

Predicting the Next Pandemic Virus

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Outline

The Limits of Prediction

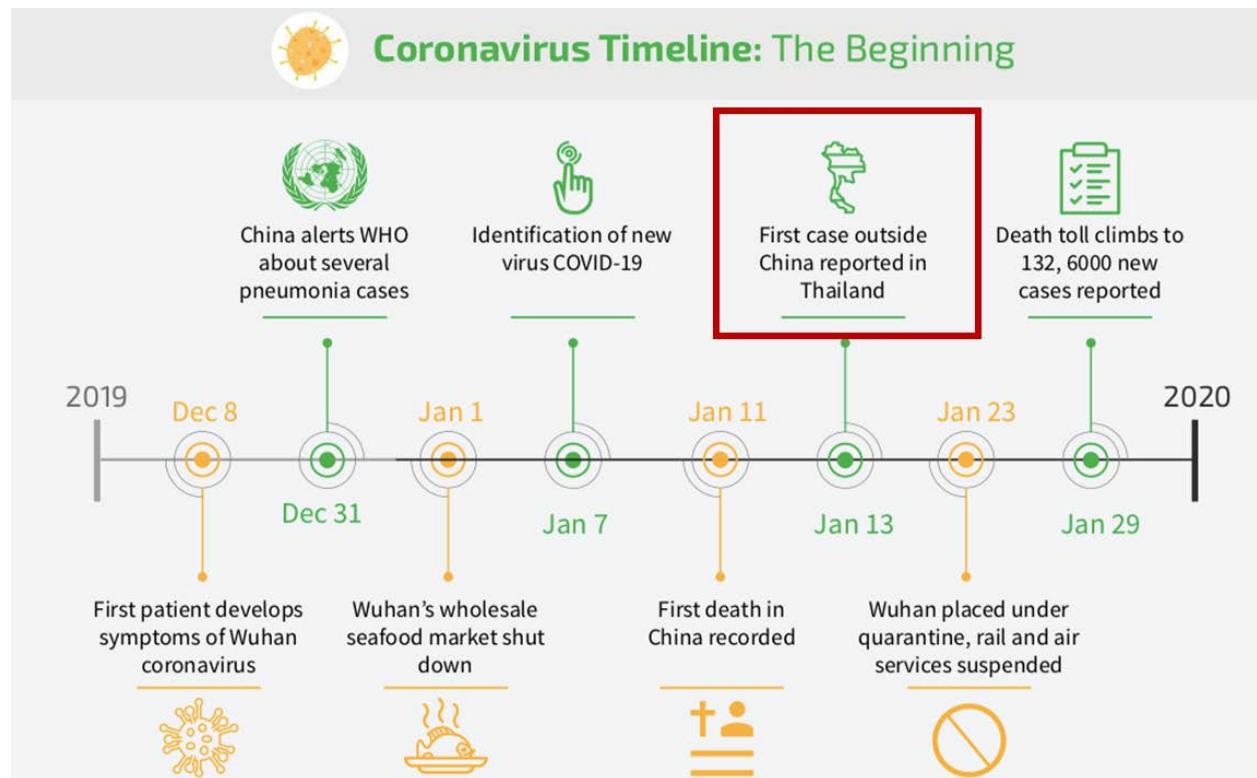
Drivers of Pandemic

The Strategic Response

Genomic Surveillance and Local Position



Can We Predict The Next Pandemic?



In January 2020, Thailand detected the first COVID-19 case outside China

What exactly are we trying to predict?

- Which virus?
- When?
- Where?
- How severe?

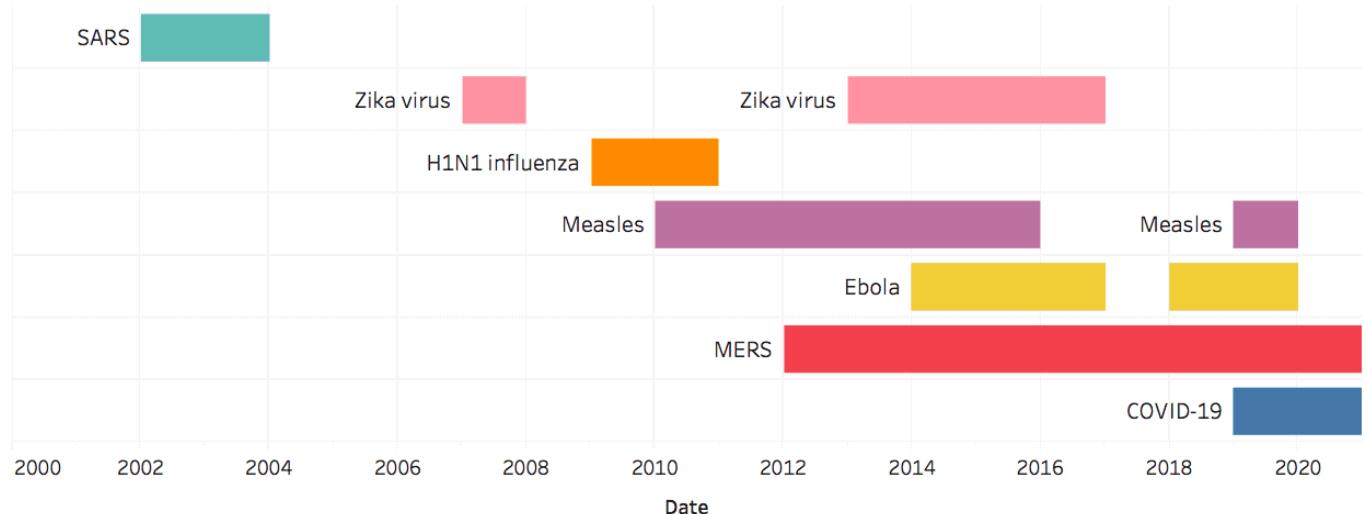
Pandemics keep surprising us —

Every major outbreak in the last 20 years —

- SARS
- MERS
- H1N1pdm2009
- Ebola
- **COVID-19**
- mPox

—arrived without prediction.

Major Emerging and Re-emerging Infectious Disease Outbreaks, 2002-2020



Adapted from: Peter Sands, et al; New England Journal of Medicine, March 31, 2016.

Data Source: World Health Organization

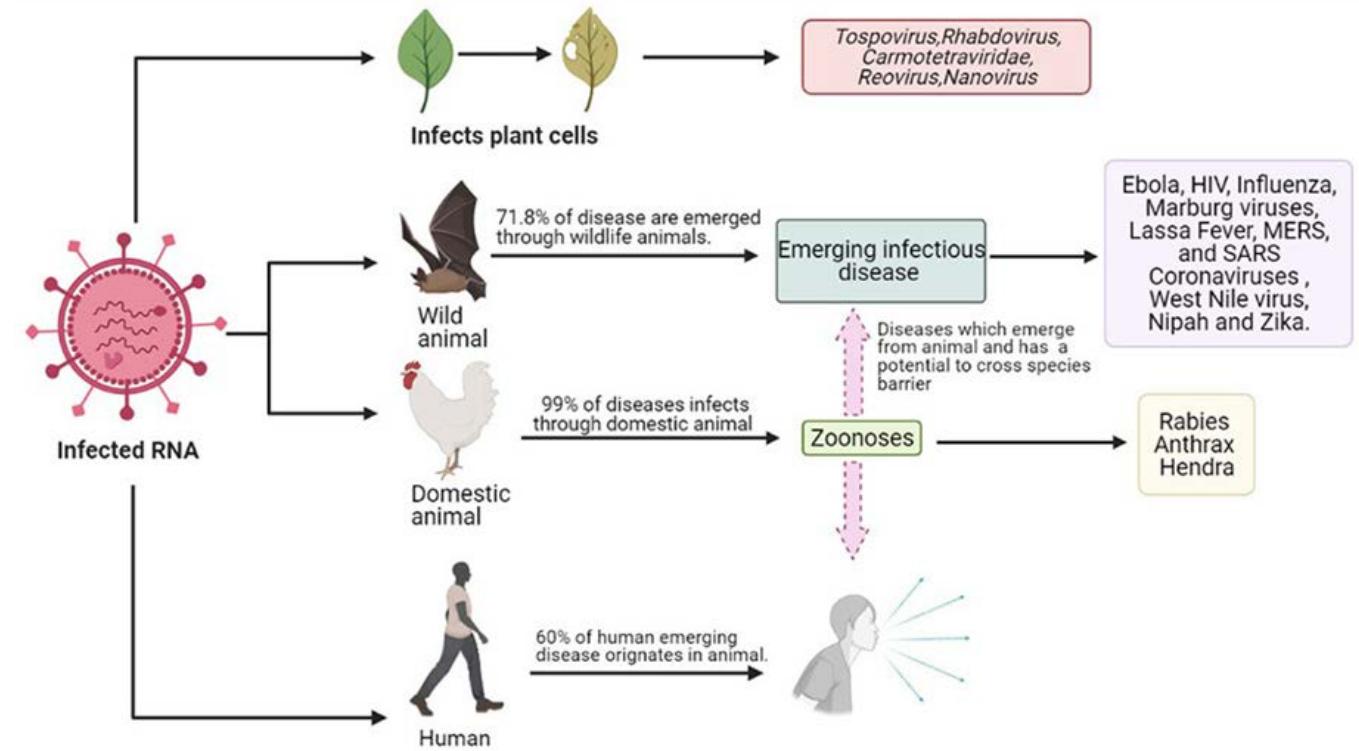
SARS, severe acute respiratory syndrome; MERS, Middle East respiratory syndrome

CDDEP THE CENTER FOR
Disease Dynamics,
Economics & Policy
WASHINGTON DC • NEW DELHI

Biology Is Not Fully Predictable

Characteristics of Potential Pandemic Viruses

- 1) High Human-to-Human Transmissibility
- 2) Antigenic Novelty to Humans
- 3) Broad Host Range & Spillover Potential
- 4) Balanced Virulence & Immune Evasion
- 5) Rapid Adaptation & Evolution Capacity



Virus Families of Greatest Concern

Orthomyxoviridae – Influenza A (H5, H7, H9; reassortment risk)

Coronaviridae – SARS-CoV, MERS-CoV, SARS-CoV-2; high recombination

Paramyxoviridae – Nipah, Hendra; high case fatality & spillover

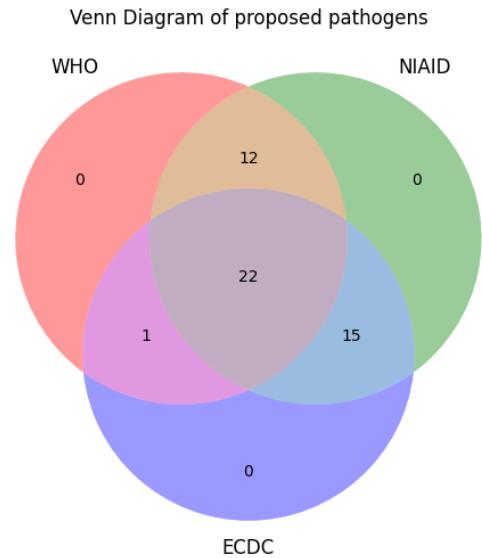
Filoviridae – Ebola, Marburg; high virulence

Arenaviridae – Lassa; rodent reservoirs

Poxviridae – Mpox; sexual networks & zoonotic potential

Togaviridae / Flaviviridae – Chikungunya, Dengue, Zika (vector-driven)

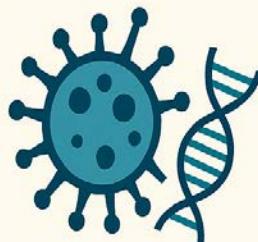
Bunyavirales – Crimean–Congo haemorrhagic fever, Rift Valley fever



- **Influenza A (H5, H7):** reassortment, airborne potential
- **Coronaviruses (SARS-like):** recombination, bat spillover
- **Paramyxoviruses (Nipah):** high mortality, bats
- **Arenaviruses (Lassa):** rodent reservoirs
- **Unknown "Disease X"**

Pandemic risk emerges when all three layers overlap:

Pandemic Drivers



Pathogen Evolution

- Mutation & recombination
- Adaptation to new hosts
- Host-range expansion & spillover potential
- Increased transmissibility or immune evasion



Host Factors

- Immunity gaps (naive or waning immunity)
- High population density & global mobility
- Behavioral / occupational exposures
- Human-animal interface intensity

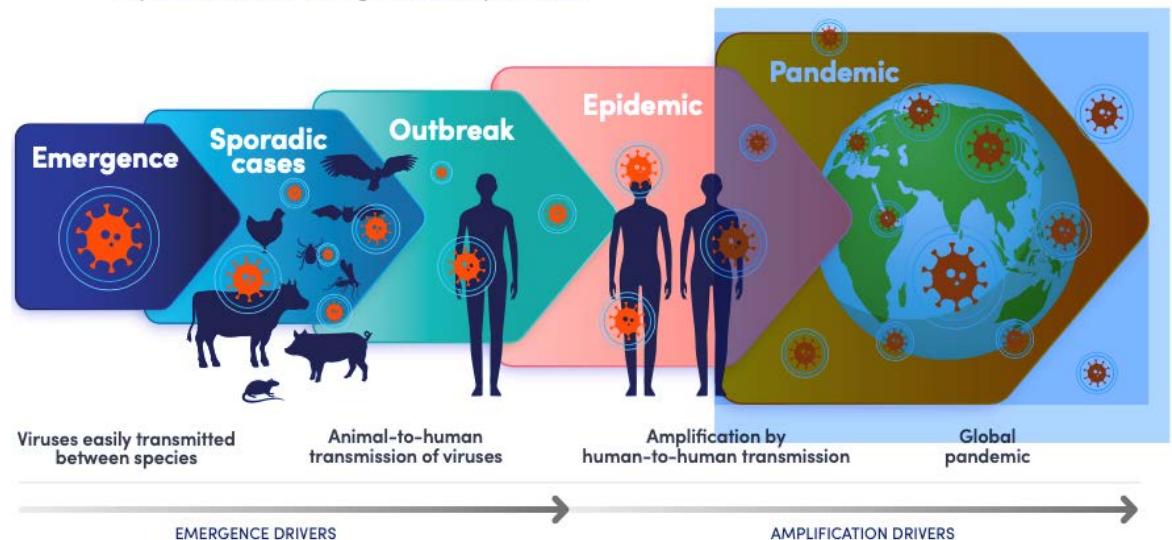


Environmental & Ecological Change

- Urbanization & megacities
- Land-use change: deforestation, agriculture, wildlife disruption
- Climate change altering vector and pathogen distribution
- Ecosystem imbalance increasing spillover events

a high-risk virus family + the right viral traits + enabling environmental/host drivers.

Steps from disease emergence to amplification



Source: GPMB

Prediction guides

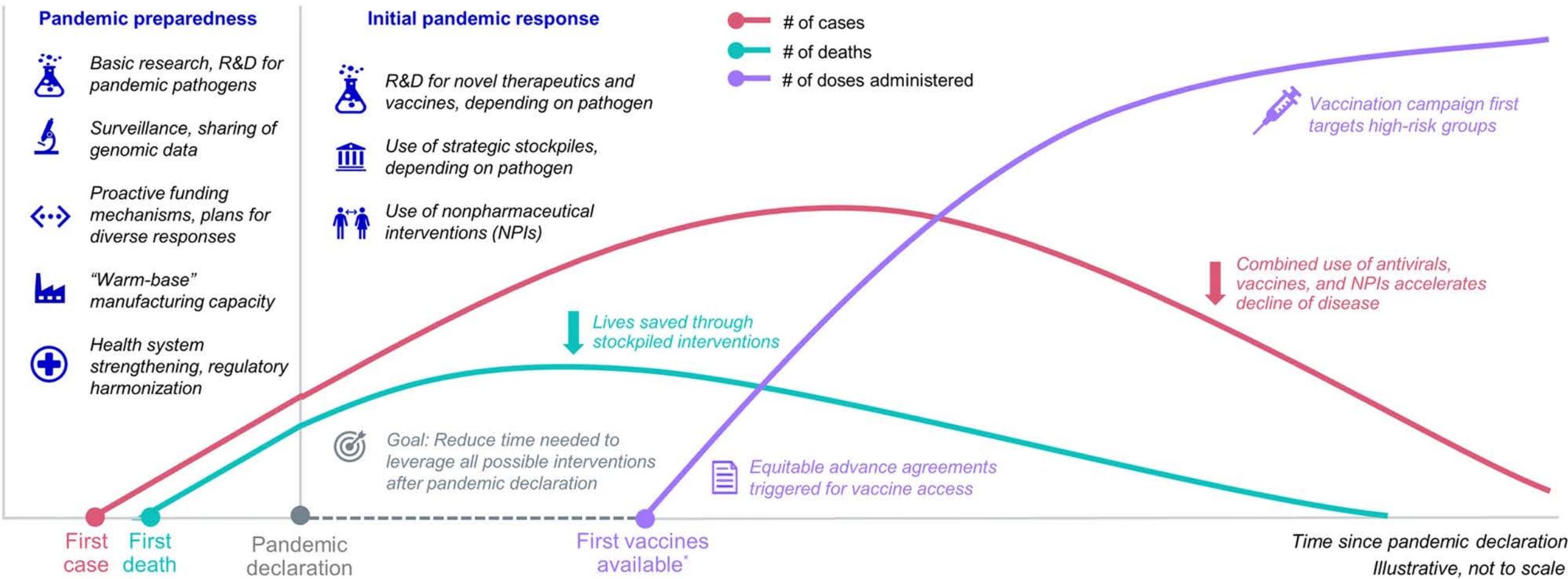
Surveillance,
preparedness
and rapid
response save us.

Prediction =

Early detection
+ Rapid
interpretation

Applying lessons from COVID-19 to reimagine the future

Pandemic Preparedness and Response Tactics



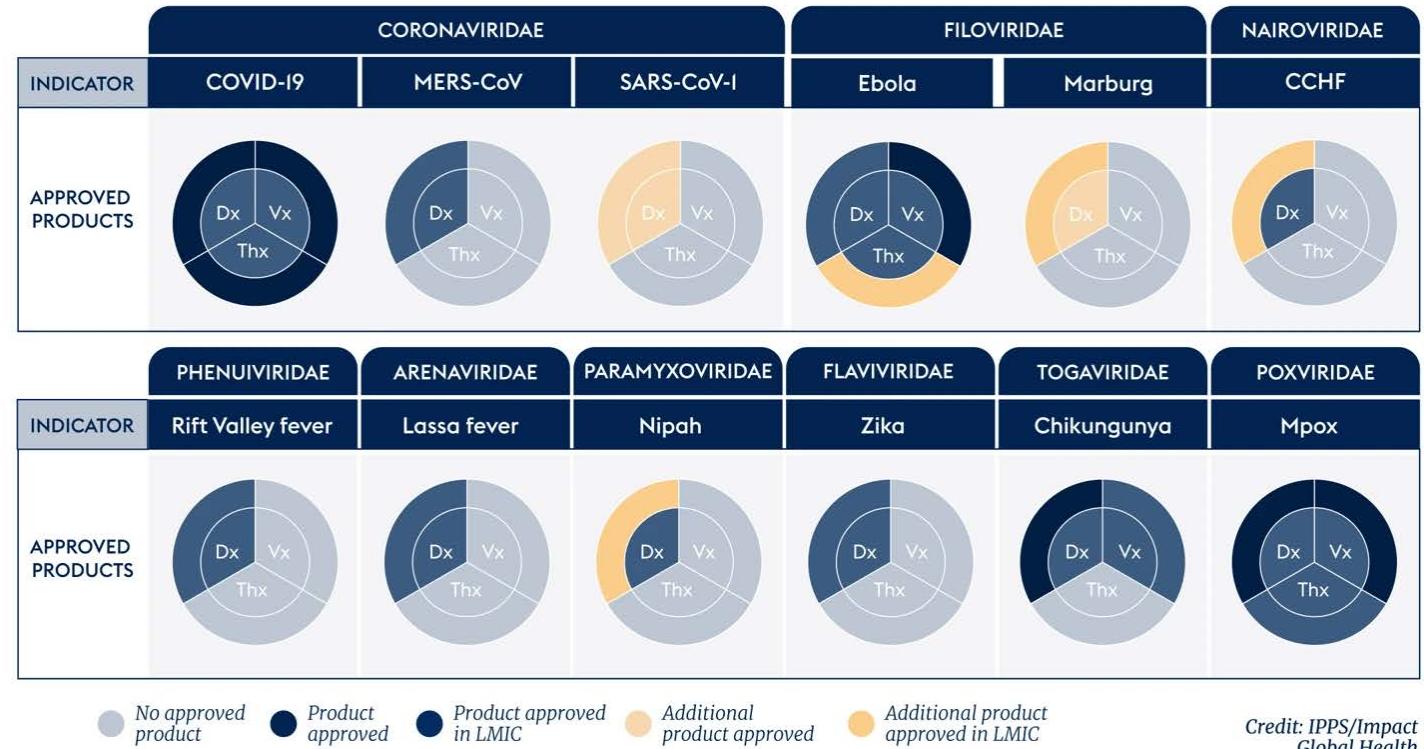
*Assumes vaccines would likely need to be developed or updated to match circulating virus.

Illustrative ecosystem of international partners for COVID-19 (non-exhaustive)



100 Days Mission Scorecard

The 100 Days Mission aims to accelerate the development of these tools to prepare for future pandemics



● No approved product ● Product approved ● Product approved in LMIC ● Additional product approved ● Additional product approved in LMIC

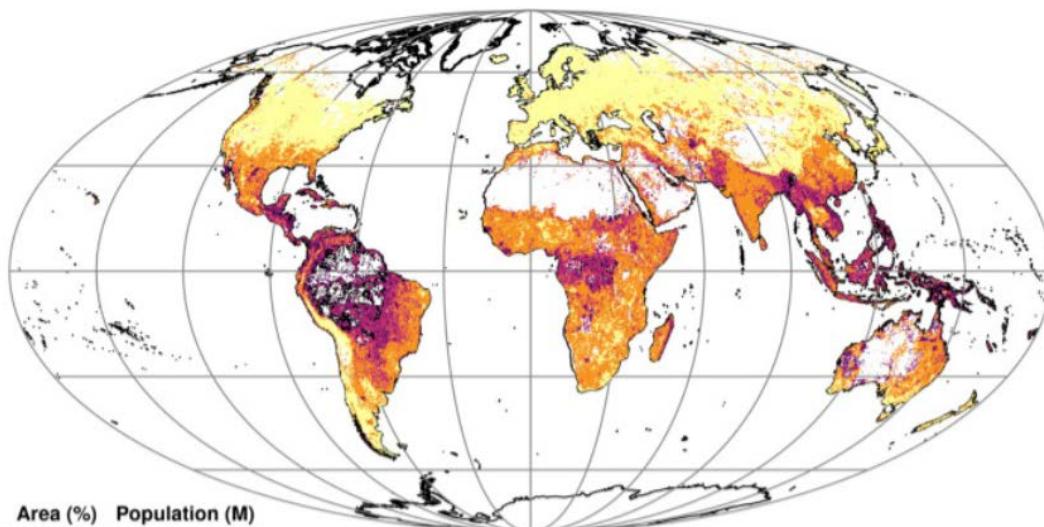
Credit: IPPS/Impact Global Health

It tracks the progress of approved diagnostics (Dx), vaccines (Vx), and therapeutics (Thx) for several priority viral diseases.

Risk of the WHO priority diseases, bias adjusted

Analysis of 9 high-threat zoonotic diseases shows risk is driven by:

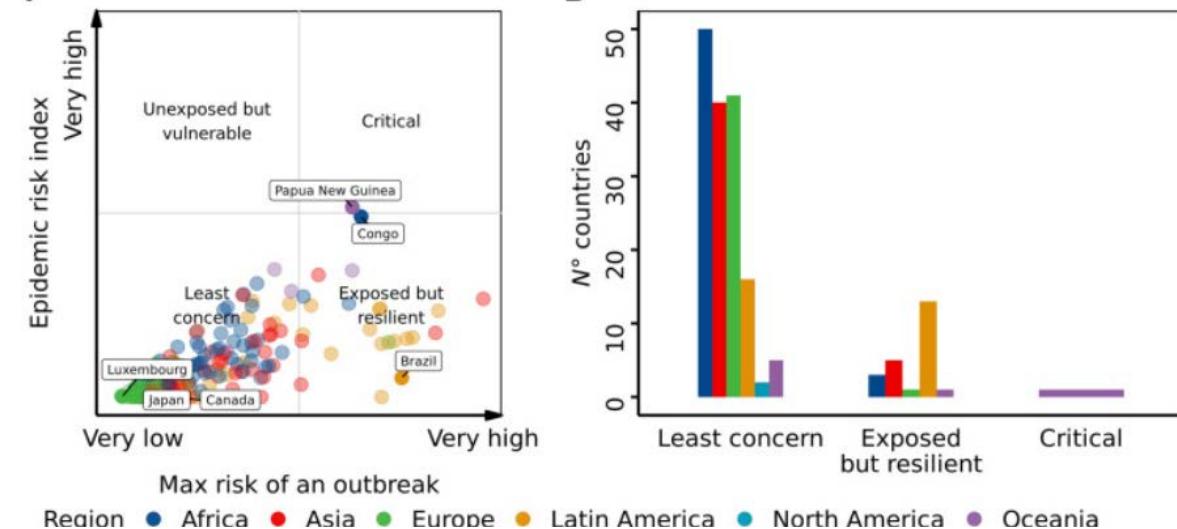
- Environmental change (deforestation, land-use change)
- Climate factors (temperature rise, rainfall shifts, drought)
- Human–animal interface (livestock density, forest proximity, wildlife contact)
- Population factors (human density, mobility)



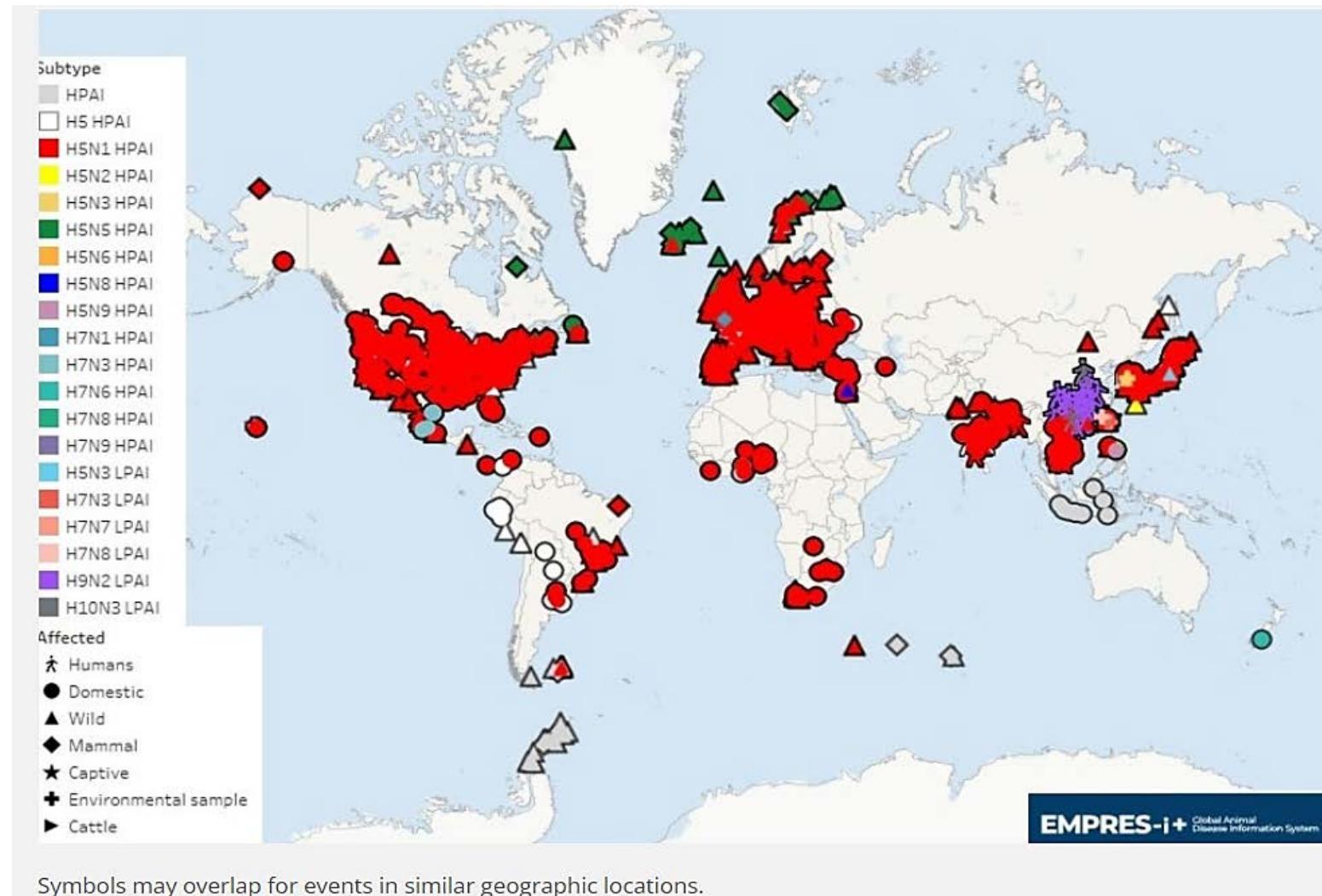
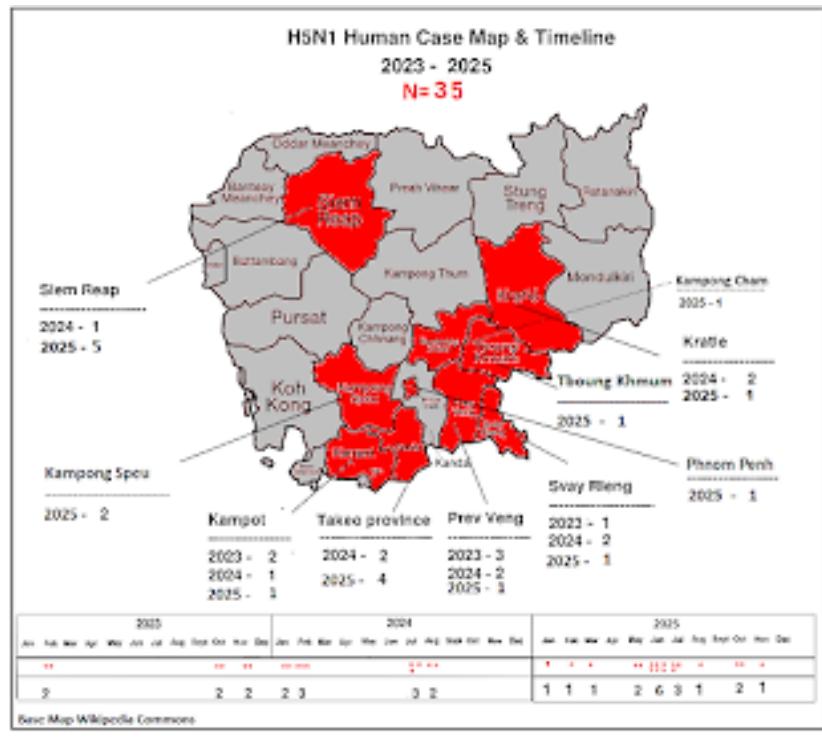
Risk	Area (%)	Population (M)
Very high	3.0	7.7
High	6.3	122.9
Medium	17.3	1198.0
Low	37.0	2965.3
Very low	36.5	1234.4

Epidemic Risk Index:

Combines outbreak risk + national response capacity → identifies countries at greatest danger due to high exposure but limited preparedness.



Global distribution of AIV with zoonotic potential*



<https://afludiary.blogspot.com/>

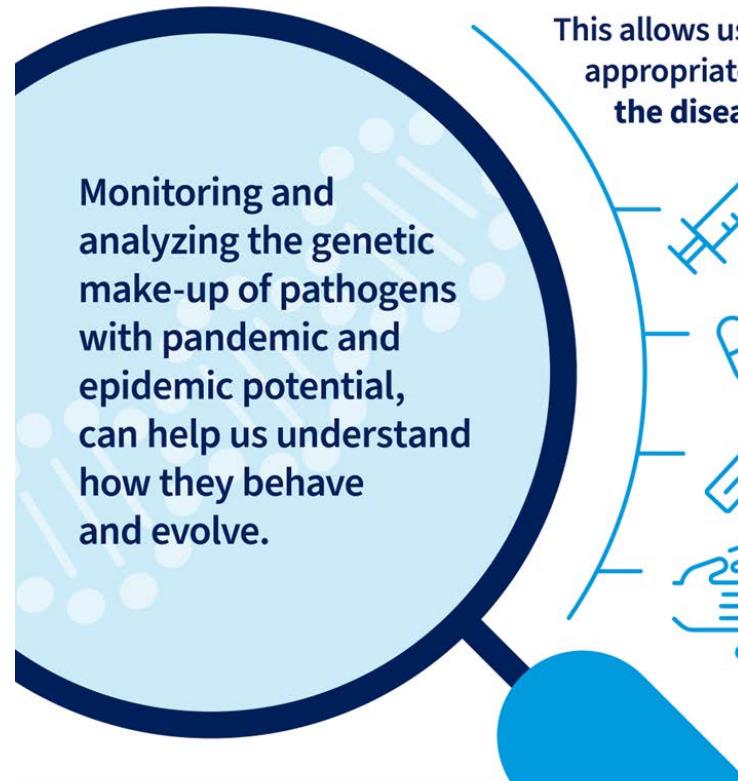
*observed in the period 1 October 2024 to 30 September 2025

<https://www.fao.org/>

What Predictive Systems Need

- Real-time sequencing & data sharing
- Wastewater + animal surveillance
- Computational modeling capacity
- Strong lab networks & BSL-3 capability
- Public communication channels

How can GENOMIC SURVEILLANCE help during a pandemic?



This allows us to develop appropriate tools to control the disease, such as:

- Vaccines
- Therapeutics
- Diagnostics
- Public health and social measures, like masks and handwashing

The Global Genomic Surveillance Strategy
for Pathogens with Pandemic and Epidemic Potential



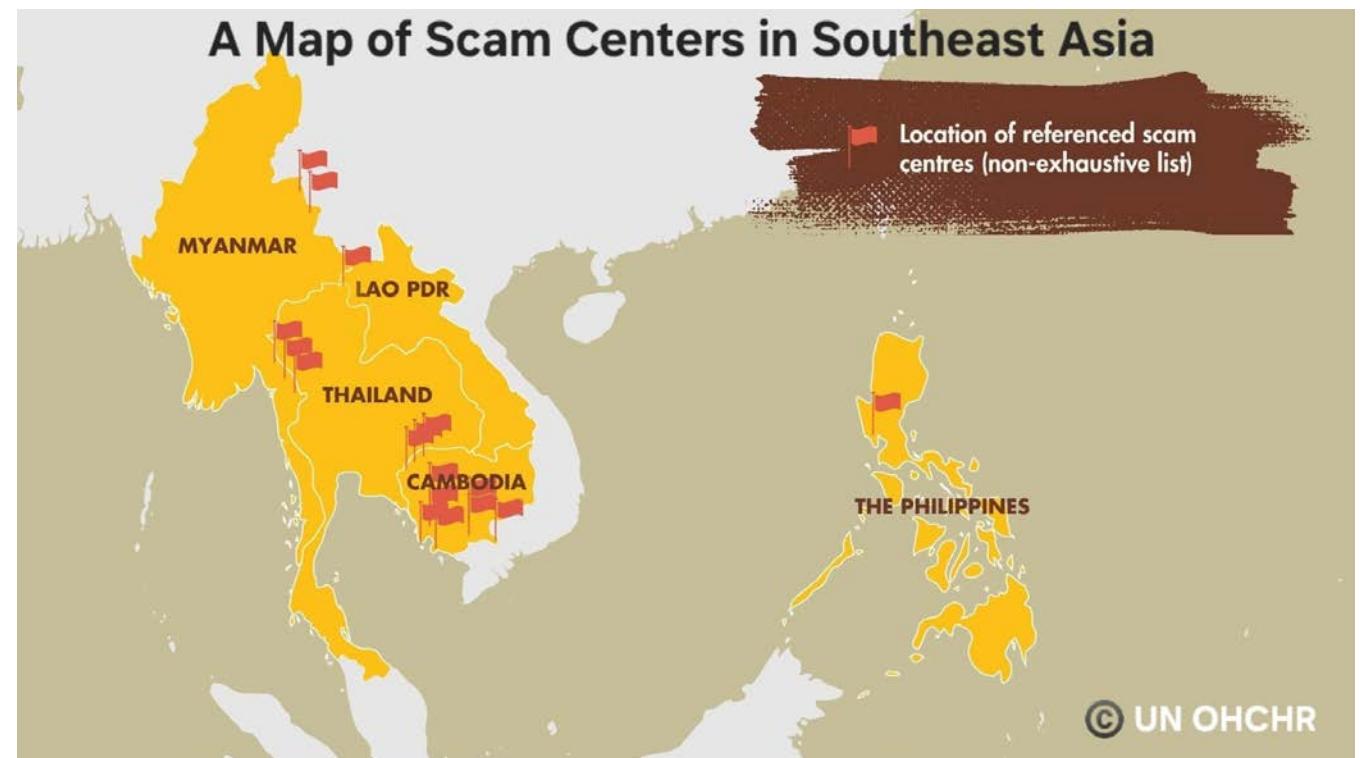
Global Genomic Surveillance Strategy

Target by 2032: every WHO Member State can rapidly sequence epidemic-risk pathogens and posts SARS-CoV-2 genomes to a public database, progress tracked by two WHO indicators.



Thailand & Southeast Asia Context

- Zoonotic hotspot
- Aquaculture, poultry, wet markets
- Cross-border migration & tourism
- **Opportunity:** build regional viral observatories



Pathogen genomic surveillance status among lower resource settings in Asia

Key barriers identified include:

- Reliance on external funding
- Supply chain challenges
- Shortages of trained personnel
- Limited quality assurance mechanisms



Genomic Surveillance in Thailand

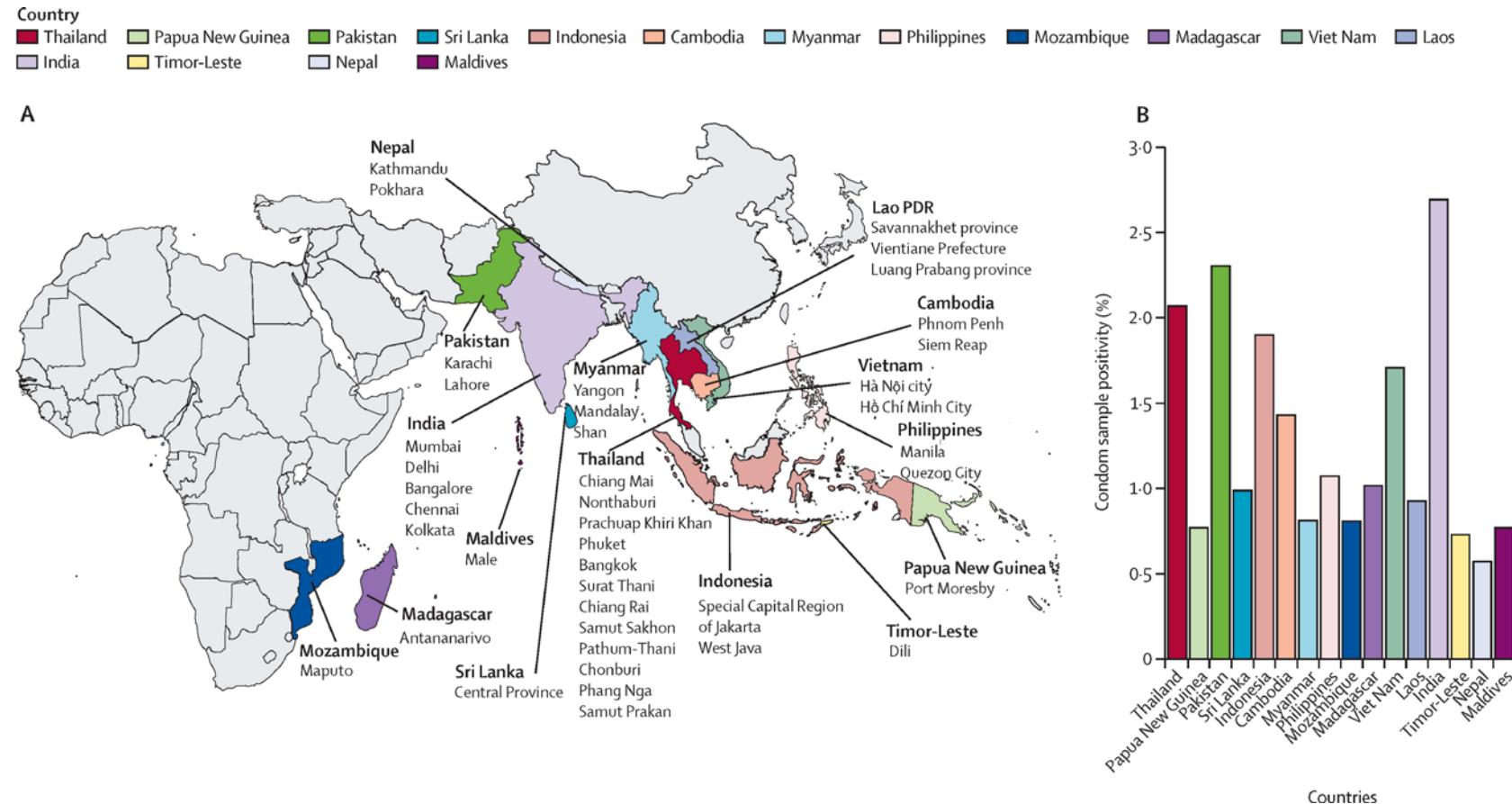
Thailand's Genomic Surveillance Strengths

- National sequencing network led by universities & MOPH
- Strong virology capacity (Mahidol, Chula, BIOTEC, Bamrasnaradura, AFRIMS)
- Proven real-time sequencing during COVID-19
- BSL-3 capabilities supporting high-risk pathogen work
- Active contributors to global platforms (e.g., GISAID)

Innovative Surveillance: Mpox Surveillance Using Discarded Condoms

Wannigama DL, Werawatte WKCP, et al. Lancet Infect Dis. 2024

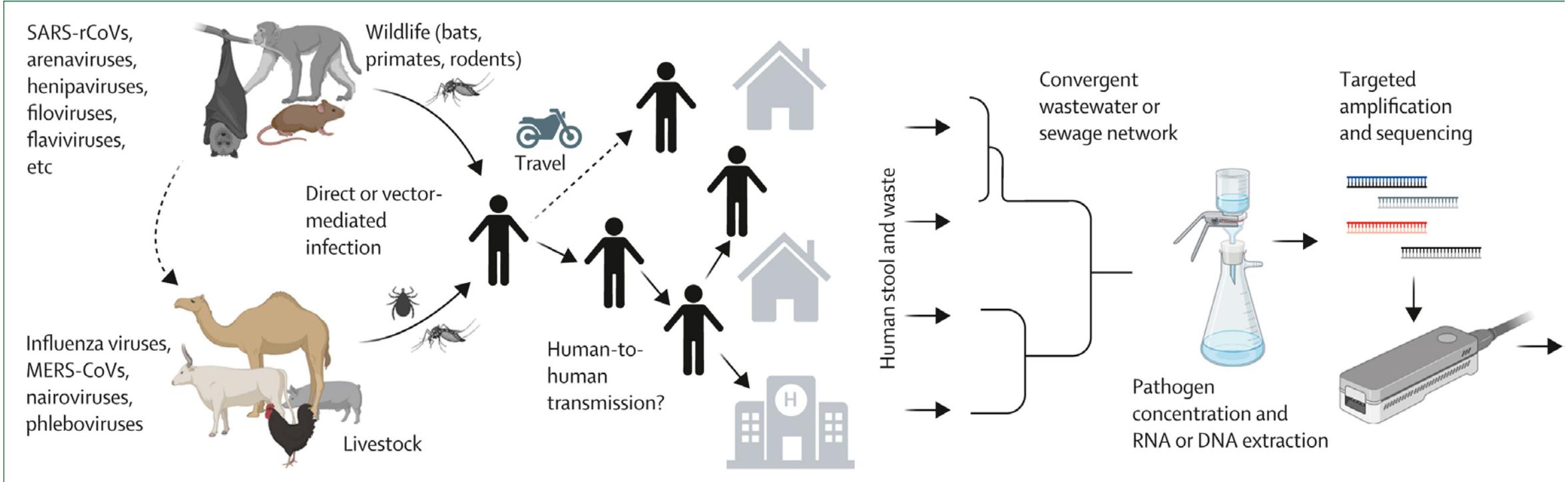
- Discarded condoms are a viable environmental sample
- Cost-effective and scalable for low-resource communities
- Provides early-warning signals



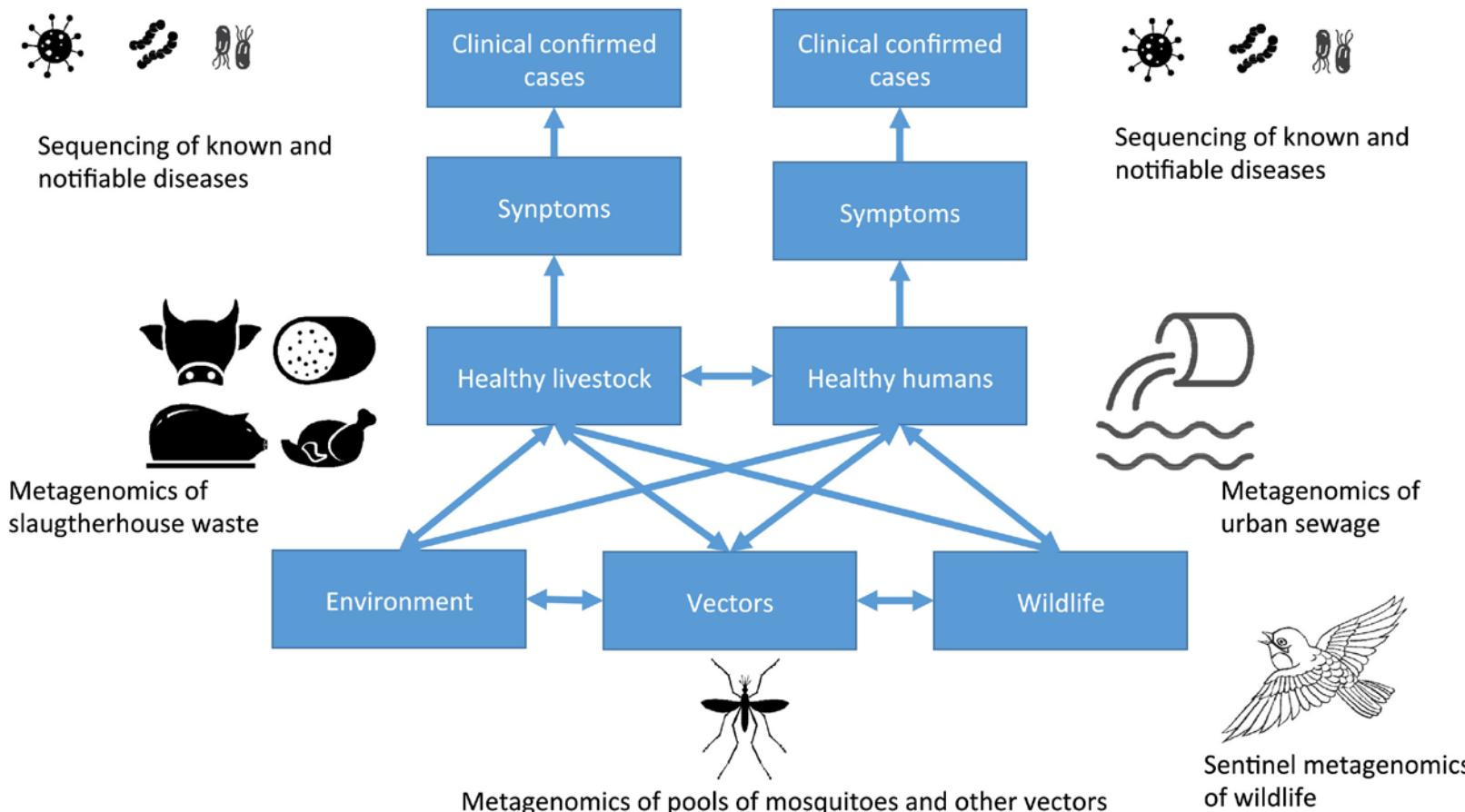
Innovative Surveillance:

Global wastewater surveillance

- Wastewater surveillance (WWPS) can detect early circulation
- WWPS is a promising early-warning tool for emerging infectious diseases

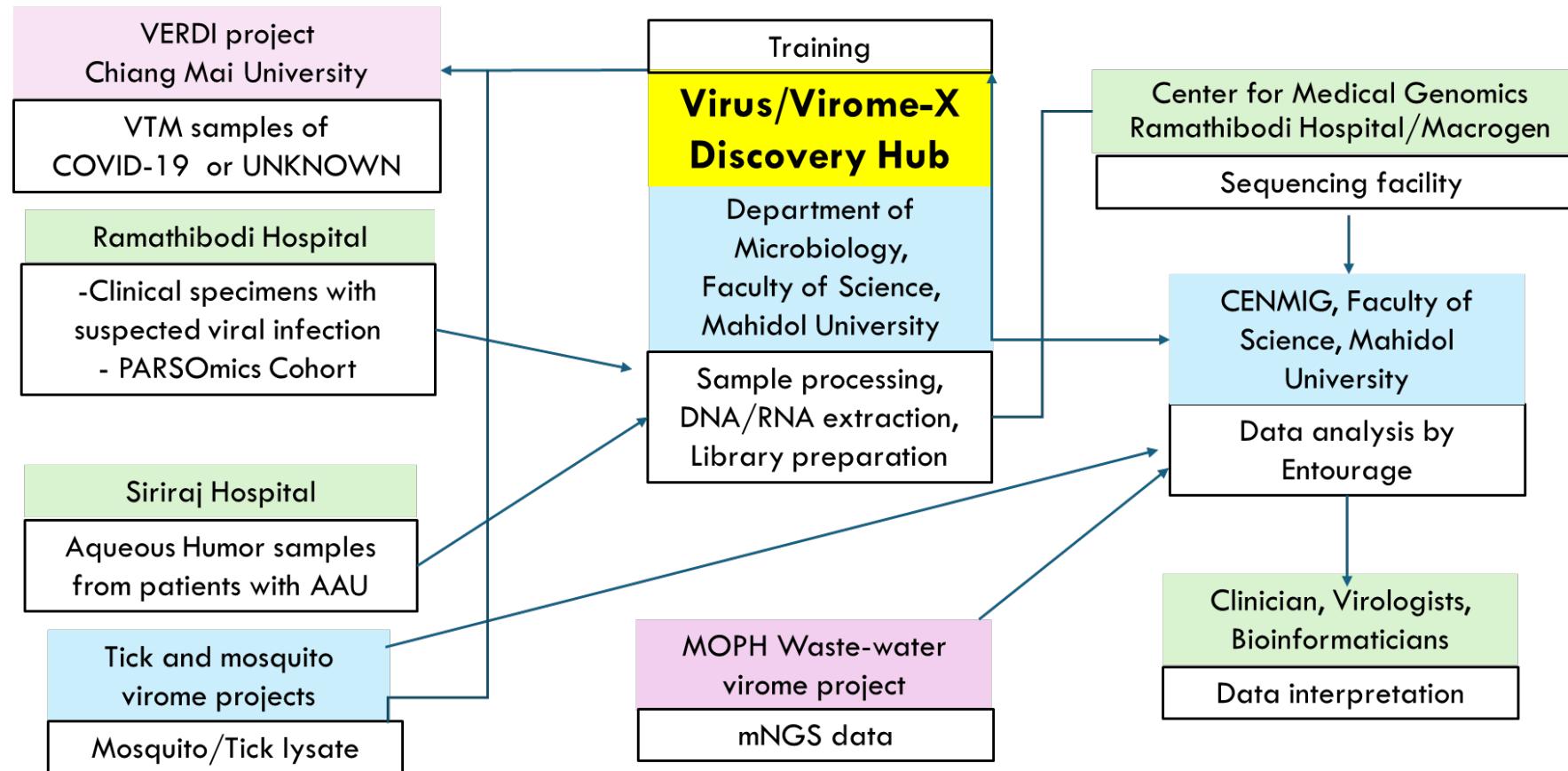


The need for One Health surveillance



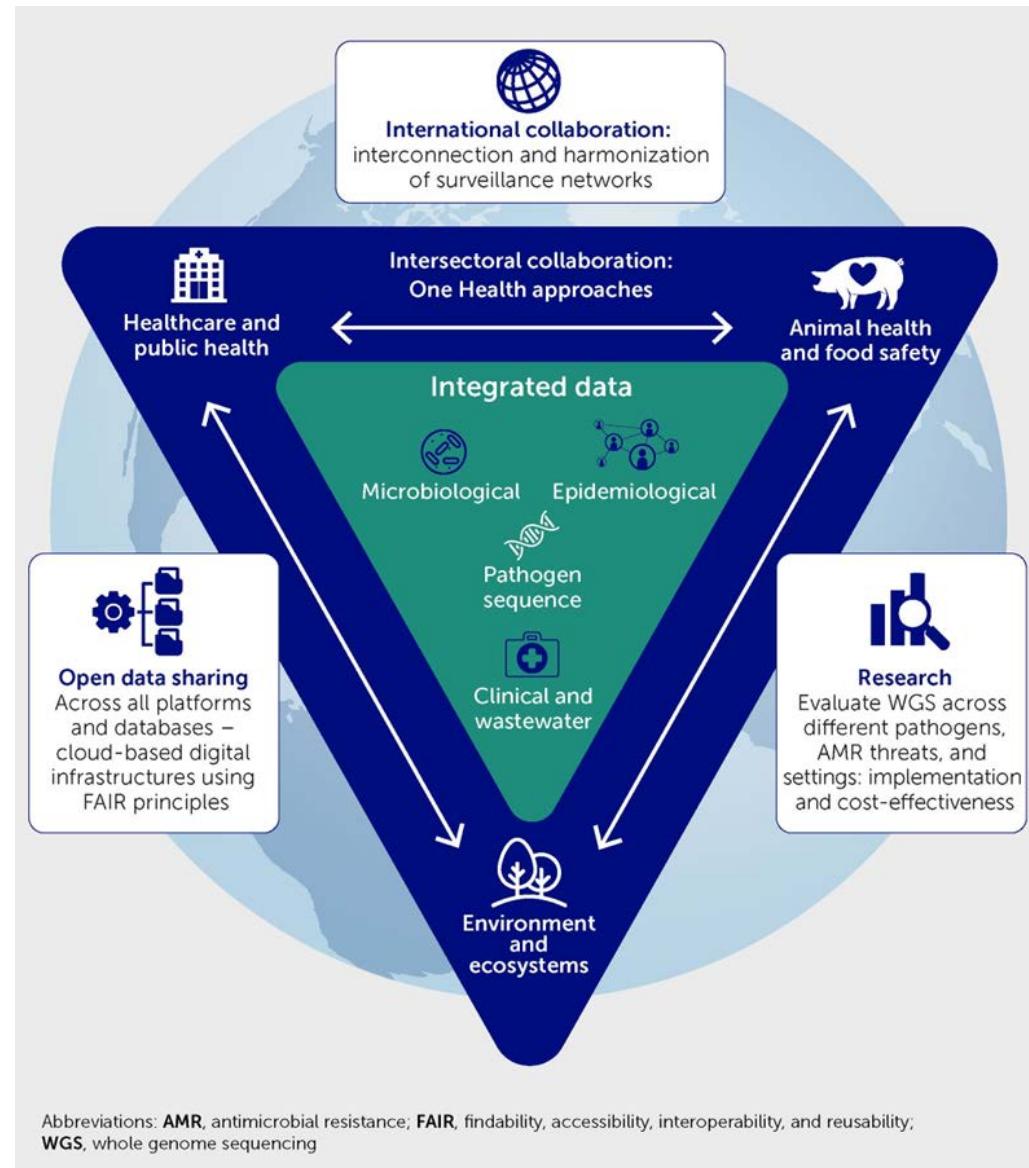
Collaborative network

Virus/Virome-X project



Challenges to Strengthen

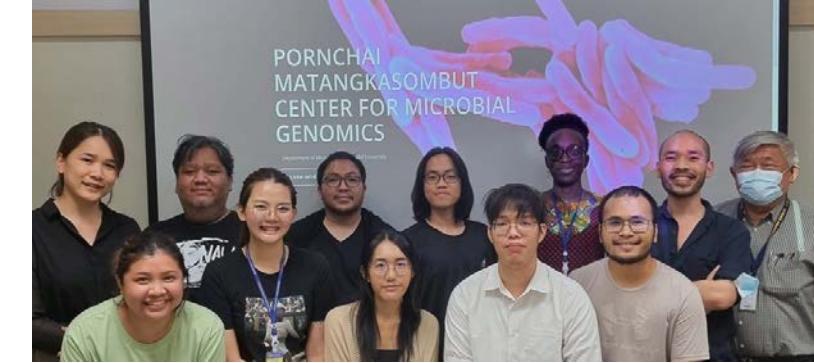
- Expand sequencing beyond major centers → regional labs
- Real-time data pipelines and automated bioinformatics
- Sustainable funding & workforce training
- Data sharing protocols across public health and agriculture
- Integration with One Health intelligence (environment + veterinary + human)



Acknowledgment



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