

# Pandemi Potansiyeli Olan Virusların Taranması ve Saptanması

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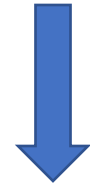
# Pandeminin Önlenmesi

## Primer Önleme

Hayvandan insana geçişin önlenmesi



Hayvanlar arasında dolaşan virüsler ???  
Hangisi insana en yakın ???



Var olup olmadığını bilmediğimiz virüs için nereye, nasıl bakacağız???

## Sekonder Önleme

Hastalık surveyansı

Hastalığın yayılmasının engellenmesi

## «Spill over» Hayvandan İnsana Geçiř

Yeni infeksiyonların %70'i zoonotik

>250 zoonotik virüs hayvandan insana geçerek insanlarda hastalık yapmıştır !

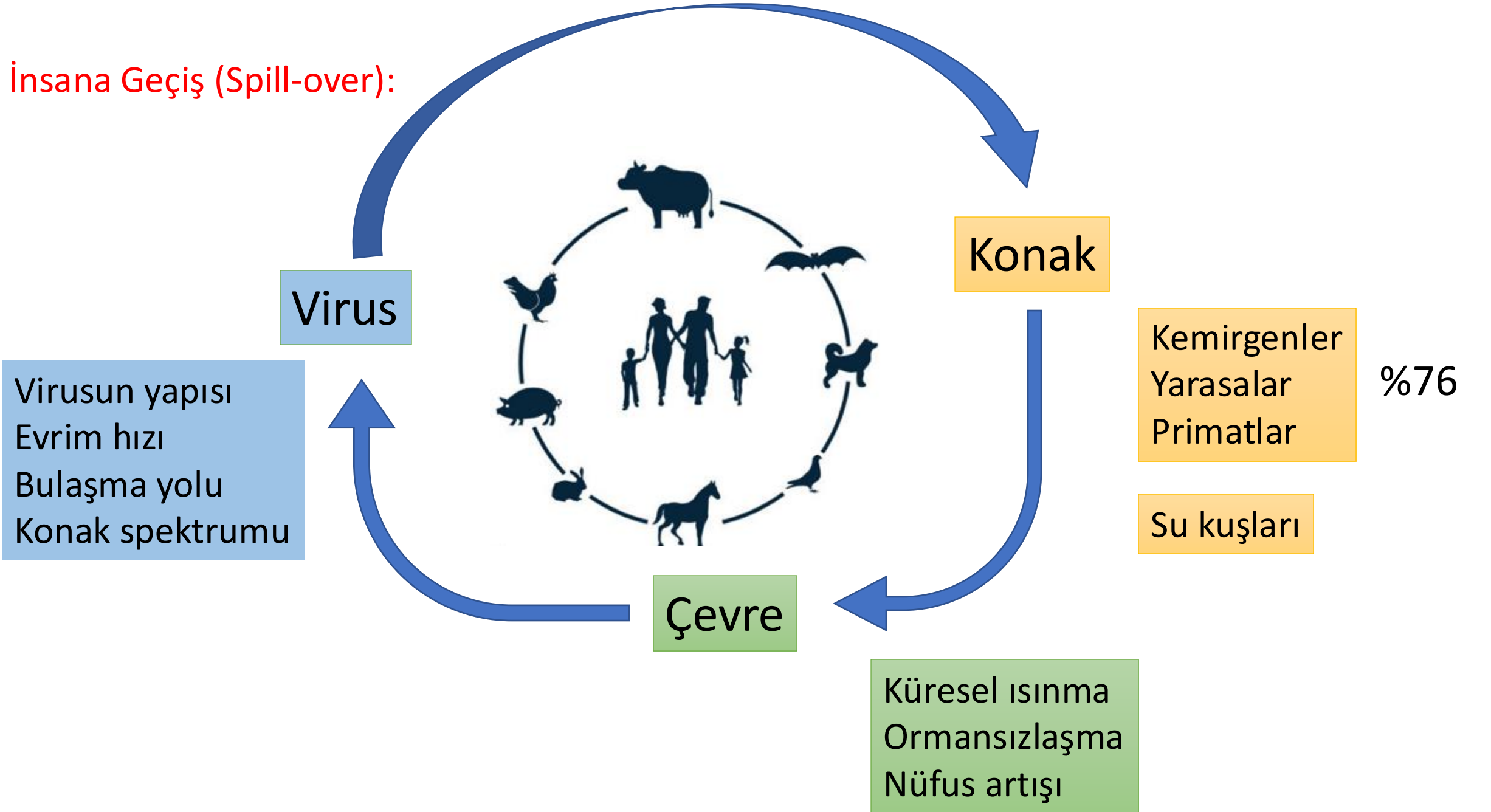


Memeli ve kuřlarda ~1.67 milyon virüs var  
~yarısı hayvandan insana geçebilir

*Mollentze N. Proc. Natl. Acad. Sci. U.S.A. 117, 9423–9430 (2020).*

*D. Carroll et al., The global virome project. Science 359, 872–874 (2018).*

## İnsana Geçiş (Spill-over):



# How many species of mammals are there?

Connor J Burgin, Jocelyn P Colella, Philip L Kahn, Nathan S Upham ✉

*Journal of Mammalogy*; 2018;99:1-14

Taxa	MSW1	MSW2	MSW3	IUCN	MDD
	1982	1993	2005	2017	This study
Species					
<i>Total</i>	4,170	4,631 <sup>a</sup>	5,416	5,560	6,495
<i>Extinct</i>	NA	NA	75	85 <sup>b</sup>	96
<i>Living</i>	NA	NA	5,341	5,475	6,399
<i>Living wild</i>	NA	NA	5,338	5,475	6,382
Genera	1,033	1,135	1,230	1,267	1,314
Families	135	132	153	159	167
Orders	20	26	29	27	27

400'ü  
Betacoronavirüs  
taşıyor

1400 yarasa  
2500 kemirgen türü

USAID, EcoHealth Alliance, Metabiota,  
Wildlife Conservation Society, Smithsonian Institution.



# PREDICT

30 ülkeden >6 800 kişi Tek Sağlık Başlığında teknisyen olarak eğitildi

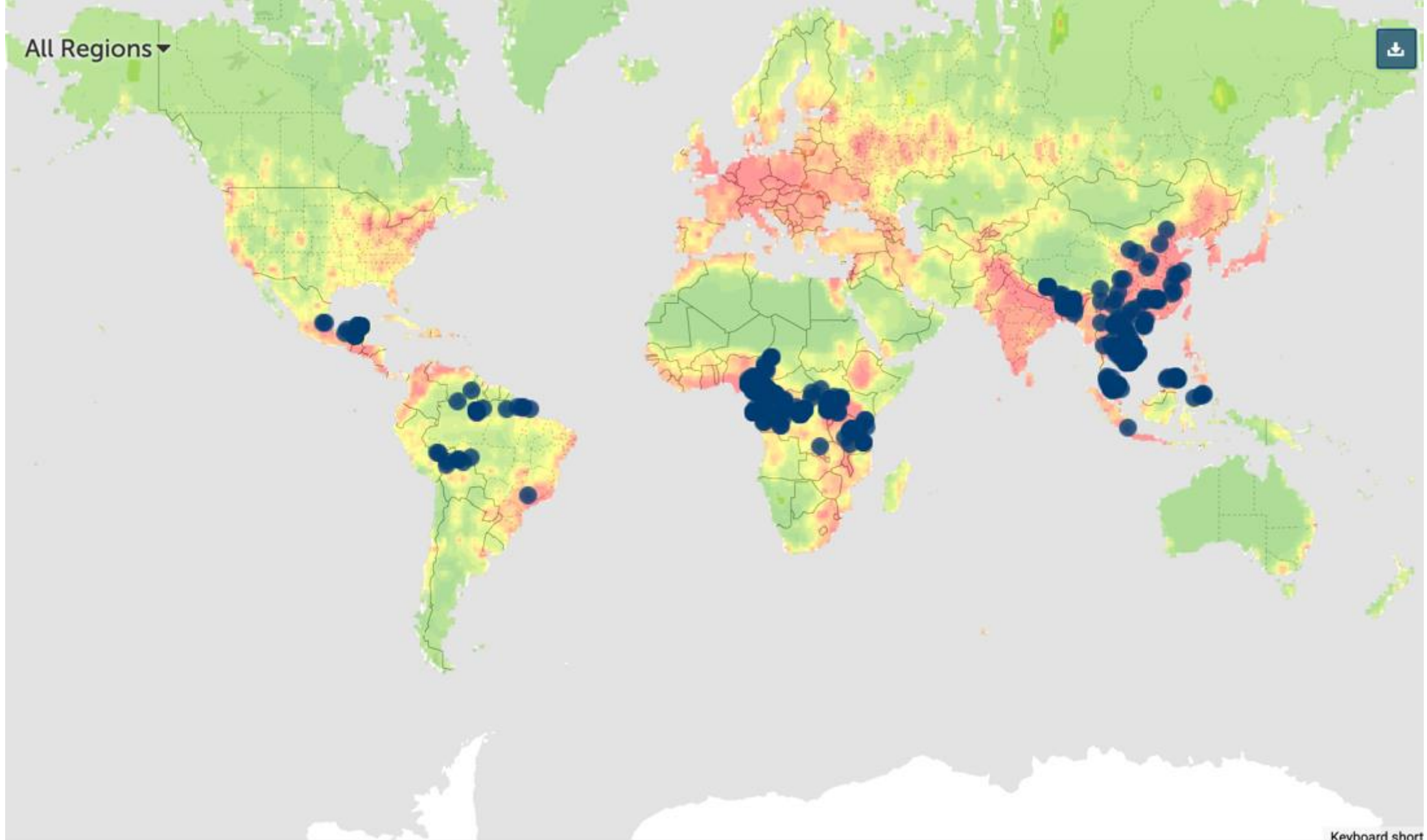
>60 lab zoonotik hastalıkları tespit etme kapasitesine kavuşturuldu (biyogüvenlik düzey 2-3)

>164,000 insan ve hayvan örnekleri toplandı

949 yeni virüs keşfedildi (Bombali ebolavirus, Zaire ebolavirus, Marburg virus,  
MERS- & SARS-ilişkili coronavirusler vb)

217 bilinen virüs tespit edildi







~1000 virüsten hangisi pandemi yapacak????

# Ranking the risk of animal-to-human spillover for newly discovered viruses

Zoë L. Grange<sup>a,1</sup> , Tracey Goldstein<sup>a,2</sup>, Christine K. Johnson<sup>a,2</sup>, Simon Anthony<sup>a,b,c,d</sup>, Kirsten Gilardi<sup>a</sup>, Peter Daszak<sup>b</sup> , Kevin J. Olival<sup>b</sup> , Tammie O'Rourke<sup>e</sup>, Suzan Murray<sup>f</sup> , Sarah H. Olson<sup>g</sup> , Eri Togami<sup>a</sup> , Gema Vidal<sup>a</sup> , Expert Panel<sup>3</sup>, PREDICT Consortium<sup>3</sup>, and Jonna A. K. Mazet<sup>a,1</sup>

PNAS 2021 Vol. 118 No. 15 e2002324118

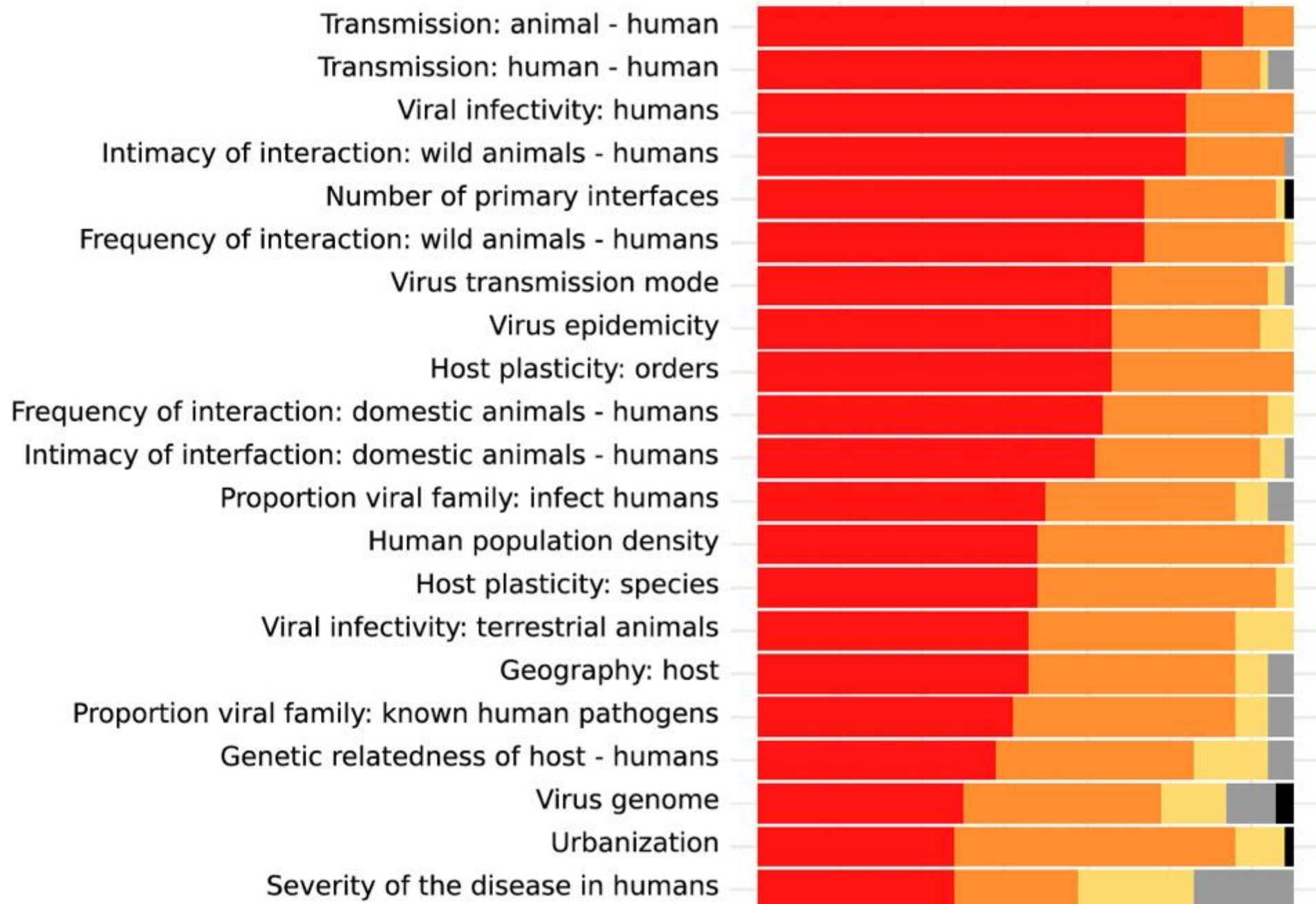
13 ülkeden 65 uzman

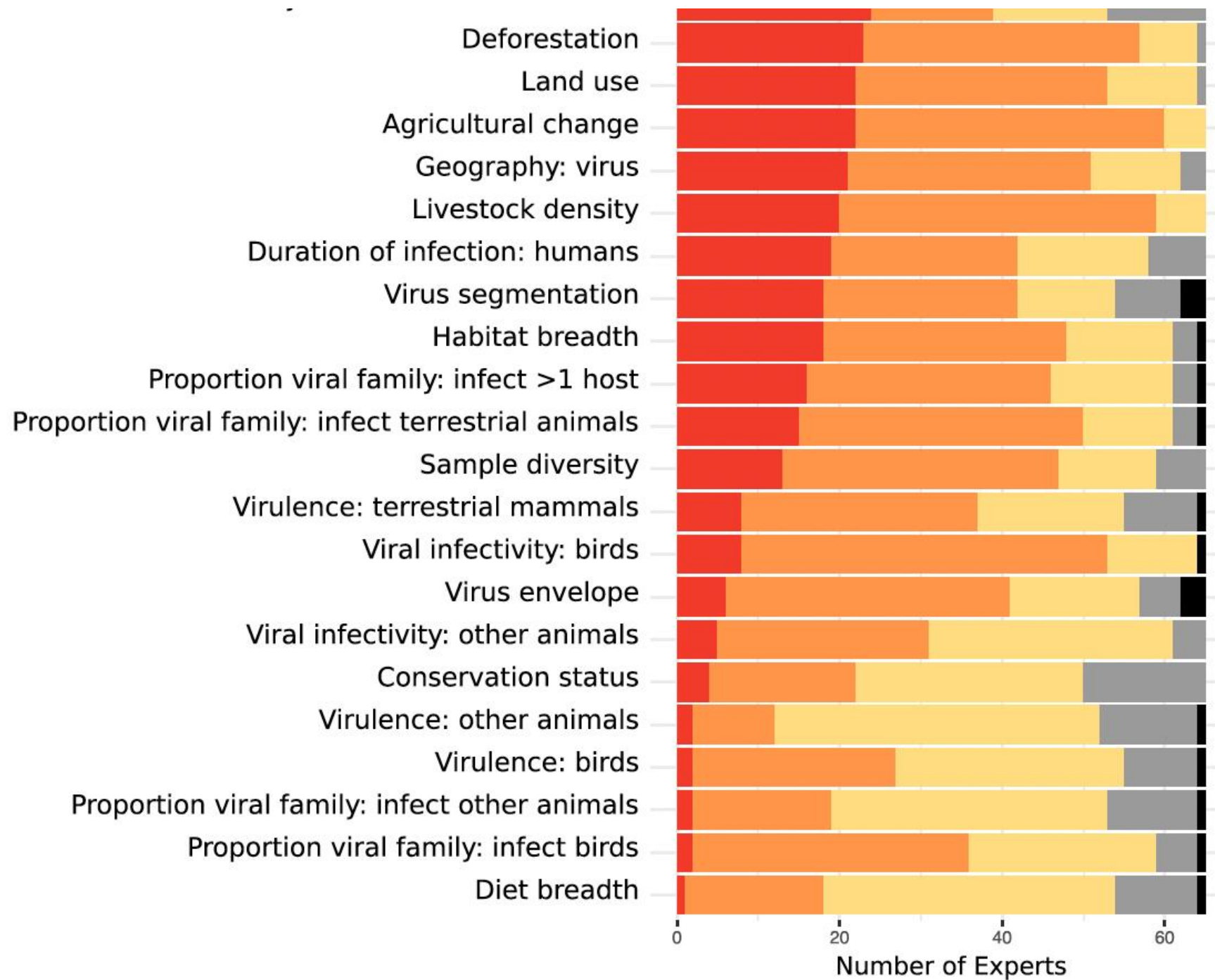
509,721 örnekten izole edilen 887 yaban hayat virüsü

38'i zoonotik, 849'u zoonotik kapasitesi ???

31 parametre üzerinden skarlama







RANKING COMPARISON

RANK YOUR VIRUS

DISCUSSION

# SPILLOVER

## VIRAL RISK RANKING

Developed by infectious disease scientists, SpillOver: Viral Risk Ranking explores and directly compares hundreds of virus, host and environmental risk factors to identify viruses with the highest risk of zoonotic spillover from wildlife to humans.

[LEARN MORE](#)[RANKING COMPARISON](#)[SEARCH FOR A VIRUS](#)



## SPILLOVER

▶ RANKING COMPARISON

RANK YOUR VIRUS

DISCUSSION

## Ranking Comparison

[Download results \(.csv\)](#)

## VIRUS

## LASSA VIRUS

**NO.2 SPILLOVER RISK** OUT OF 88g VIRUSES[NOT SEEING THE VIRUS YOU'RE LOOKING FOR?](#)RISK SCORE  
(OUT OF 155)

## CONTRIBUTIONS TO RISK SCORE



HOST



ENVIRONMENT



VIRUS

## SEARCH BY:

Virus Name

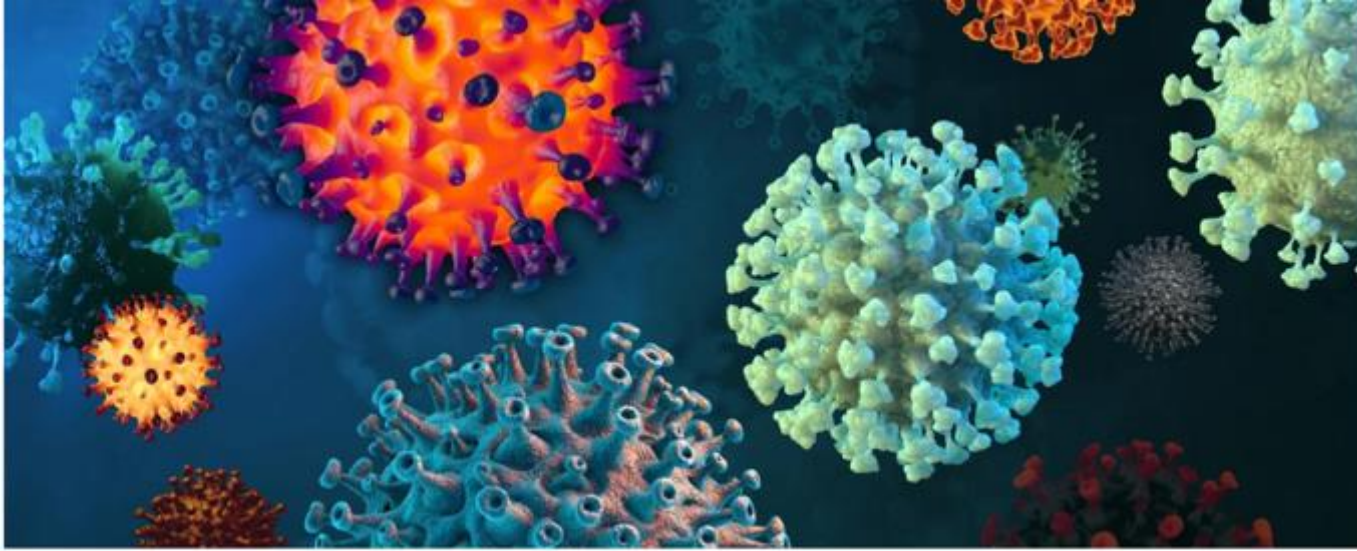
## ORDER BY:

Overall Rank ▼

## SHOW KNOWN ZONOTICS:

Show all viruses ▼

RISK POSITION	RISK SCORE	VIRUS	GENUS	FAMILY
1	97	Severe acute respiratory syndrome coronavirus 2	Betacoronavirus	Coronaviridae ▼
2	91	Lassa virus	Mammarenavirus	Arenaviridae ▼
3	87	Ebola virus	Ebolavirus	Filoviridae ▼
4	86	Seoul virus	Hantavirus	Bunyaviridae ▼
5	86	Nipah virus	Henipavirus	Paramyxoviridae ▼
6	86	Hepatitis E virus	Orthohepevirus	Hepeviridae ▼



# Virus Intelligence & Strategic Threat Assessment

**New global collaboration uses experts and AI to spot the next pandemic**

by CEPI | September 05, 2025

Coalition for Epidemic Preparedness Innovations (CEPI) and University of California, Davis (UC Davis) working with the Boston University-based Biothreats Emergence, Analysis and Communication Network ([BEACON project](#)) to integrate BEACON's open-source disease surveillance program with UC Davis's [Virus Intelligence & Strategic Threat Assessment \(VISTA\) project](#) (formerly "SpillOver 2.0").

VISTA aims to provide risk rankings in near real time through the use of AI-assisted tools along with expert oversight and curation.

CEPI is providing up to \$1 million to support the integration of data between BEACON and VISTA.



# **ViSTA**

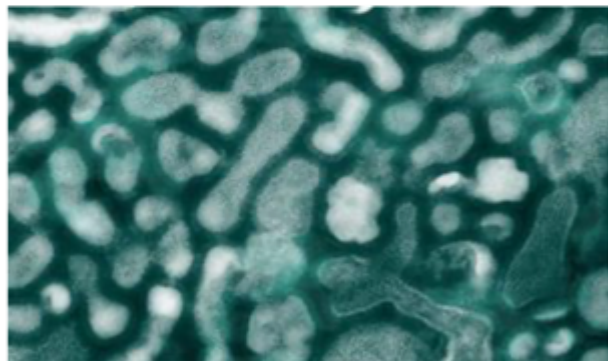
Virus Intelligence  
& Strategic Threat Assessment

Developed by infectious disease scientists, VISTA uses AI-assisted tools and expert opinion to explore and compare hundreds of virus, host, and environmental risk factors to identify viruses with pandemic potential.

[Health Topics](#) ▾[Countries](#) ▾[Newsroom](#) ▾[Emergencies](#) ▾[Data](#) ▾[About WHO](#) ▾

[Home](#) / [Initiatives](#) / [Global Influenza Surveillance and Response System \(GISRS\)](#)

## Global Influenza Surveillance and Response System (GISRS)



Global influenza surveillance has been conducted through WHO's Global Influenza Surveillance and Response System (GISRS) since 1952.

GISRS is a system fostering global confidence and trust for over half a century, through effective collaboration and sharing of viruses, data and benefits based on Member States' commitment to a global public health model.

The mission of GISRS is to protect people from the threat of influenza by continuously functioning as a:

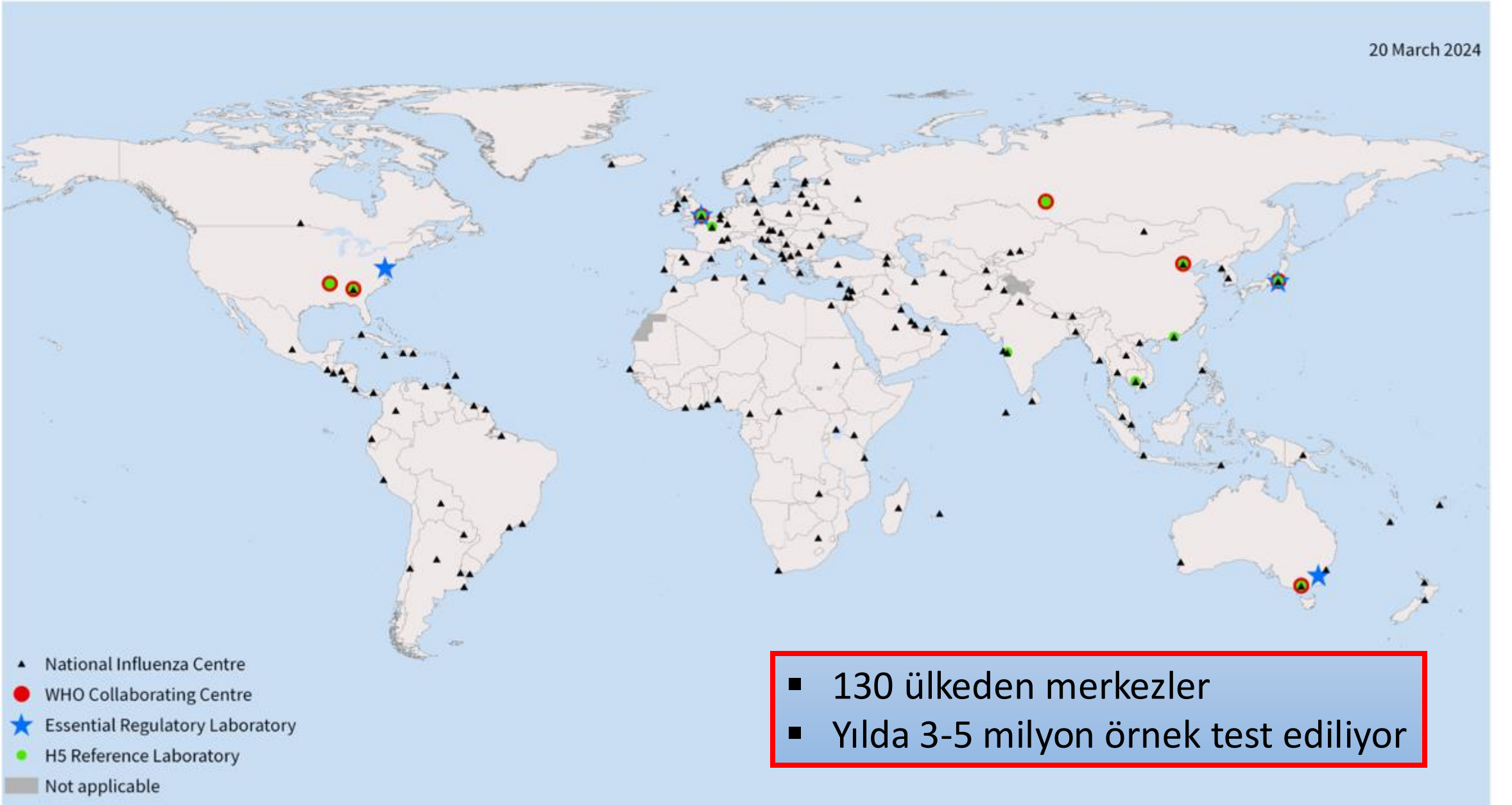
- global mechanism of surveillance, preparedness and response for seasonal, pandemic and zoonotic influenza;
- global platform for monitoring influenza epidemiology and disease; and
- global alert for novel influenza viruses and other respiratory pathogens.

**GISRS 70th Anniversary**

**National Influenza  
Centres**

# WHO Global Influenza Surveillance and Response System (GISRS)

20 March 2024





# Surveillance data generated by GISRS

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*RespiMart* is a central data platform exchanging, harmonizing, consolidating, and storing surveillance data on respiratory viruses with epidemic and pandemic potential, including influenza, SARS-CoV-2, and RSV. Two databases within RespiMart are used routinely to monitor and report on global and regional activity of these respiratory viruses: FluNet and FluID

*FluNet* is a global database of virologic surveillance for respiratory viruses conducted and reported through GISRS.

*FluID* is a global database of epidemiologic surveillance for respiratory illness conducted and reported through GISRS.



Food and Agriculture  
Organization of the  
United Nations



UN  
environment  
programme



World Health  
Organization



World Organisation  
for Animal Health  
Founded in 1924

## ONE HEALTH JOINT PLAN OF ACTION (2022-2026)

WORKING TOGETHER FOR  
THE HEALTH OF HUMANS, ANIMALS,  
PLANTS AND THE ENVIRONMENT

**FIGURE 3: THE SIX OH JPA ACTION TRACKS**





Food and Agriculture  
Organization of the  
United Nations



World Health  
Organization



World Organisation  
for Animal Health

# **Updated joint FAO/WHO/WOAH public health assessment of recent influenza A(H5) virus events in animals and people**

**Assessment based on data as of 1 July 2025**

**28 July 2025**



[Health Topics ▾](#)[Countries ▾](#)[Newsroom ▾](#)

The WHO R&D Blueprint for Epidemics has a primary goal to accelerate the development of medical countermeasures (MCMs). Since 2015, its primary goal is to make these countermeasures available for diseases with epidemic and pandemic potential, thereby contributing to the prevention of Public Health Emergencies of International Concern (PHEICs) and saving lives during outbreaks. The WHO R&D Blueprint for Epidemics functions as a global platform for research and development collaboration, stressing the significance of international cooperation in expediting the research and development of medical countermeasures (MCMs) to respond to epidemics and pandemics. At the same time, it also provides the support of

# WHO R&D Blueprint for Epidemics

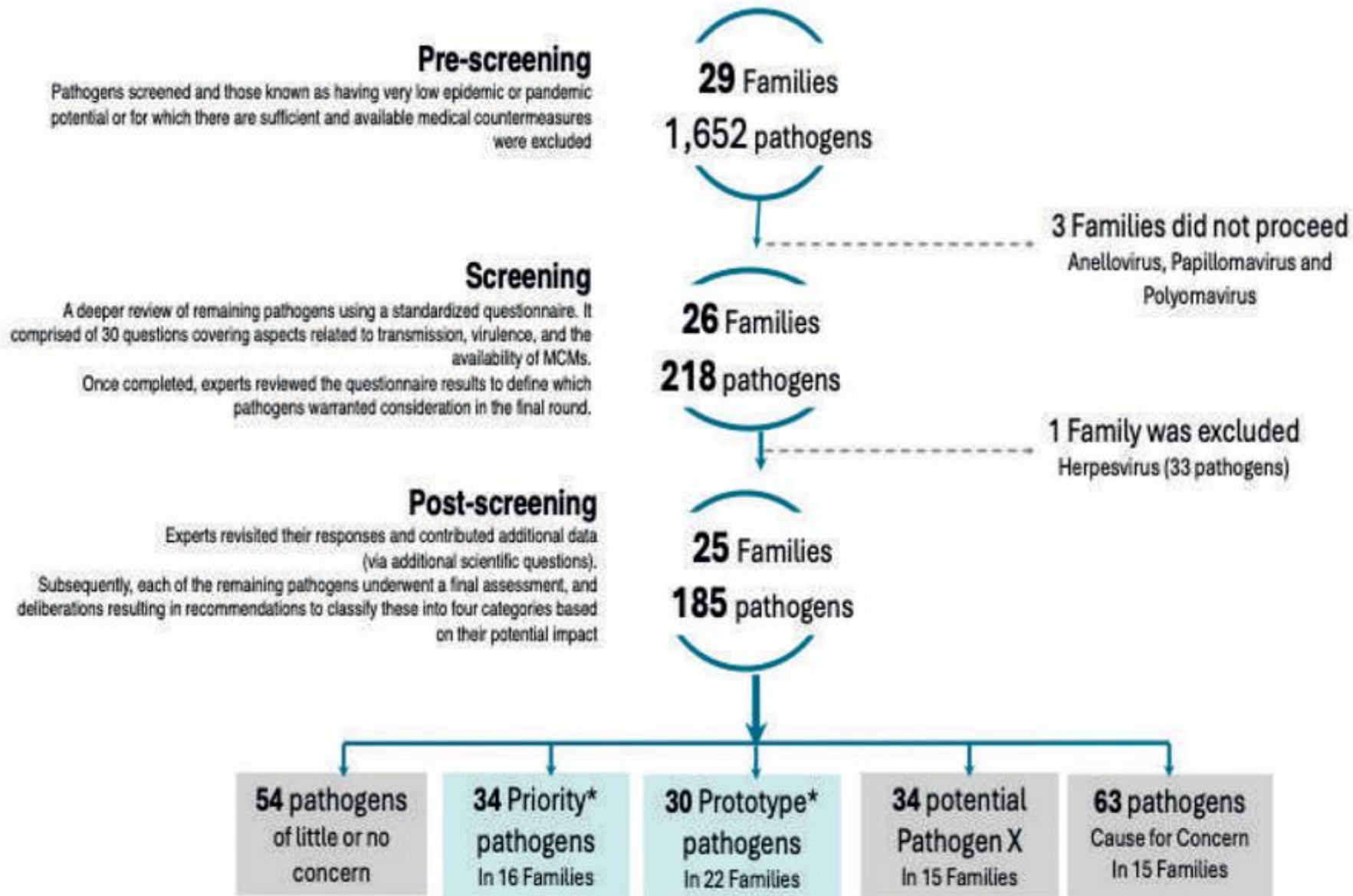
## PATHOGENS PRIORITIZATION

A SCIENTIFIC FRAMEWORK  
FOR EPIDEMIC AND PANDEMIC  
RESEARCH PREPAREDNESS

HEALTH  
EMERGENCIES  
programme

JUNE 2024

50 ülkeden 200 bilim insanı





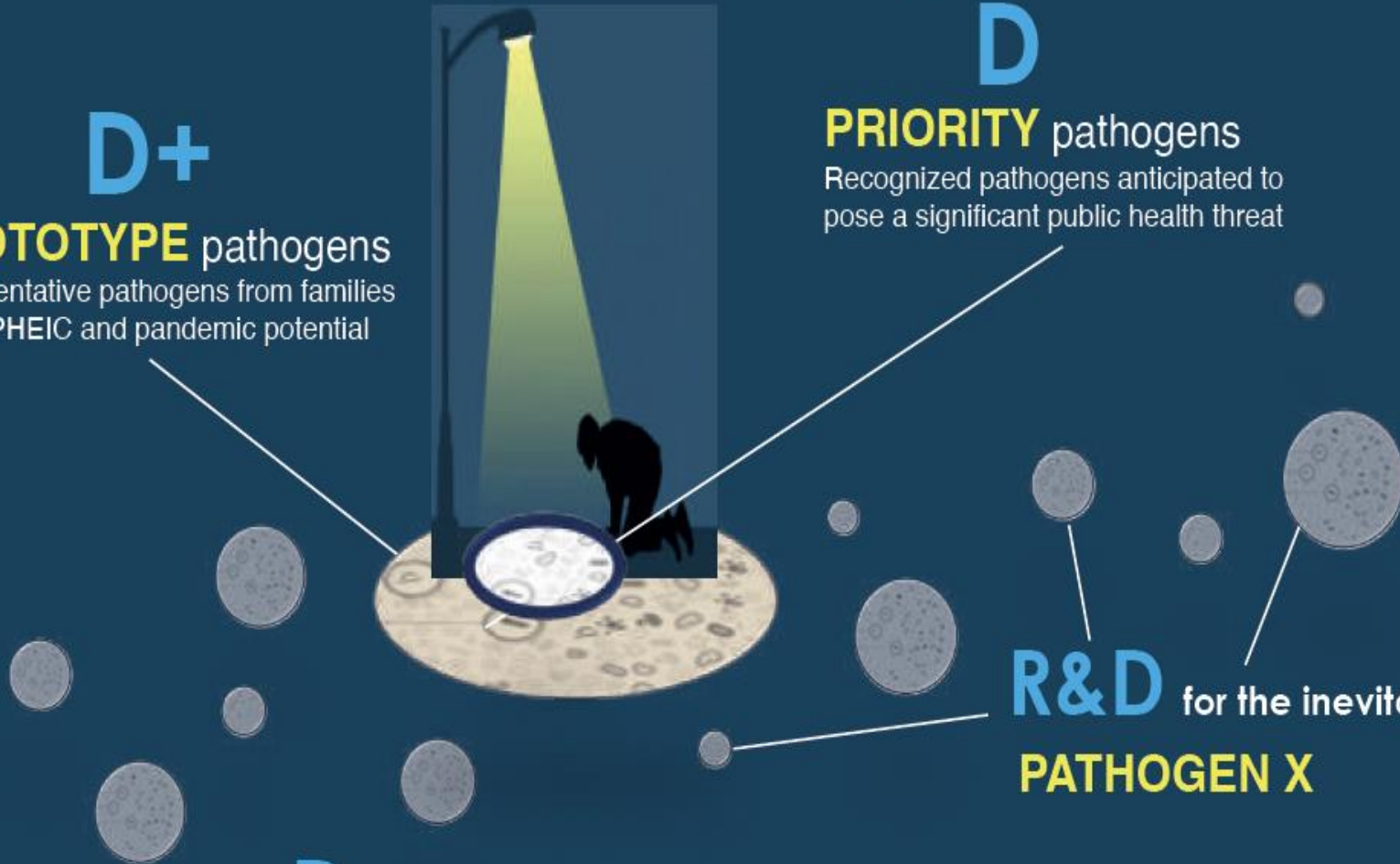
# Preparing for the next pandemic threat

**D+**  
**PROTOTYPE** pathogens  
Representative pathogens from families  
with PHEIC and pandemic potential

**D**  
**PRIORITY** pathogens  
Recognized pathogens anticipated to  
pose a significant public health threat

**R&D** for the inevitable  
**PATHOGEN X**

**R** for Research across all **FAMILIES**  
regardless of perceived PHEIC/pandemic potential





# Global genomic surveillance strategy

for pathogens with pandemic and epidemic potential

2022–2032

A 10-year unifying framework to strengthen country, regional and global genomic surveillance.



Monitoring and evaluation are key to understand progress towards and drive the achievement of the strategy's results hierarchy. The Strategy's key measure of success is:

By 2032, all 194 WHO Member States have, or have access to, timely genomic sequencing for pathogens with pandemic and epidemic potential.<sup>1</sup>

**Genomic surveillance is monitoring the genetic make-up of pathogens, such as viruses and bacteria, to understand how they behave and how we can control them.**

It involves constantly monitoring pathogens...



...and analyzing their similarities and differences.



**IT HELPS US TO:**



Monitor diseases



Control pathogens



Tailor interventions and recommendations for the public



Develop countermeasures, like vaccines



Stamp out disease



For example, genomic surveillance is used to monitor for changes in SARS-CoV-2 virus, and to identify new variants.



## GOAL

Genomic surveillance is strengthened and scaled for quality, timely and appropriate public health actions within local to global surveillance systems

## OBJECTIVES



### Objective 1

Improve access to tools for better geographic representation



### Objective 2

Strengthen the workforce to deliver at speed, scale and quality



### Objective 3

Enhance data sharing and utility for streamlined local to global public health decision-making and action



### Objective 4

Maximize connectivity for timely value-add in the broader surveillance architecture



### Objective 5

Maintain a readiness posture for emergencies

## STRATEGIC ACTIONS

- **Advocate for the value of genomic surveillance** with policy makers
- **Map and monitor** capability and capacity landscape
- **Deliver contextualized and sustainable** technology solutions
- **Stimulate innovation and research** to address local to global needs
- **Shape a sustainable and quality market to maximize access**

- Roll-out training packages in **genomics and bioinformatics**
- Promote **communities of practice and knowledge exchange**
- Implement **external quality assessment programmes**
- Strengthen programmes for **workforce development and retention**

- Develop consensus on **data and meta data standards**
- Establish **data sharing and access principles**
- Ensure **data sharing agreements**
- **Harmonize** norms, standards, benchmarks and reference materials
- **Make the use of genomics routine** in surveillance practice

- **Facilitate data, specimen and information sharing**
- **Increase network linkages** at local, regional and global levels
- Implement targeted collaboration with **One Health partners**
- **Strengthen networks** in routine, epidemic and pandemic contexts

- **Test the surge and stretch** of genomic surveillance systems
- **Establish or sustain joint projects** to maintain capacities
- **Implement inter- or after-action reviews** to strengthen practices



# Global wastewater surveillance for pathogens with pandemic potential: opportunities and challenges



Nicholas C Grassly, Alexander G Shaw, Michael Owusu

Wastewater surveillance holds great promise as a sensitive method to detect spillover of zoonotic infections and early pandemic emergence, thereby informing risk mitigation and public health response. Known viruses with pandemic

*Lancet Microbe* 2025;  
6: 100939

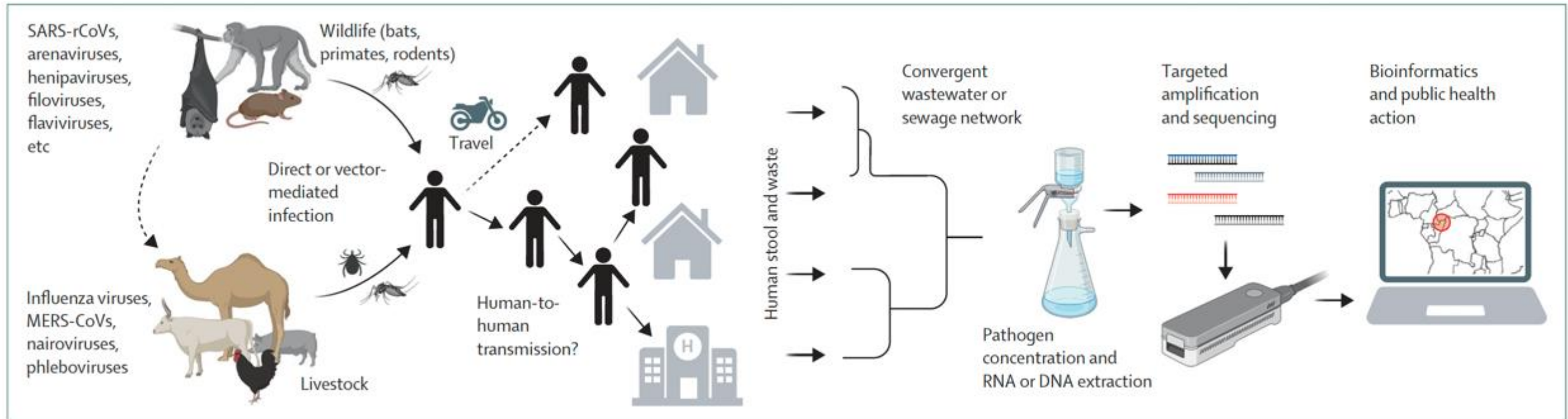


Figure 1: Illustration of wastewater surveillance for viruses with pandemic potential as an early warning for human infection (spillover), transmission, and adaptation

Virus family (prototype or priority virus)	Reported in human stool or urine	Mean quantity shed (genome copies per mL) <sup>a</sup>	Mean duration of shedding (weeks)	Reported in wastewater or sewage	Clinical characteristics
Coronaviruses (SARS-CoV-2, MERS-CoV)	Yes	1.9×10 <sup>6</sup> (stool, SARS-CoV-2); <sup>40</sup> 10 <sup>4</sup> (stool, MERS-CoV) <sup>41</sup>	3 (stool, SARS-CoV-2) <sup>40</sup>	Yes (many studies on SARS-CoV-2, not on MERS-CoV)	Non-specific respiratory illness, approximately 30% asymptomatic for SARS-CoV-2 <sup>42</sup>
Flaviviruses (Zika virus, Dengue Virus, Yellow Fever virus)	Yes	10 <sup>2</sup> –10 <sup>5</sup> (urine, n=4); <sup>43</sup> similar for dengue virus, higher for West Nile virus <sup>44</sup>	1–3 (urine), 1 (rectal swab) <sup>45</sup>	Yes <sup>13</sup>	Mild, non-specific illness, 50–70% asymptomatic <sup>46</sup>
Filoviruses (Ebola virus, Marburg virus)	Yes	approximately 10 <sup>5</sup> (stool) <sup>47</sup>	2 (stool)	No	Case definition, 70% sensitivity; <sup>48</sup> rarely asymptomatic <sup>49</sup>
Paramyxoviruses (Nipah virus)	Yes	Not quantified <sup>50</sup>	NA	No	Variable clinical presentation, less than 45% asymptomatic <sup>51</sup>
Nairoviruses (CCHF virus)	Yes	10 <sup>2</sup> –10 <sup>4</sup> (urine and stool) <sup>52</sup>	NA	No	Severe febrile illness, approximately 80% asymptomatic <sup>53</sup>
Phenuiviruses (Rift Valley fever virus)	No <sup>b</sup>	NA	NA	No	Non-specific symptoms, frequently asymptomatic <sup>54</sup>
Arenaviruses (Lassa virus)	Yes	10 <sup>4</sup> –10 <sup>5</sup> (max, n=1) (urine and stool) <sup>55</sup>	4–12 (urine) <sup>56</sup>	No	Non-specific symptoms, greater than 90% asymptomatic or mild <sup>57</sup>
Orthomyxoviruses (influenza virus)	Yes	approximately 10 <sup>4</sup> (stool) <sup>58</sup>	Less than 3 (stool) <sup>59</sup>	Yes <sup>8</sup>	Non-specific respiratory illness, 20–85% asymptomatic <sup>60</sup>
Picornaviruses (EV-71, EV-D68)	Yes	approximately 10 <sup>5</sup> (stool) <sup>c</sup> <sup>61</sup>	2–6 (depending on serotype) <sup>62</sup>	Yes <sup>63</sup>	Severe neurological disease in less than 1% <sup>64</sup>

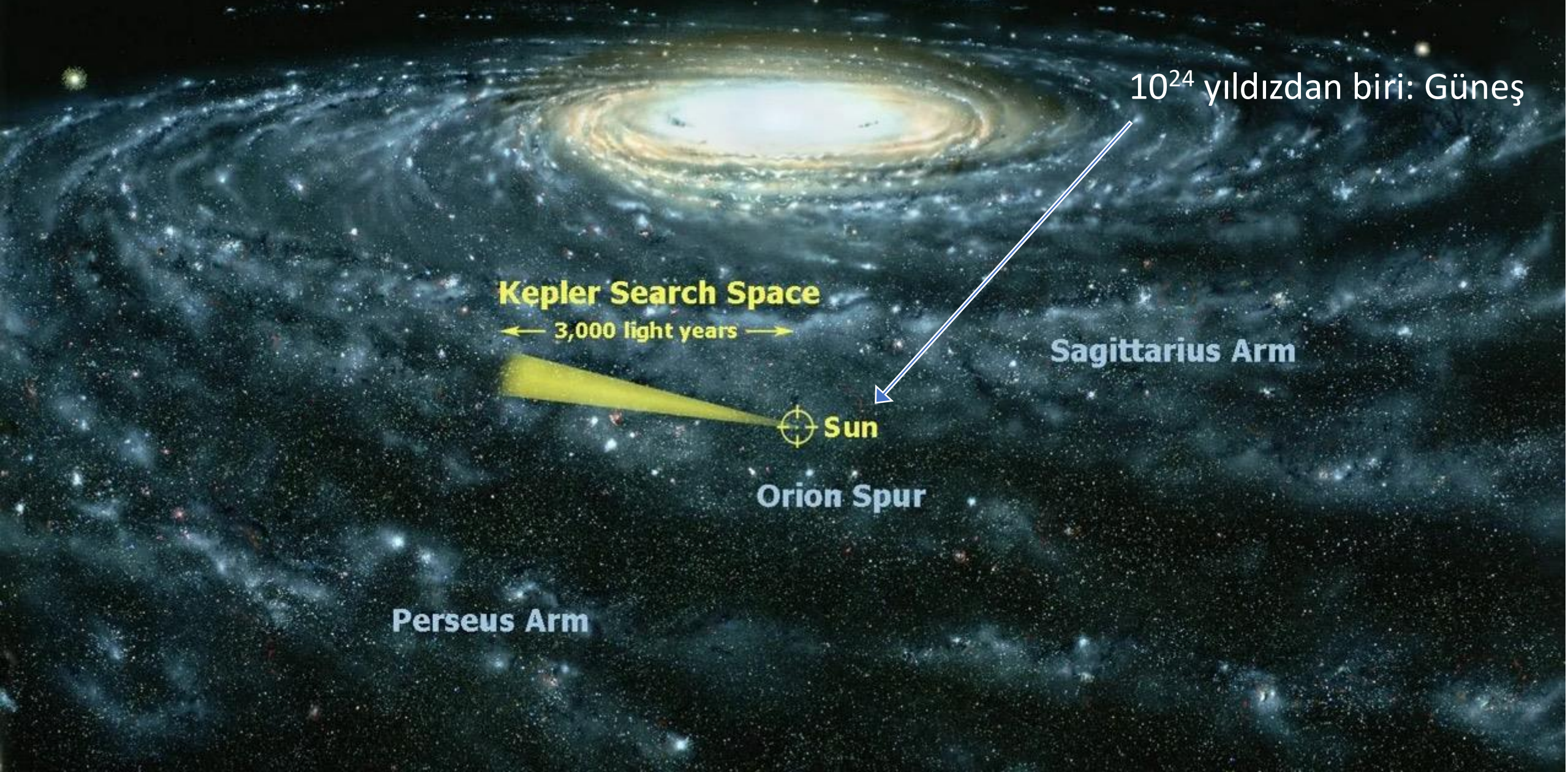
CCHF=Crimean-Congo haemorrhagic fever. EV=enterovirus. NA=not available. <sup>a</sup>Direct comparison between pathogens or sample types of viral load is difficult because viral loads are reported as genome copies per mL, but whether this is per mL of sample or RNA extraction volume and the extent of dilution of stool samples before extraction are unclear. <sup>b</sup>Shedding most likely based on wild-type challenge in a non-human primate model. <sup>65</sup>  
<sup>c</sup>Reported for vaccine poliovirus.

**Table:** Characteristics of prototype and priority viruses from viral families of concern for pandemic emergence that influence the potential value of wastewater surveillance, relative to that of clinical surveillance



# Milky Way Galaxy

2 trilyon galaksiden biri: Samanyolu



$10^{24}$  yıldızdan biri: Güneş

**Kepler Search Space**

← 3,000 light years →

**Sagittarius Arm**

**Sun**

**Orion Spur**

**Perseus Arm**