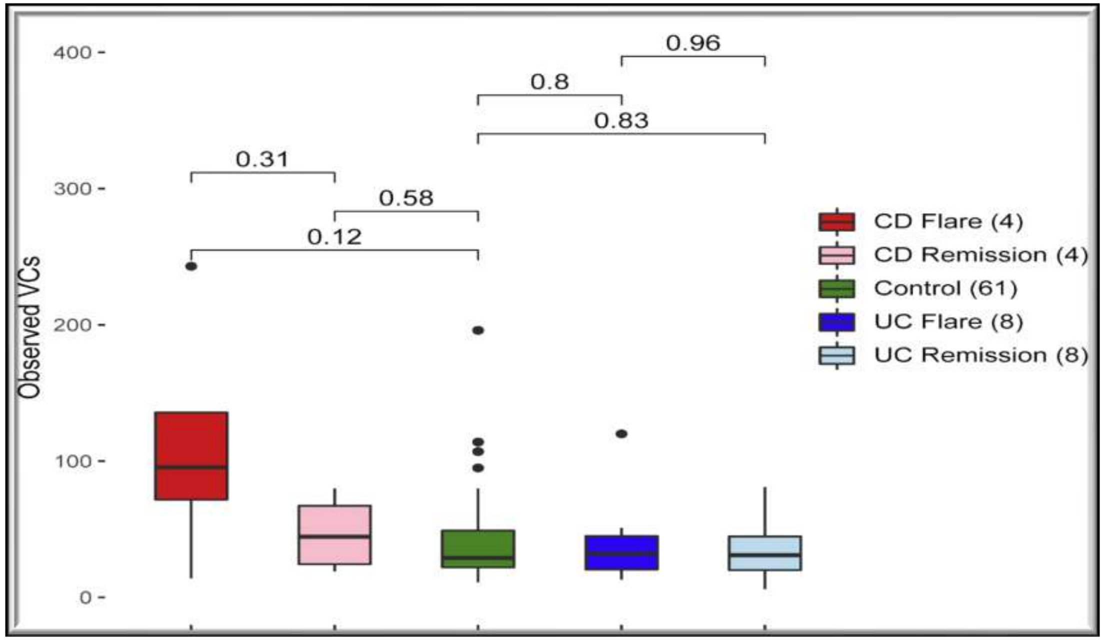
Whole-Virome Analysis Sheds Light on Viral Dark Matter in Inflammatory Bowel Disease

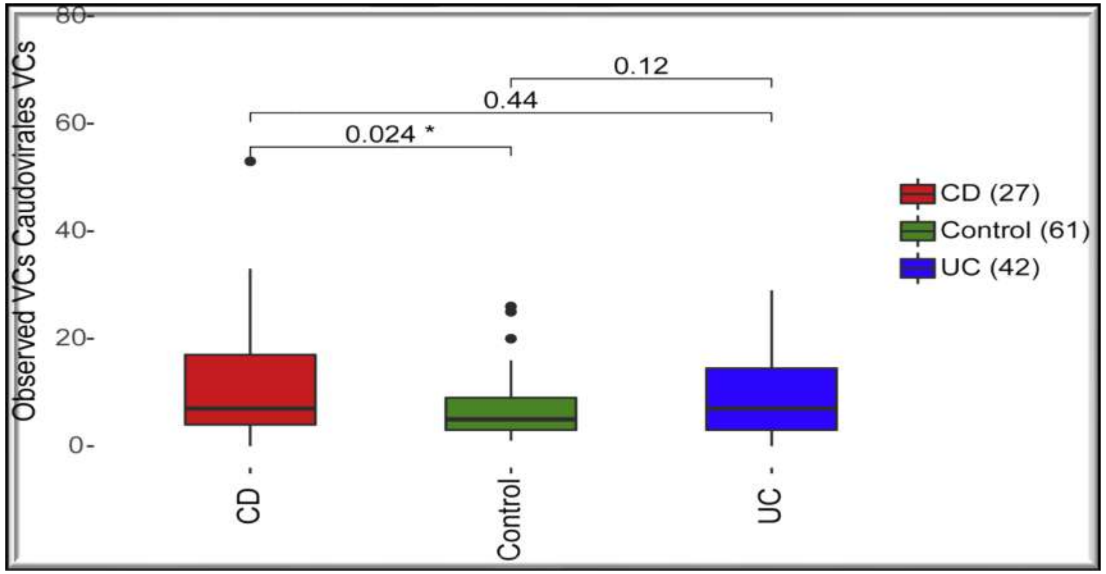
Adam G. Clooney [1,3,6] · Thomas DS Sutton [1,3] · Andrey N. Shkoporov [1] · ... · Scott E. Plevy [2,5] · R. Paul Ross [1] · Colin Hill [1] ... Show more

Highlights

- Analyzing viral dark matter changes our understanding of the gut virome
- Gene-based clustering can address the challenges of high inter-individual variation
- Healthy human gut virome is dominated by a stable core of virulent bacteriophages
- In Crohn's disease, the virulent core is replaced with temperate bacteriophages

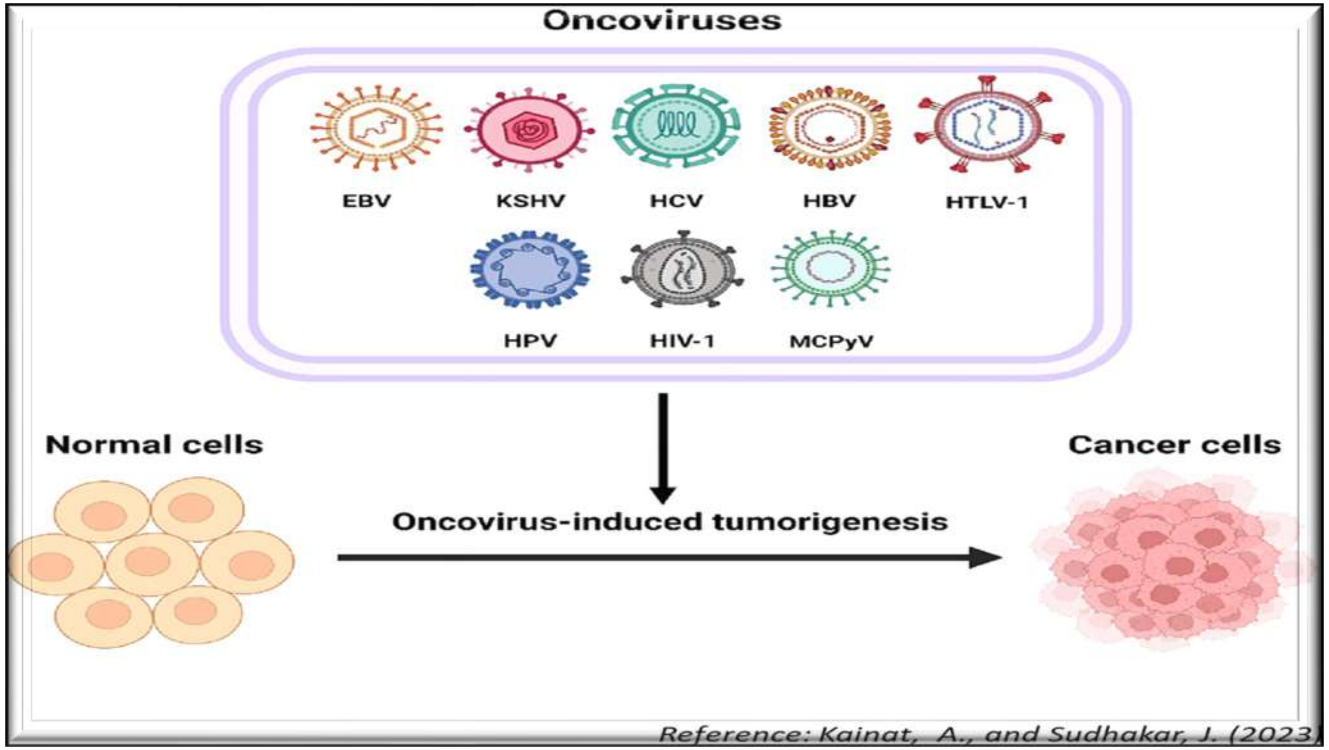






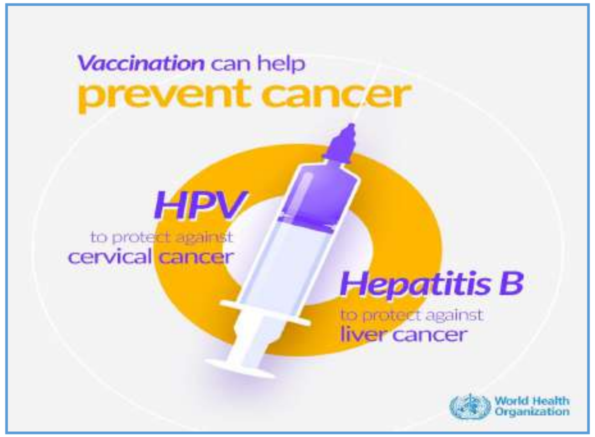
Crohn hastalığı olan bireylerde virulan core kaybı fajlarda litik replikasyon yönünde değişim.

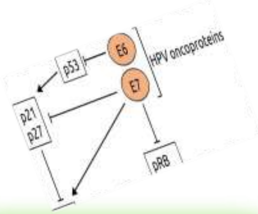
Onkovirüsler & Sessiz Tehdit

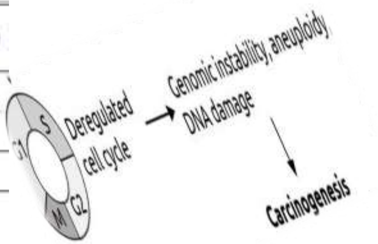


Reference: Kainat, A., and Sudhakar, J. (2023)

HPV, HIV ve *Hepatit B* ve *C*
Bazı Kanserle İlişkili Virüsler için Tarama Testleri





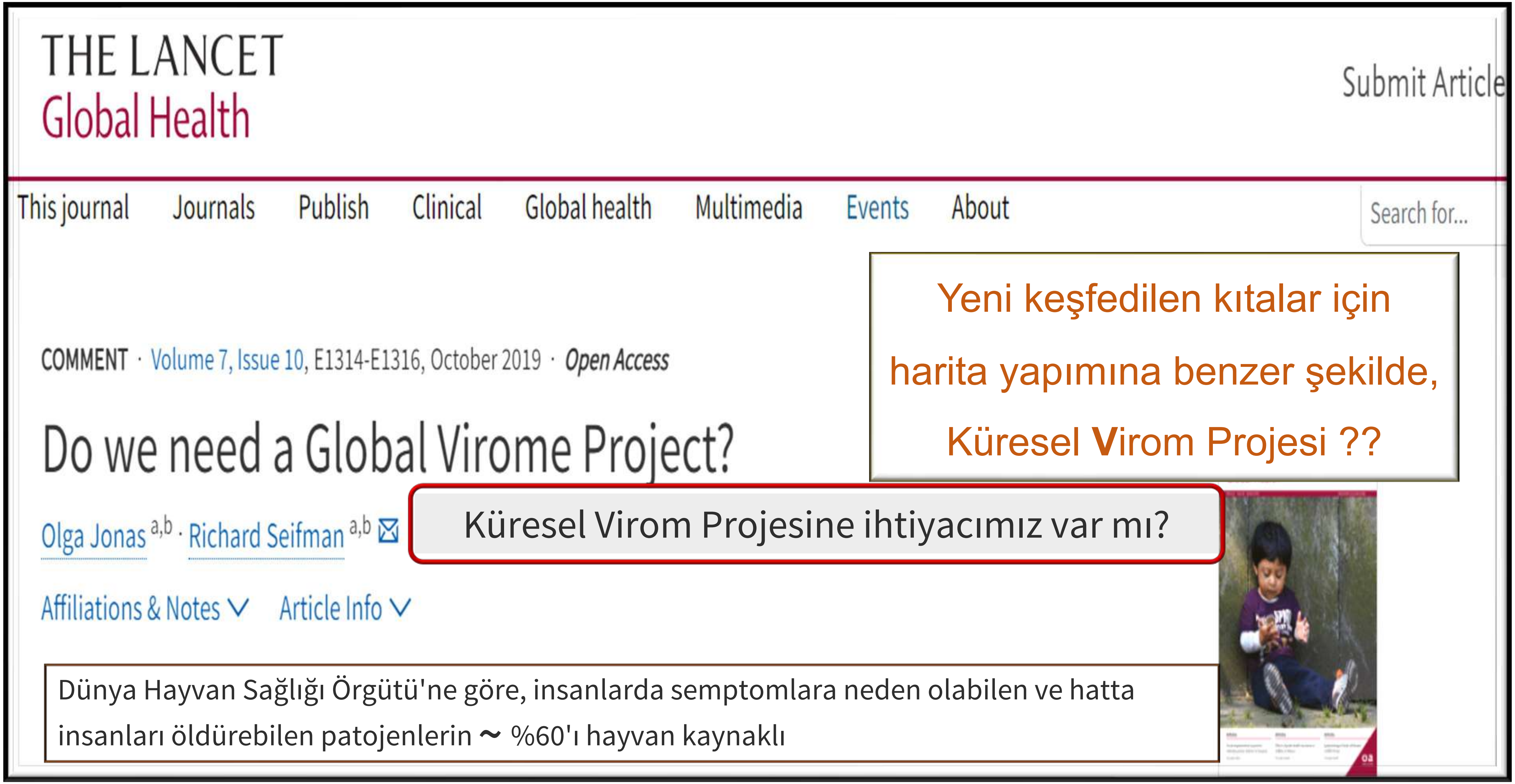


Virus Family	Virus	Cancer Type
Papillomaviridae	HPV-16	Anal
	HPV	Bladder
	HPV-16, -18	Cervical
	HPV-18	Colorectal
	HPV-16, -18, -26, -57	Esophageal
	HPV-16	Head and neck (SCC)
	HPV-6	Oral
	HPV-16	Prostate
	HPV-16, -18, -58	Renal
	HPV-5, -8	Skin and mucosal
	HPV-16	Vulvar
Polyomaviridae	BKV	Bladder
	BKV	Colorectal
	JCV	Colorectal
	MCV	Merkel cell carcinoma
Retroviridae	HIV	Anal
	HIV	Cervical
	HIV	Kaposi sarcoma
	HIV	Lymphoma (NHL)
	HTLV-1	Lymphoma (ATLL)
Herpesviridae	CMV (HHV5)	Colorectal
	EBV (HHV4)	Colorectal
	EBV (HHV4)	Esophageal
	EBV (HHV4)	Gastric
	EBV (HHV4)	Hepatic
	EBV (HHV4)	Lymphoma (Burkitt)
	EBV (HHV4)	Lymphoma (DLBCL)
	EBV (HHV4)	Lymphoma (PTCL)
	EBV (HHV4)	Oral
	EBV (HHV4)	Skin and mucosal
	HHV6	Lymphoma (DLBCL)
	HHV6	Malignant melanoma
	HHV7	Bladder
	HHV7	Lymphoma (CTCL)
	HHV7	Oral
	HSV (HHV1/2)	Oral
	KSHV (HHV8)	Kaposi sarcoma
Others	HBV	Bile duct
	HBV	Colorectal
	HBV	Hepatic
	HBV	Pancreatic
	HCV	Bile duct
	HCV	Hepatic
	TTV	Hepatic
	HBoV	Colorectal
	HBoV	Lung
	HBoV	Tonsillar
	Orthobunyaviruses	Colorectal
	Parvoviruses	Skin
	Anelloviruses	Mucosal
	Anelloviruses	Leukemias

Broecker F, Moelling K. The Roles of the Virome in Cancer. Microorganisms. 2021 Dec 8;9(12):2538.

- İnsanlarda bilinen çok sayıda virüs
- Bilinmeyen virüsler potansiyel zoonozların ~%99,9'u
- Genellikle insanlarda hastalığa neden olana kadar tespit edilemiyor

Carroll, D · Watson, B · Togami, E · et al.
Building a global atlas of zoonotic viruses *Bull World Health Organ.* 2018; **96**:292-294



THE LANCET
Global Health

COMMENT · Volume 7, Issue 10, E1314-E1316, October 2019 · *Open Access*

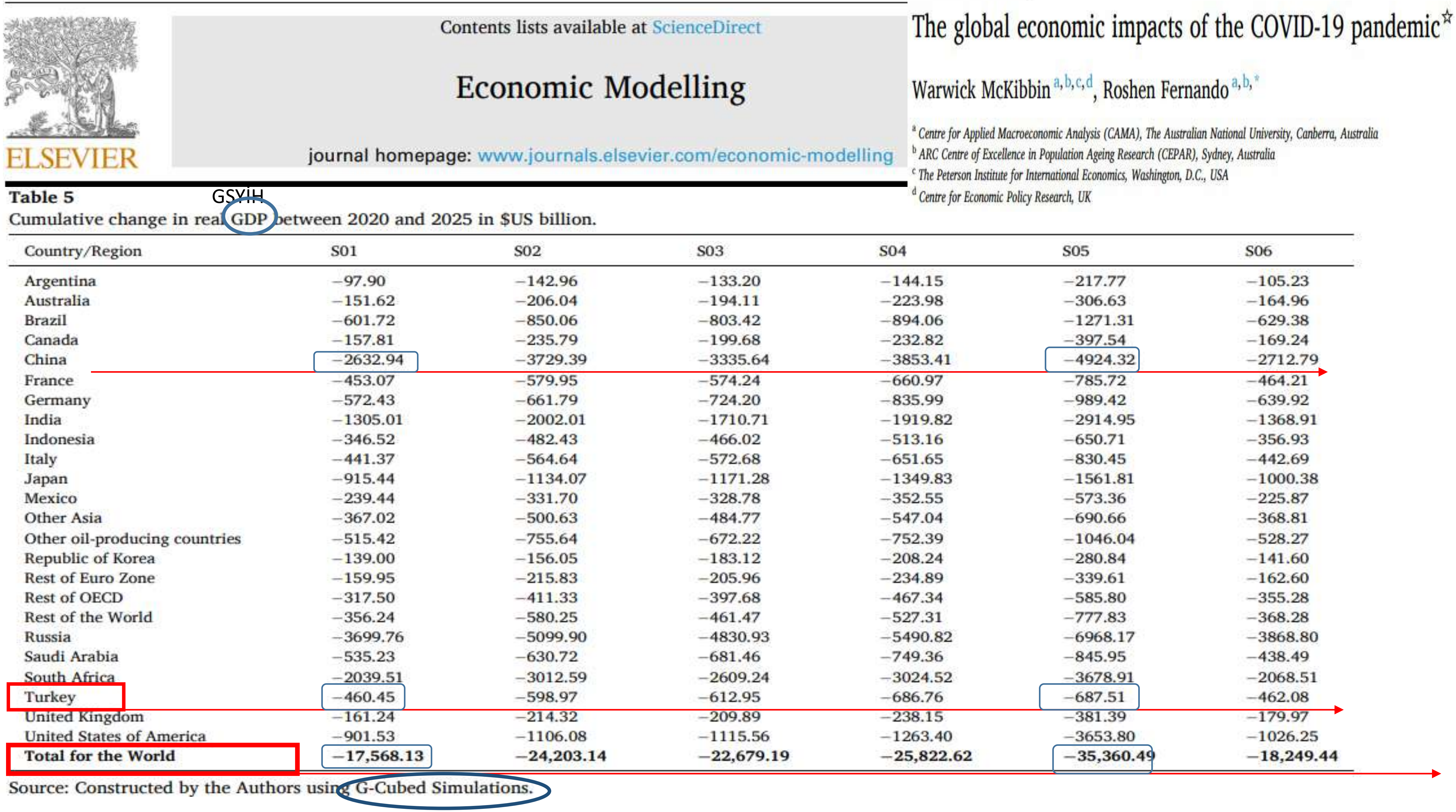
Do we need a Global Virome Project?

Olga Jonas [a,b] · Richard Seifman [a,b] ✉

Yeni keşfedilen kıtalar için
harita yapımına benzer şekilde,
Küresel **V**irom Projesi ??

Küresel Virom Projesine ihtiyacımız var mı?

Dünya Hayvan Sağlığı Örgütü'ne göre, insanlarda semptomlara neden olabilen ve hatta insanları öldürebilen patojenlerin ~ %60'ı hayvan kaynaklı



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Economic Modelling

journal homepage: www.journals.elsevier.com/economic-modelling

The global economic impacts of the COVID-19 pandemic☆

Warwick McKibbin[a,b,c,d], Roshen Fernando[a,b,*]

[a] Centre for Applied Macroeconomic Analysis (CAMA), The Australian National University, Canberra, Australia
[b] ARC Centre of Excellence in Population Ageing Research (CEPAR), Sydney, Australia
[c] The Peterson Institute for International Economics, Washington, D.C., USA
[d] Centre for Economic Policy Research, UK

Table 5

GSYİH

Cumulative change in real GDP between 2020 and 2025 in $US billion.

Country/Region	S01	S02	S03	S04	S05	S06
Argentina	−97.90	−142.96	−133.20	−144.15	−217.77	−105.23
Australia	−151.62	−206.04	−194.11	−223.98	−306.63	−164.96
Brazil	−601.72	−850.06	−803.42	−894.06	−1271.31	−629.38
Canada	−157.81	−235.79	−199.68	−232.82	−397.54	−169.24
China	−2632.94	−3729.39	−3335.64	−3853.41	−4924.32	−2712.79
France	−453.07	−579.95	−574.24	−660.97	−785.72	−464.21
Germany	−572.43	−661.79	−724.20	−835.99	−989.42	−639.92
India	−1305.01	−2002.01	−1710.71	−1919.82	−2914.95	−1368.91
Indonesia	−346.52	−482.43	−466.02	−513.16	−650.71	−356.93
Italy	−441.37	−564.64	−572.68	−651.65	−830.45	−442.69
Japan	−915.44	−1134.07	−1171.28	−1349.83	−1561.81	−1000.38
Mexico	−239.44	−331.70	−328.78	−352.55	−573.36	−225.87
Other Asia	−367.02	−500.63	−484.77	−547.04	−690.66	−368.81
Other oil-producing countries	−515.42	−755.64	−672.22	−752.39	−1046.04	−528.27
Republic of Korea	−139.00	−156.05	−183.12	−208.24	−280.84	−141.60
Rest of Euro Zone	−159.95	−215.83	−205.96	−234.89	−339.61	−162.60
Rest of OECD	−317.50	−411.33	−397.68	−467.34	−585.80	−355.28
Rest of the World	−356.24	−580.25	−461.47	−527.31	−777.83	−368.28
Russia	−3699.76	−5099.90	−4830.93	−5490.82	−6968.17	−3868.80
Saudi Arabia	−535.23	−630.72	−681.46	−749.36	−845.95	−438.49
South Africa	−2039.51	−3012.59	−2609.24	−3024.52	−3678.91	−2068.51
Turkey	−460.45	−598.97	−612.95	−686.76	−687.51	−462.08
United Kingdom	−161.24	−214.32	−209.89	−238.15	−381.39	−179.97
United States of America	−901.53	−1106.08	−1115.56	−1263.40	−3653.80	−1026.25
Total for the World	**−17,568.13**	**−24,203.14**	**−22,679.19**	**−25,822.62**	**−35,360.49**	**−18,249.44**

Source: Constructed by the Authors using G-Cubed Simulations.

Bull World Health Organ. 2018 Apr 1; 96(4): 292–294.
Published online 2018 Mar 5. doi: 10.2471/BLT.17.205005

PMCID: PMC5872013
PMID: 29695886

Building a global atlas of zoonotic viruses

Dennis Carroll,[a] Brooke Watson,[b] Eri Togami,[c] Peter Daszak,[b] Jonna AK Mazet,[c] Cara J Chrisman,[a] Edward M Rubin,[d] Nathan Wolfe,[d] Carlos M Morel,[e] George F Gao,[f] Gian Luca Burci,[g] Keiji Fukuda,[h] Prasert Auewarakul,[j] and Oyewale Tomori[k]

▸ Author information ▸ Article notes ▸ Copyright and License information PMC Disclaimer

At the Prince Mahidol Awards Conference on 30 January 2018 in Bangkok, Thailand, policy- and decision-makers, experts, researchers, donors and private sector representatives from across the globe came together to introduce and explore the dynamics of the Global Virome Project. The project is an innovative 10-year proposed partnership to develop a global atlas of most of the planet's naturally occurring potentially zoonotic viruses. The project aims to transform the study of emerging diseases by building an unprecedented database of viruses in their ecological contexts.

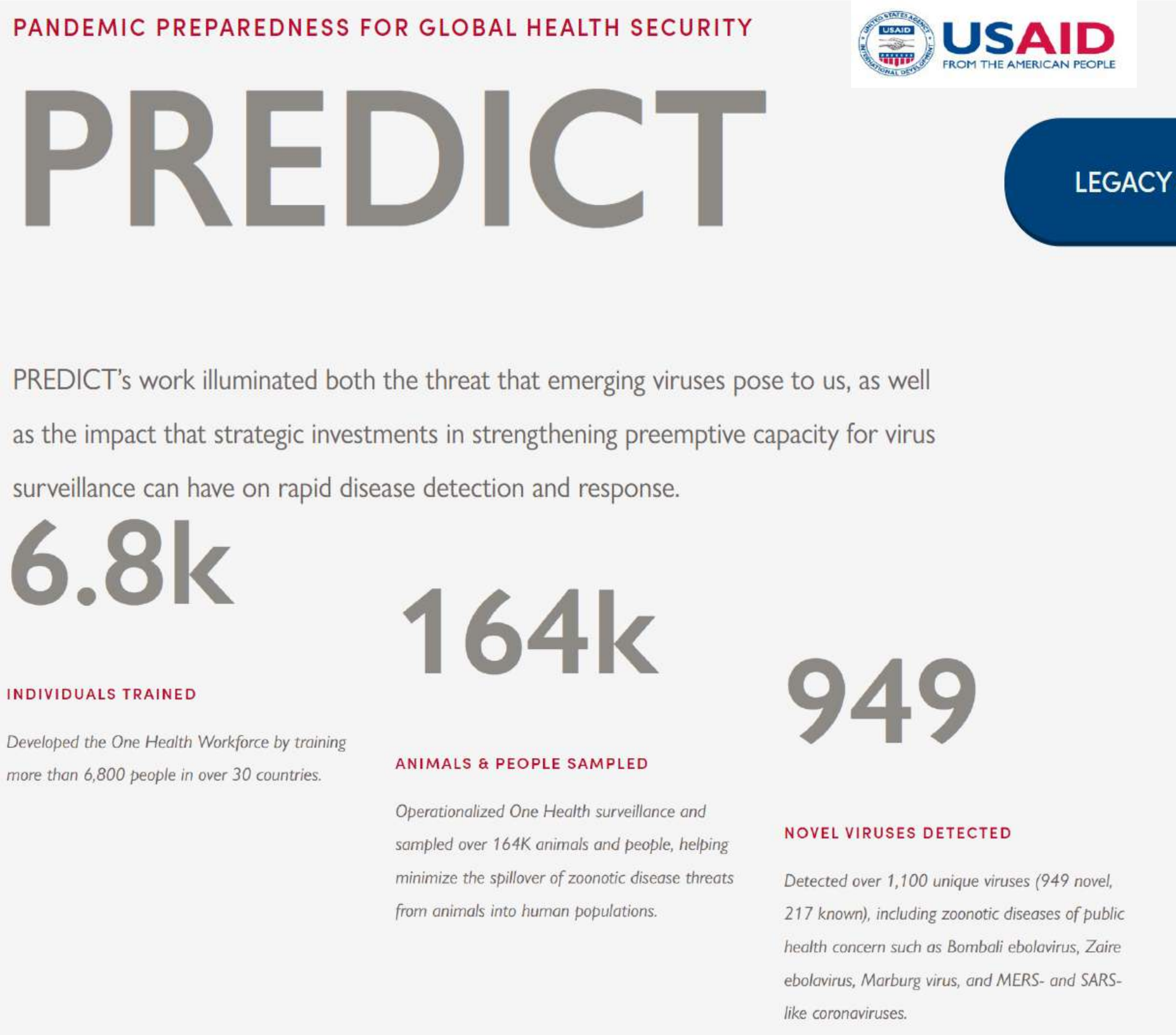
Küresel **V**irom **P**rojesi

potansiyel zoonotik virüslerinin çoğunun küresel bir atlasını geliştirmek için önerilen 10 yıllık

Çin (Hastalık Kontrol ve Önleme Merkezi) Küresel Virom Projesi için maliyet tahminleri, 10 yıllık bir süre için 1,2-3,4 milyar $

Küresel kayıplar 2020'de 283 milyar-1,9 trilyon $

~ %0,2 den daha az



PANDEMIC PREPAREDNESS FOR GLOBAL HEALTH SECURITY

PREDICT

PREDICT's work illuminated both the threat that emerging viruses pose to us, as well as the impact that strategic investments in strengthening preemptive capacity for virus surveillance can have on rapid disease detection and response.

6.8k

INDIVIDUALS TRAINED

Developed the One Health Workforce by training more than 6,800 people in over 30 countries.

164k

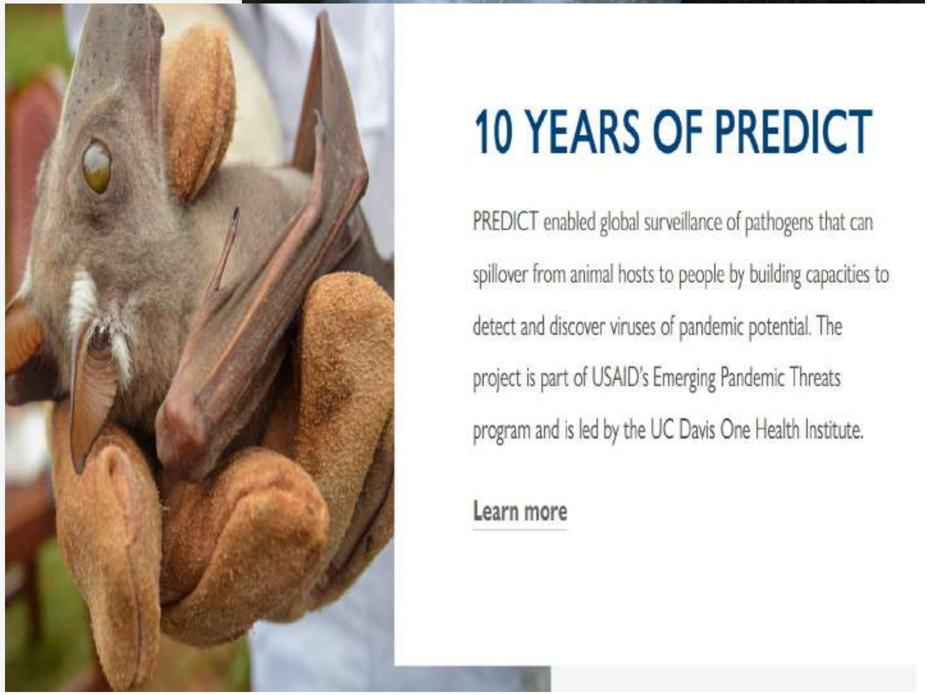
ANIMALS & PEOPLE SAMPLED

Operationalized One Health surveillance and sampled over 164K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.

949

NOVEL VIRUSES DETECTED

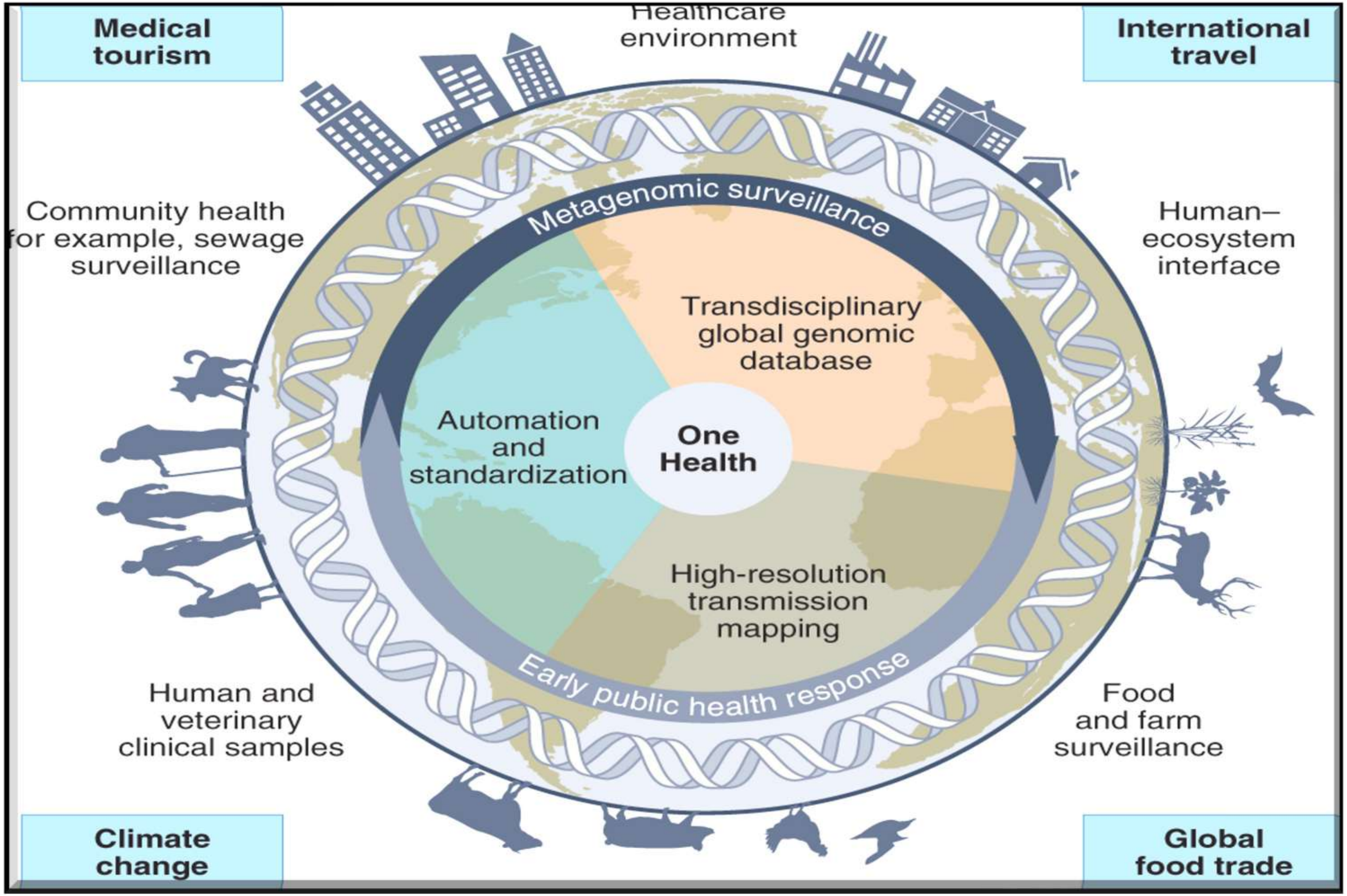
Detected over 1,100 unique viruses (949 novel, 217 known), including zoonotic diseases of public health concern such as Bombali ebolavirus, Zaire ebolavirus, Marburg virus, and MERS- and SARS-like coronaviruses.



10 YEARS OF PREDICT

PREDICT enabled global surveillance of pathogens that can spillover from animal hosts to people by building capacities to detect and discover viruses of pandemic potential. The project is part of USAID's Emerging Pandemic Threats program and is led by the UC Davis One Health Institute.

- **V**iral diziler,
- Coğrafi aralıklar ve
- Konak dağılımları hakkındaki bilgi tabanını genişletmek, insanlığın zorlu mikrobiyal düşmanı hakkında bilgiler edinmek



Tüm ülkelerin aktif katılımı

Özellikle en yoksul ülkelerde kamu sağlığına ve kalkınmaya daha fazla yatırım

Hastalık birçok ülkeye yayılıp küresel bir pandemi başladığında sınırların kapatılması çok geç olabilir

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Gelecekte

İnsan Virobiyomunun

bilinmeyen yönlerini, potansiyel tehdit oluşturabilecek virüsleri ve olası salgınlara karşı proaktif yaklaşımları yeni bilgiler ile analiz ederek daha iyi anlayabileceğiz.

TEŞEKKÜRLER…

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- virüsler evrimin atölyesi

- Virom, mikrobiyomu düzenleyebilir ve bakteri karmaşıklığını etkileyebilir,'kazananı öldür' ekolojik modeli
- Bu modelde, en bol bulunan bakteriler fajları tarafından öldürülür, diğer bakteri taksonları ekolojik nişi ele geçirir ve daha sonra fajları tarafından öldürülür
- ancak gözlemlenen farklılıklar, disbiyozu tersine çevirmeyi amaçlayan hedefli mikrobiyota manipülasyonları