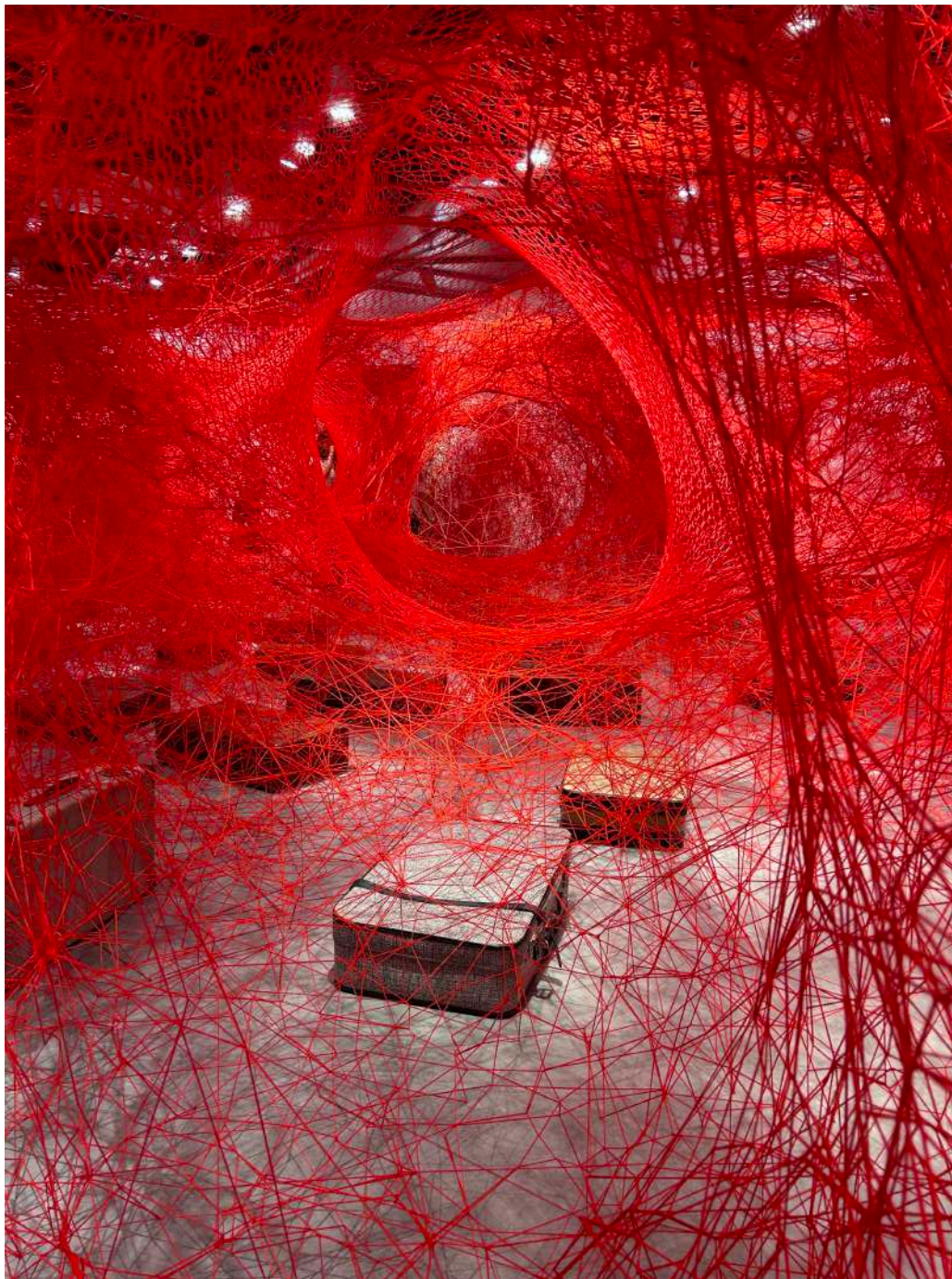


# Viral Evrimin Sonuçları

Ahmet Çağkan İnkaya  
Hacettepe Üniversitesi Tıp Fakültesi  
Enfeksiyon Hastalıkları Anabilim Dalı  
inkaya@hacettepe.edu.tr



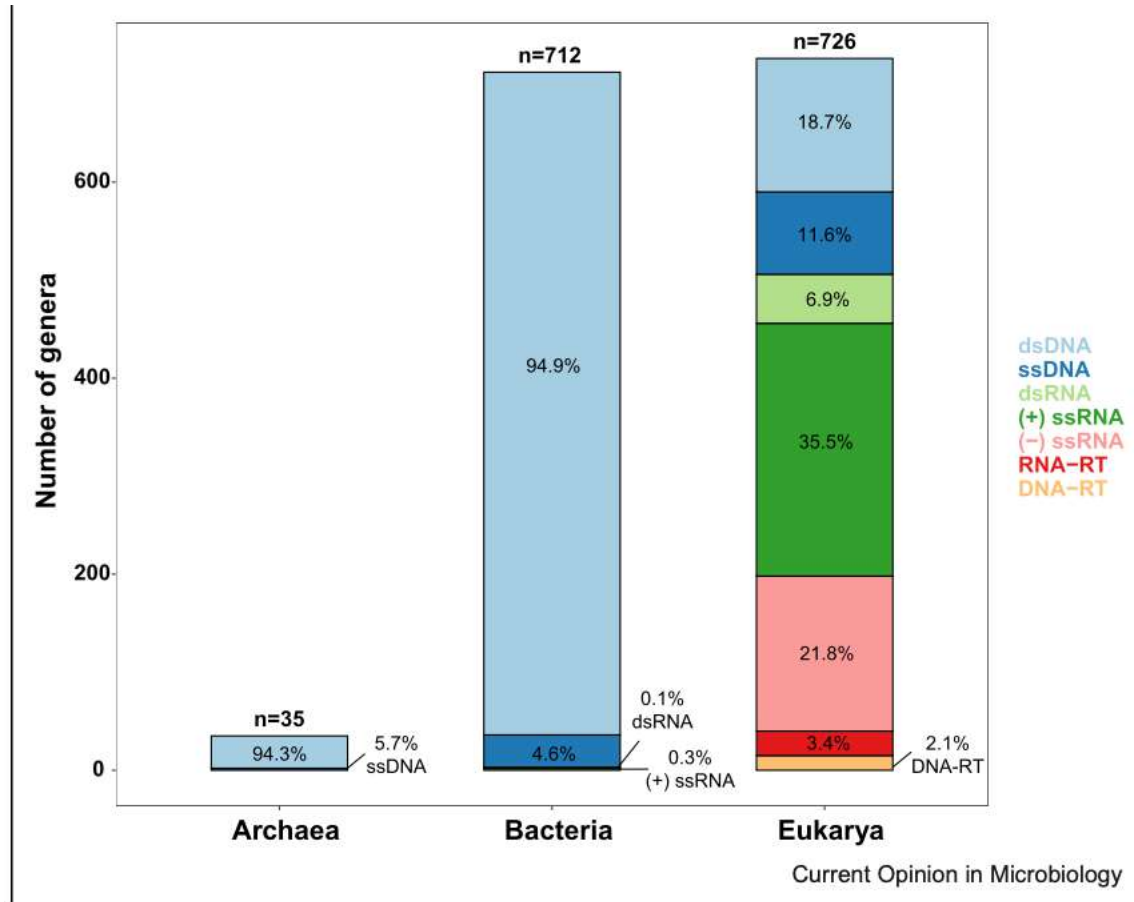


**Dünyalar Arasında**

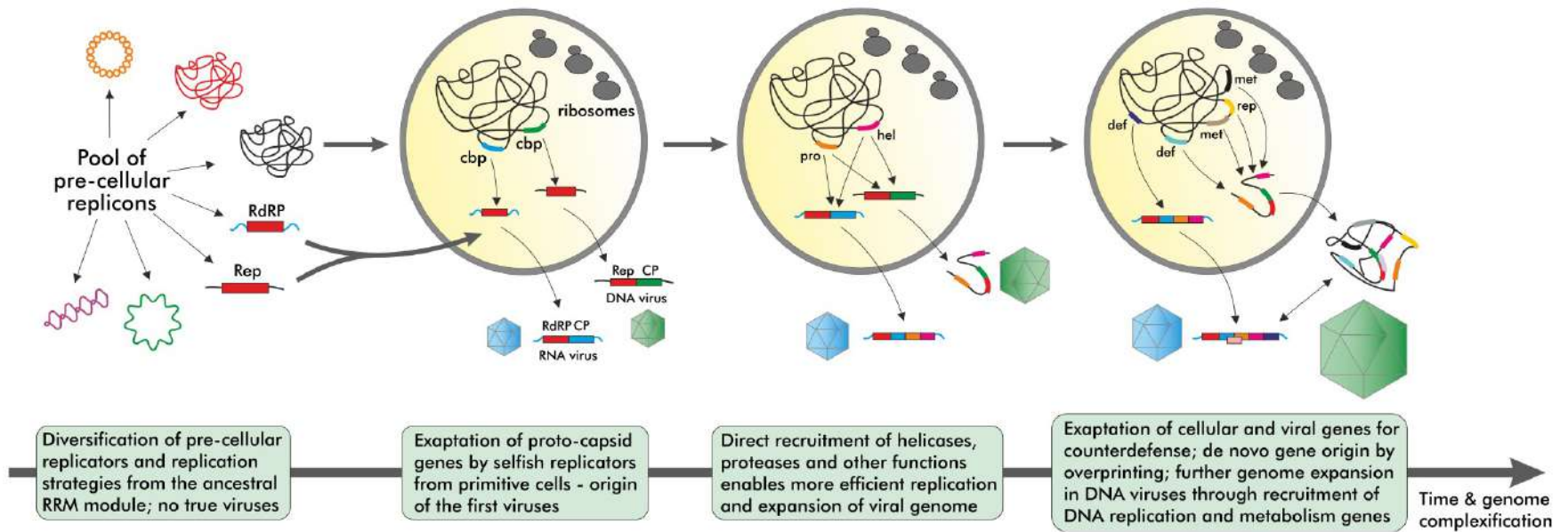
**Chiharu Shiota**

**İstanbul Modern**

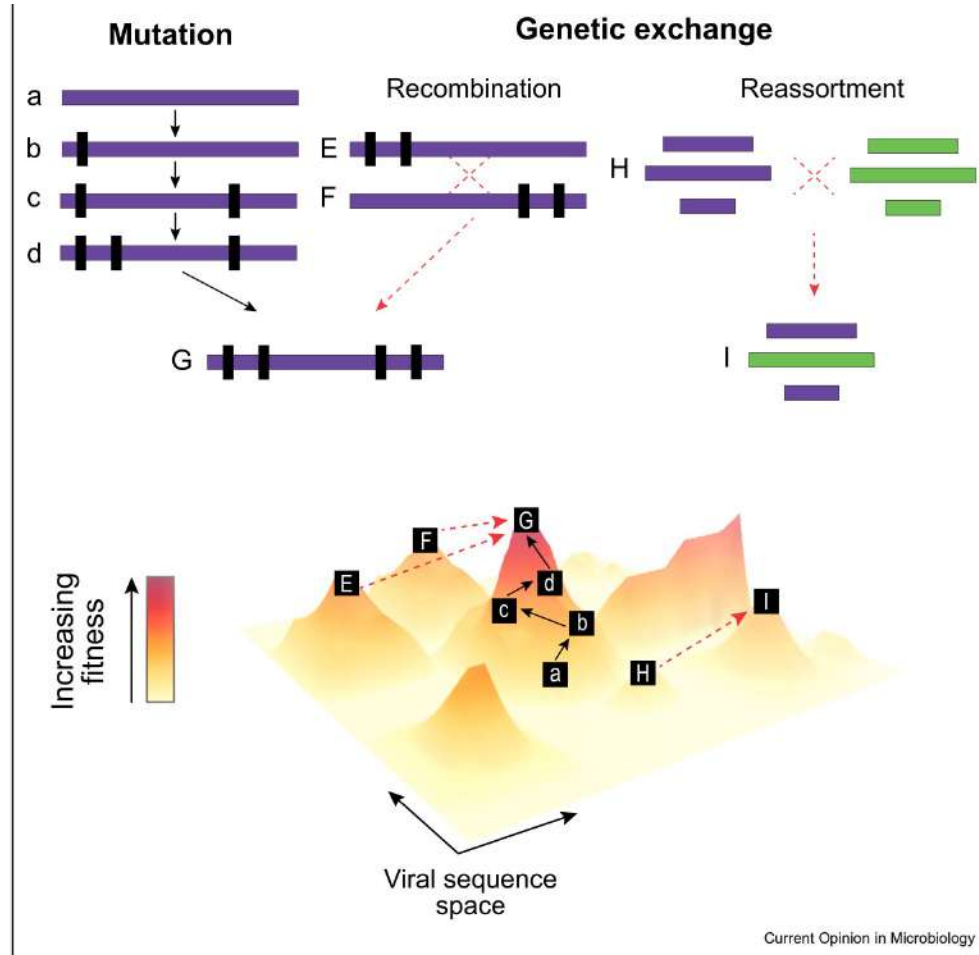
# Viral Genlerin Kökenleri



# Virüsler Gereken Bilgiyi Nasıl Depoladı?



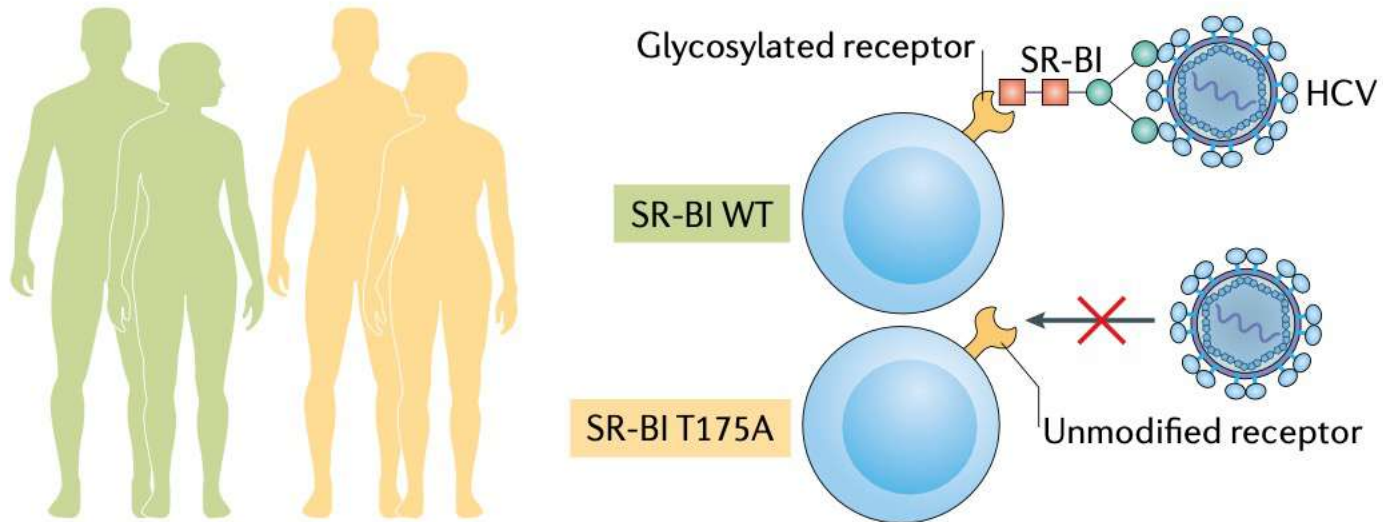
# Evrin Temel Mekanizmalar



İmmun kaçış:  
İnfluenza → 1  
Kızamık → 8

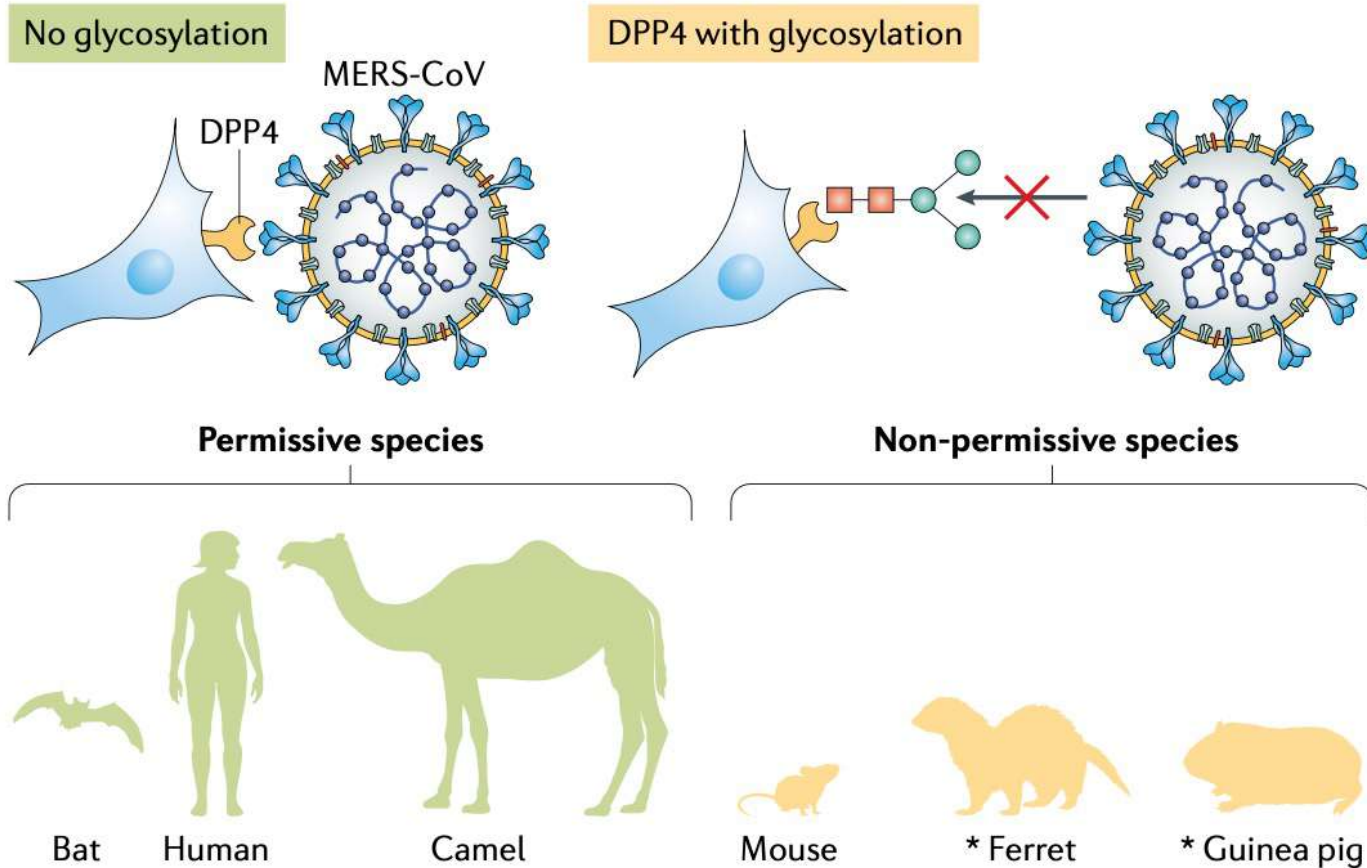
# Sadece Sekans Değil I

## a Host-level determinants: HCV example



# Sadece Sekans Değil II

## b Species-level determinants: MERS-CoV example



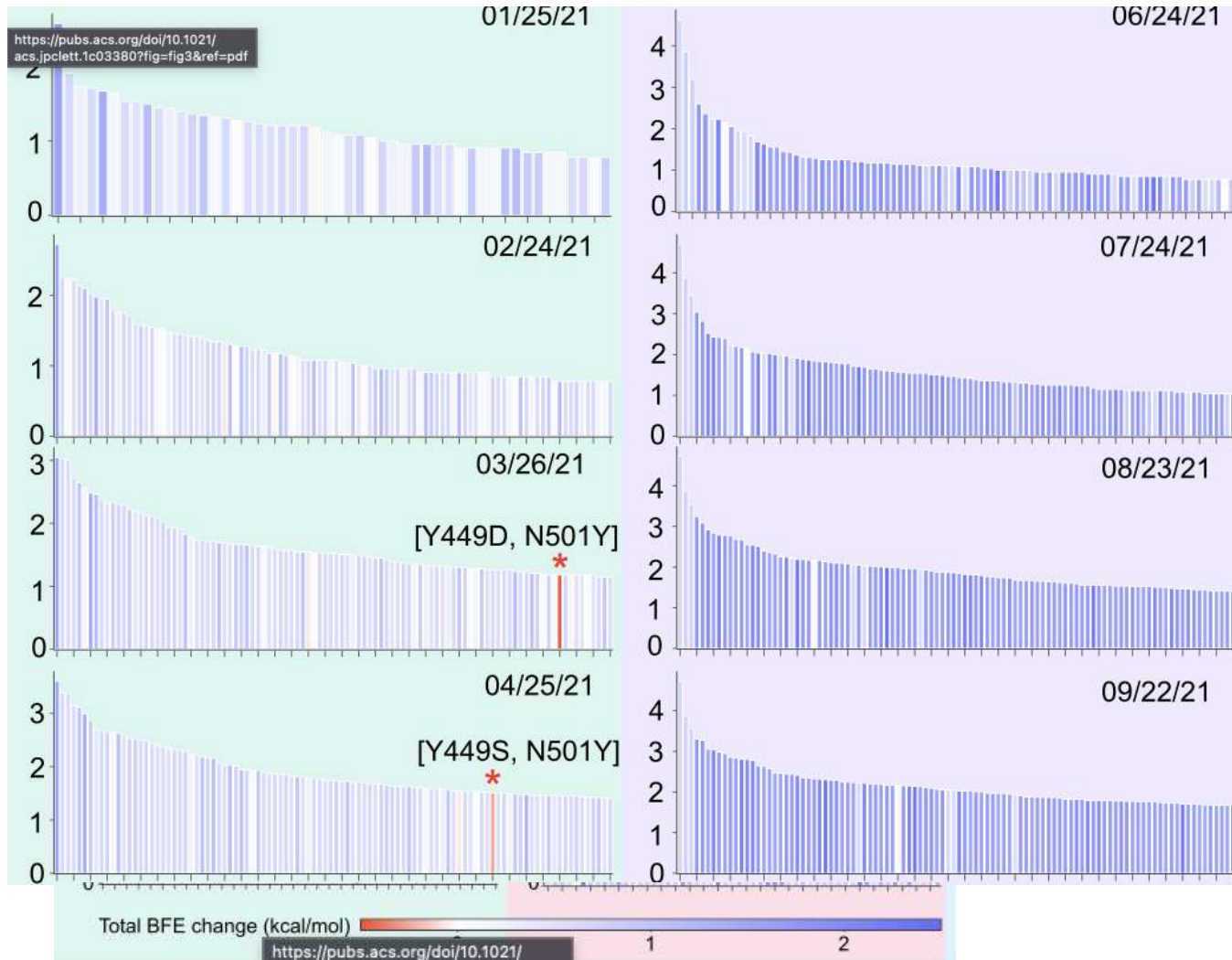
# Yeni Yöntemler Gerek

Step of replication cycle	Technology	Application	Refs
Entry	Glycan microarray	Receptor specificity and avidity	30
Replication	Single-cell RNA sequencing	Cell-to-cell replication variability	6–17
	Single-cell RNA labelling		59
	Rare sequence detection and single-virion genomics		136,137
Assembly	Cryo-electron tomography	Pleomorphic virion morphology	19–21
	Small-molecule labelling		86
	Live cell tracking	Intracellular particle tracking	18
Egress	Air–liquid interface cultures of the human epithelium	Cell-type specific entry or egress mechanisms	3–5



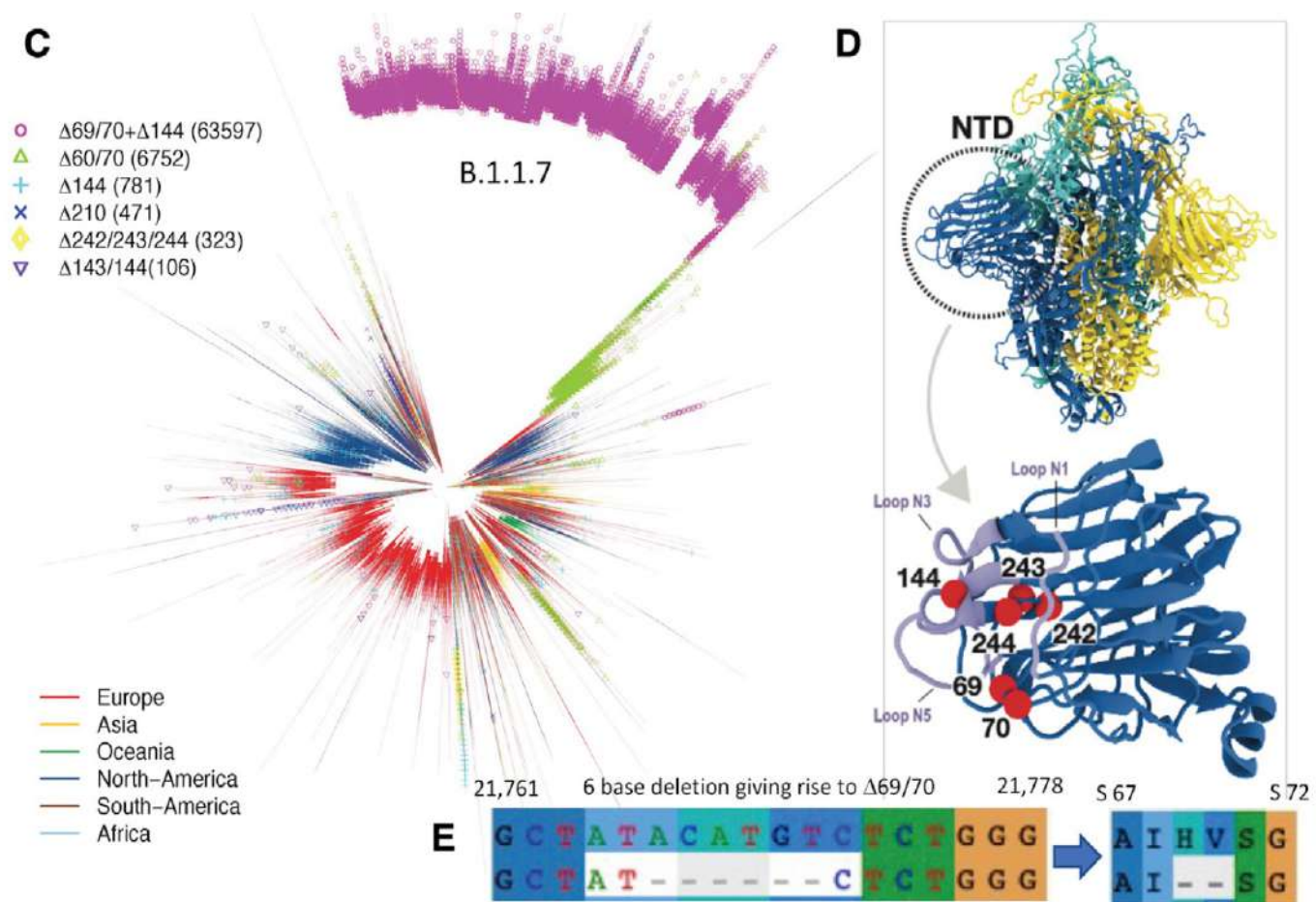


# SARSCoV2 ve Mutasyonları II



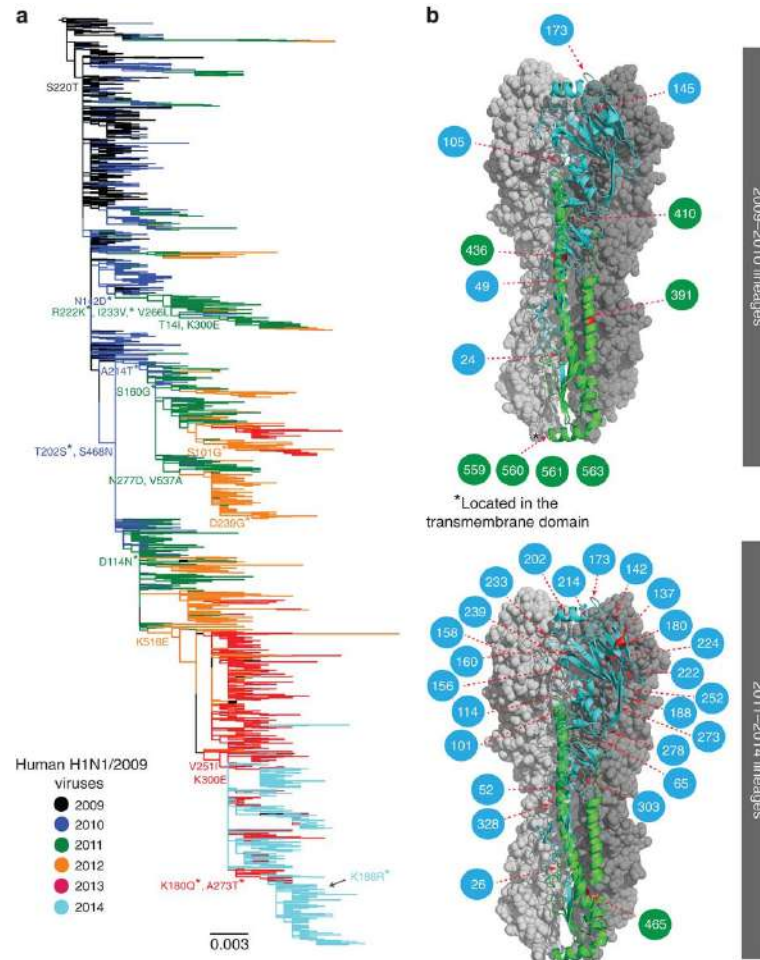
Wang R et al 2021 Mechanisms of SARS-CoV-2 Evolution Revealing Vaccine-Resistant Mutations in Europe and America J Phys Chem Lett

# SARSCoV2 Evrim: $\Delta$ H69/V70



Fischer W et al 2021 *HIV-1 and SARS-CoV-2: Patterns in the evolution of two pandemic pathogens* Cell Host Microbe

# Influenza A H1N1pdm09 Evrim 2009-2014



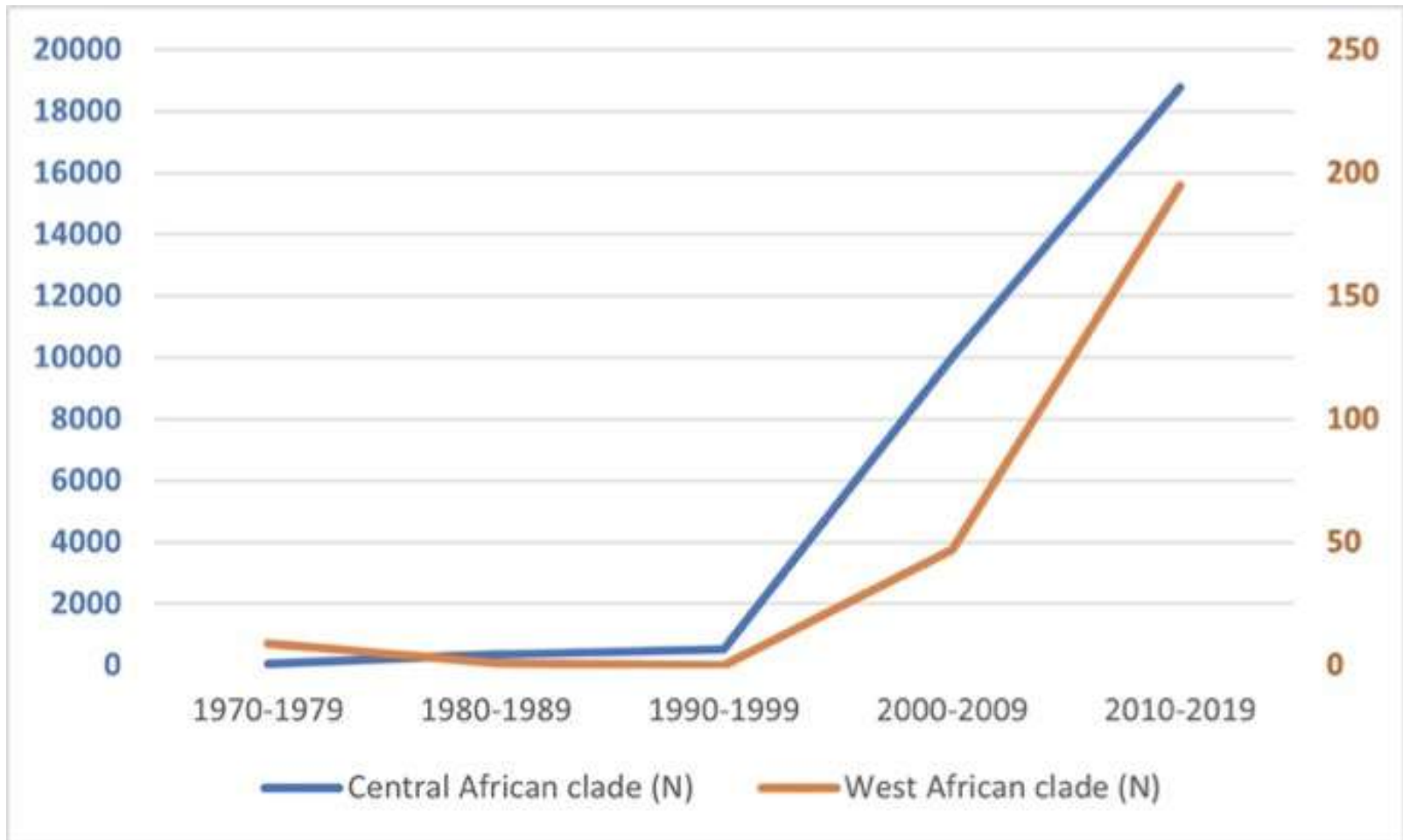
Su Y et al 2015 *Phylogenetics of H1N1/2009 influenza reveals the transition from host adaptation to immune-driven selection* Nat Commun



# Mpox: Hikayesi

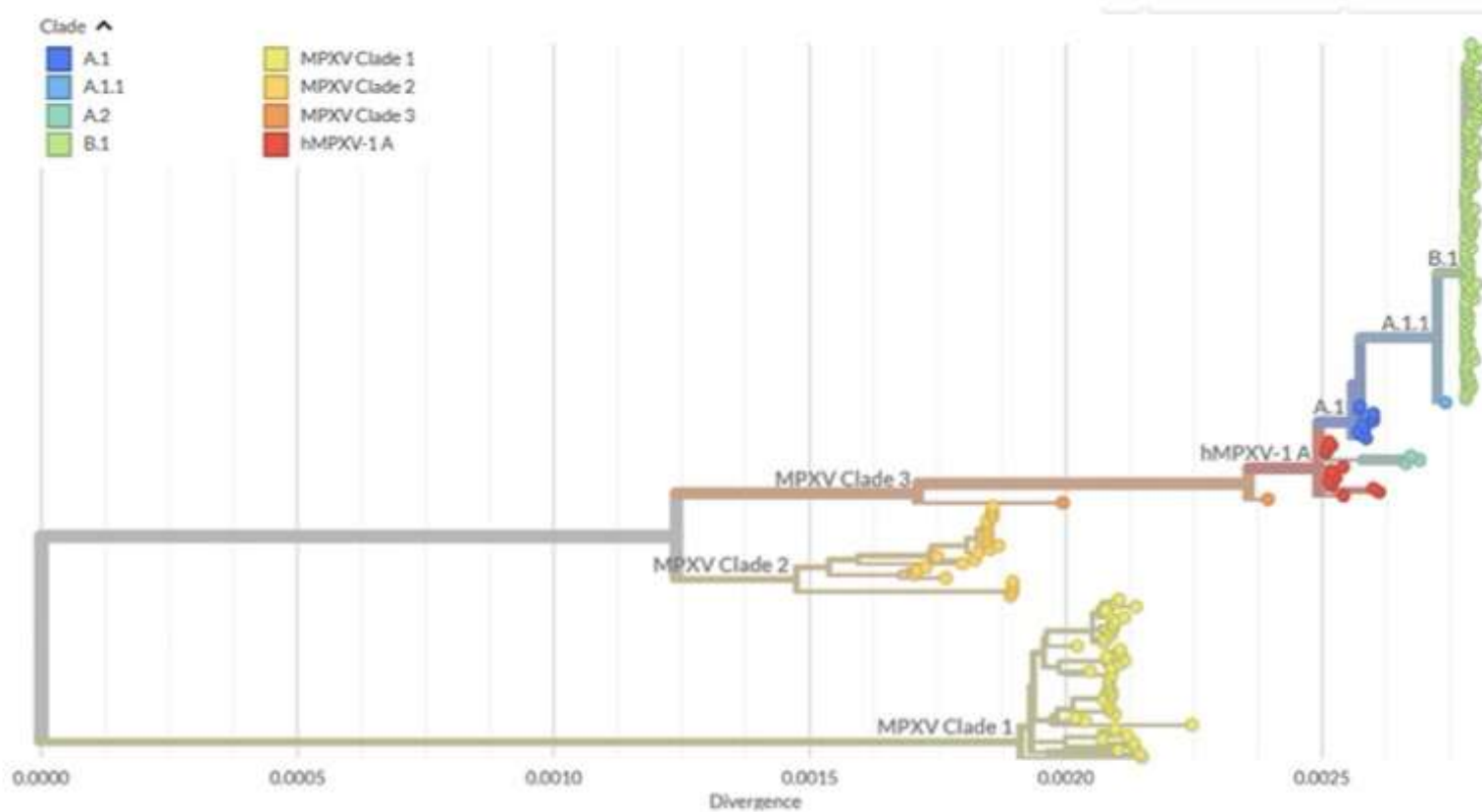
- Yakın temas
  - Isırık
  - Bush-meat
  - Kontamine yüzey
  - Cinsel uygulamalar
- Vücut sıvıları
  - Cinsellik dahil
- Damlacık
- Perkütan
- Plasental
- **Aerosolizasyon?**

# Göz Göre Göre



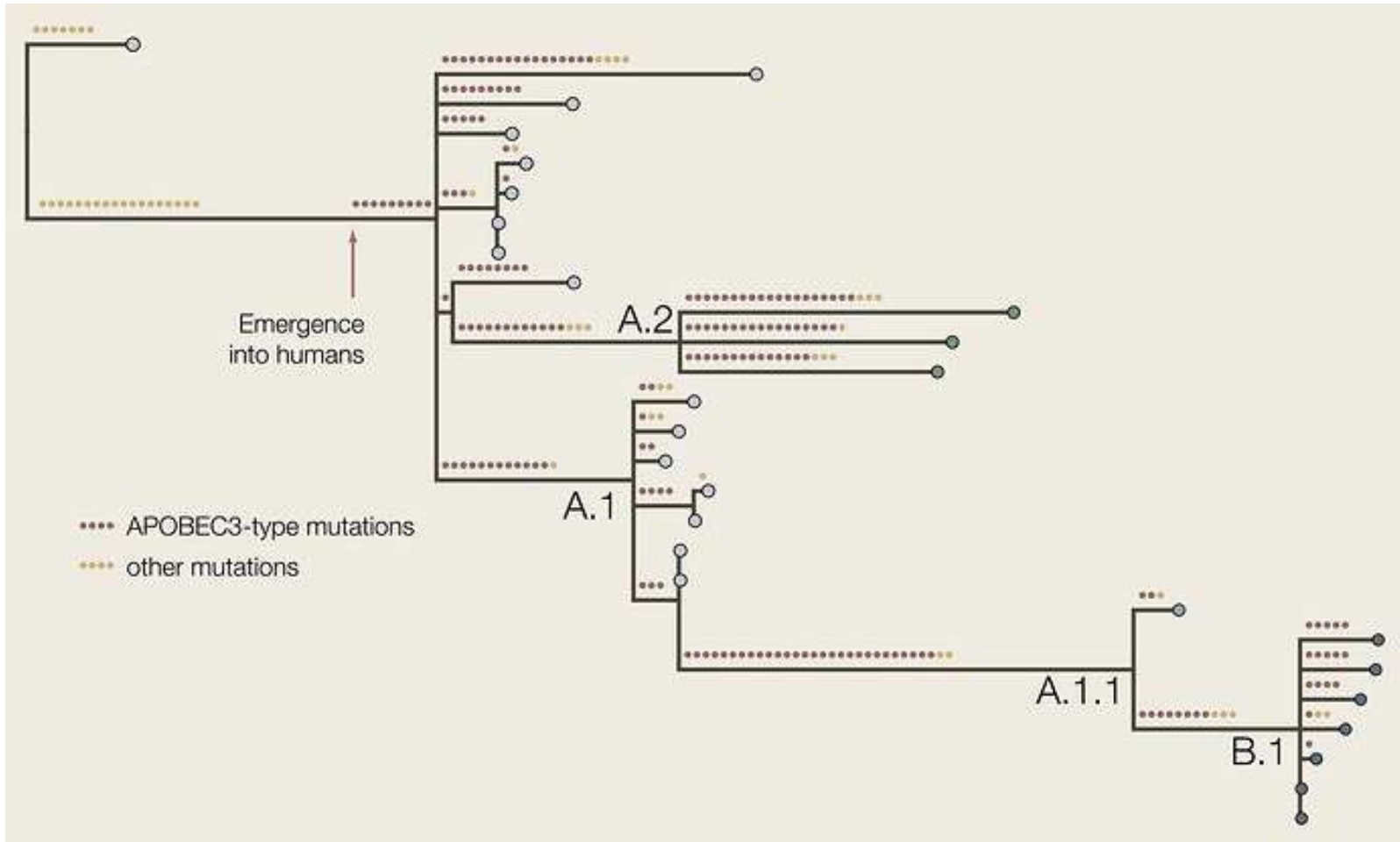
Bunge EM et al 2022 *The changing epidemiology of human monkeypox—A potential threat? A systematic review* PLoS Negl Trop Dis

# Mpox Evrim





# Peki Ne Oldu da İnsan Hastalığı Oldu?



[https://virological.org/t/an-apobec3-molecular-clock-to-estimate-the-date-of-emergence-of-hmpxv/885#post\\_1](https://virological.org/t/an-apobec3-molecular-clock-to-estimate-the-date-of-emergence-of-hmpxv/885#post_1)

# Mpox: *Low complexity regions (LCR)*

	MPXV-M5312_HM12_Rivers	MPXV_USA_2022_MA001	353R
Genome length	197,209	197,205	198,547
SNPs <sup>a</sup>	NA	67	69
Indels <sup>a</sup>	NA	10del 7ins	11del 6 ins
Homopolymeric sites <sup>b</sup>	408	405	399
Unique SNPs	NA	0	2
LCR pair 1/4	8	8	<b>16</b>
LCR2	22	24	<b>25</b>
LCR3	18	16	<b>52</b>
LCR5	25	28	<b>24</b>
LCR6	<b>2</b>	1	1
LCR7	<b>19</b>	17.6	17.6
LCR8	10	10	10
LCR9	<b>8</b>	6	6
LCR pair 10/11	17	14	<b>13</b>
LCR12	9	9	9
LCR13	9	9	9
LCR14	9	9	9
LCR15	7	7	7
LCR16	9	9	9
LCR17	6.1	6.1	6.1
LCR18	3.5	3.5	3.5
LCR19	9.3	9.3	9.3
LCR20	9	9	9
LCR21	4.5	4.5	4.5

Monzón S et al 2024 *Monkeypox virus genomic accordion strategies* Nat Commun



# Apo abi imzayı attıysa 😊

Annals of Internal Medicine

ORIGINAL RESEARCH

## A Possible Sterilizing Cure of HIV-1 Infection Without Stem Cell Transplantation

Gabriela Turk, PhD\*; Kyra Seiger, BSc\*; Xiaodong Lian, PhD; Weiwei Sun, PhD; Elizabeth M. Parsons, BSc; Ce Gao, PhD; Yelizaveta Rassadkina, BSc; Maria Laura Polo, PhD; Alejandro Czernikier, MSc; Yanina Ghiglione, PhD; Alejandra Vellicce, MD; Joseph Varriale, MSc; Jun Lai, MSc; Yuko Yuki, DDM; Maureen Martin, MD; Ajantha Rhodes, BSc; Sharon R. Lewin, PhD; Bruce D. Walker, MD; Mary Carrington, PhD; Robert Siliciano, MD; Janet Siliciano, PhD; Mathias Lichterfeld, MD, PhD†; Natalia Laufer, MD, PhD†; and Xu G. Yu, MD, MSc†

**Table.** HIV-1 Reservoir Profiling Assays Performed on Cells From the Esperanza Patient

Assay	Cells, <i>n</i>	Cell Type	Intact Proviruses, <i>n</i>	Defective Proviruses, <i>n</i>	Replication-Competent Proviruses, <i>n</i>
Near-full-length individual proviral sequencing assay	1.188 billion	Peripheral blood mononuclear cells	0	7	-
Near-full-length individual proviral sequencing assay	503 million	Isolated mononuclear cells from placenta	0	0	-
Viral outgrowth assay	150 million	Resting CD4 <sup>+</sup> T cells	-	-	0

# Antik Mücadeleler I

## HERV-K(HML-2) genome



## HERV-L genome



## HERV-W genome



Figure 2. The structures of HERV-K (HML-2), HERV-L and HERV-W. As seen in the illustration, the location of the same protein coding sequence may be in different locations in different HERV genomes, and may be absent in other HERVs. In this example, while dUTPase is located in the *pol* sequence of HML-2; it is located closer to the 3' end of the HERV-L genome, after the *pol* sequence. The sequence coding dUTPase is absent in the HERV-W genome.

# Antik Mücadele II

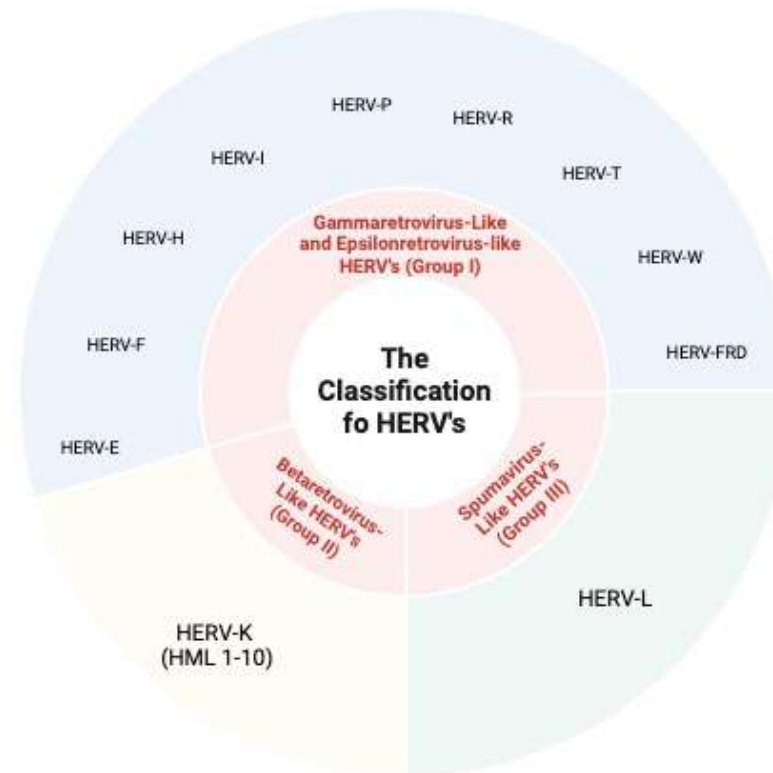


Figure 3. HERV's are classified according to their similarity to their exogenous counterparts. While HERV-K has structural similarity to Betaretroviruses; HERV-L resemble Spumaviruses. A majority of HERV's are structurally similar to Gammaretroviruses and Epsilonretroviruses.

# Antik Mücadele III

## Some examples of HERVs in diseases

HERV types	Protein	Disease	Role	Mechanism	Reference
HERV-K HML-2	env	Breast cancer	Proliferation, metastasis, progression	ERK 1/2 MAPK activation, EMT induction in normal cells	[47]
HERV-H	env	Fibrosarcoma, melanoma	Proliferation of cancers	Evading the immune system, immunosuppression	[61]
HERV-W	env	Multiple Sclerosis	Causing inflammation	TLR-4 and iNOS activation	[64]
HERV-W	syncytin-1	Mycosis Fungoides	Intercellular signalling	Formation of extracellular vesicles	[97]
HERV-K	dUTPase	Pulmonary Hypertension	Pathogenesis	Apoptosis of endothelial cells, mesenchymal transformation	[79]
HERV-K HML-2	dUTPase	Psoriasis	Pathogenesis	TLR-2 activation, Th cell differentiation	[78]

Figure 4. Examples of some well-known HERVs in various diseases together with the mechanisms.