

# COVID-19 through a One Health Lens: The Wonders of Wildlife and Wilderness



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FROM THE AMERICAN PEOPLE



**UC DAVIS**  
One Health Institute  
School of Veterinary Medicine



**SEA HUN**  
Southeast Asia One Health  
University Network



Ata Health Strategies



**Berkeley**  
UNIVERSITY OF CALIFORNIA



**UCI** University of  
California, Irvine

# USAID One Health Workforce – Next Generation Project 2019-2024

## AFROHUN

AFRICA ONE HEALTH UNIVERSITY NETWORK



## SEAOHUN

SOUTHEAST ASIA ONE HEALTH UNIVERSITY  
NETWORK



# USAID PREDICT Project 2009-2020

# We are a globally-connected society...



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**EcoHealth  
Alliance**



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**We start, and end, in communities...**













# What is risk?



**EXPOSURES → OUTCOMES**



**What kind of wildlife do we live with?**





# One Health Approach





# ENDANGERED POLLINATORS



# AND THEIR HABITATS

Art by Carol Schwartz



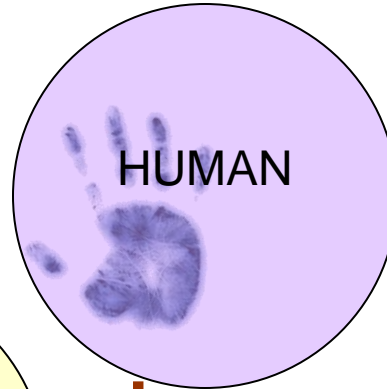
# Bats and Mosquito Control



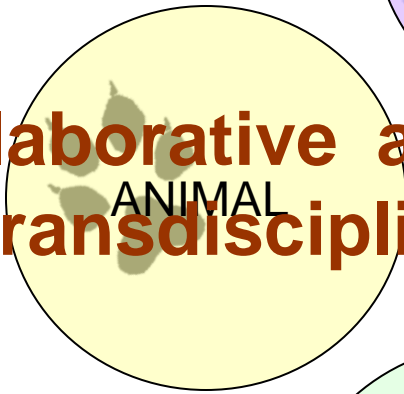
# One Health



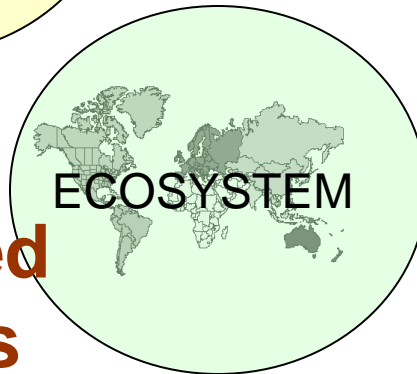
**Holistic**



**Collaborative and  
transdisciplinary**



**Focused on  
integrated  
solutions**





# One Health



<http://www.cdc.gov/onehealth>

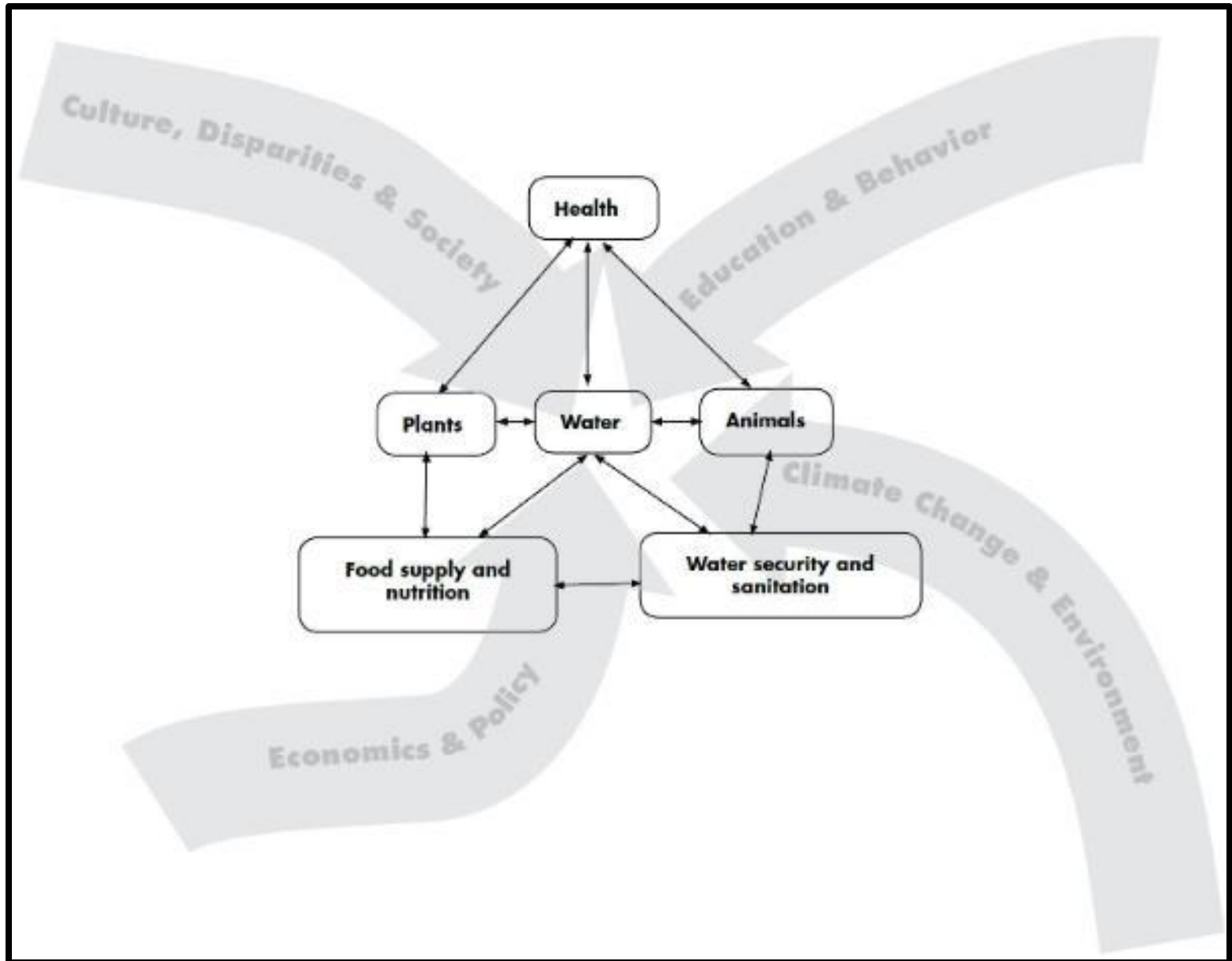
The collaborative efforts of multiple disciplines working locally, nationally and globally to attain optimal health for people, animal and our environment

(FAO, OIE, WHO, WB...)

## From theoretical to operational definition:

“One Health” can be defined as the ***added value*** in terms of ***lives*** of animals and humans ***saved, financial savings and improved ecosystem services*** from a ***closer cooperation of human and animal health*** as compared to single sector approaches (Zinsstag et al., 2012)

# One Health Framework





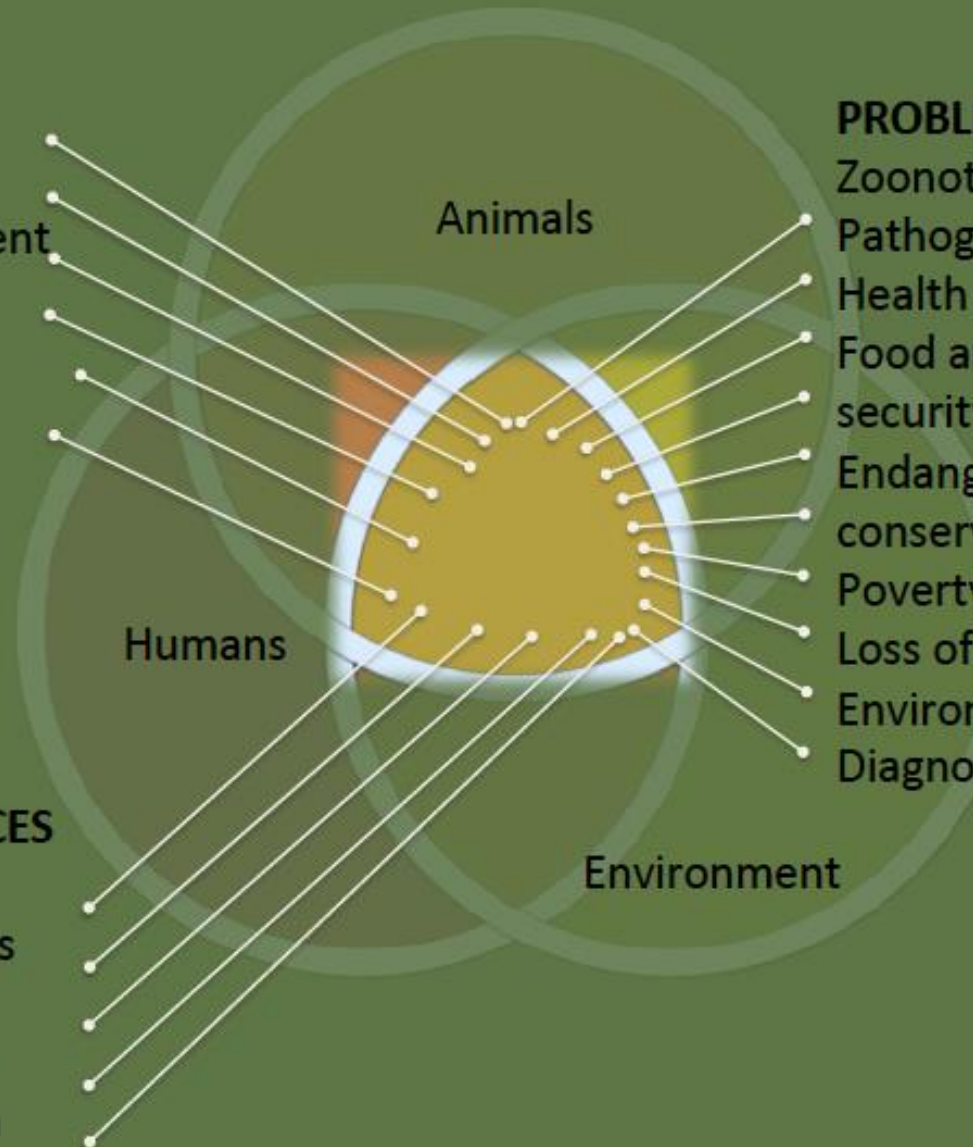
# Transdisciplinary Problems

## DRIVERS

- Land use
- Climate change
- Economic development
- Globalization
- Energy extraction
- Migration

## INFLUENCES

- Culture
- Economics
- Policy
- Behavior
- Education



## PROBLEMS

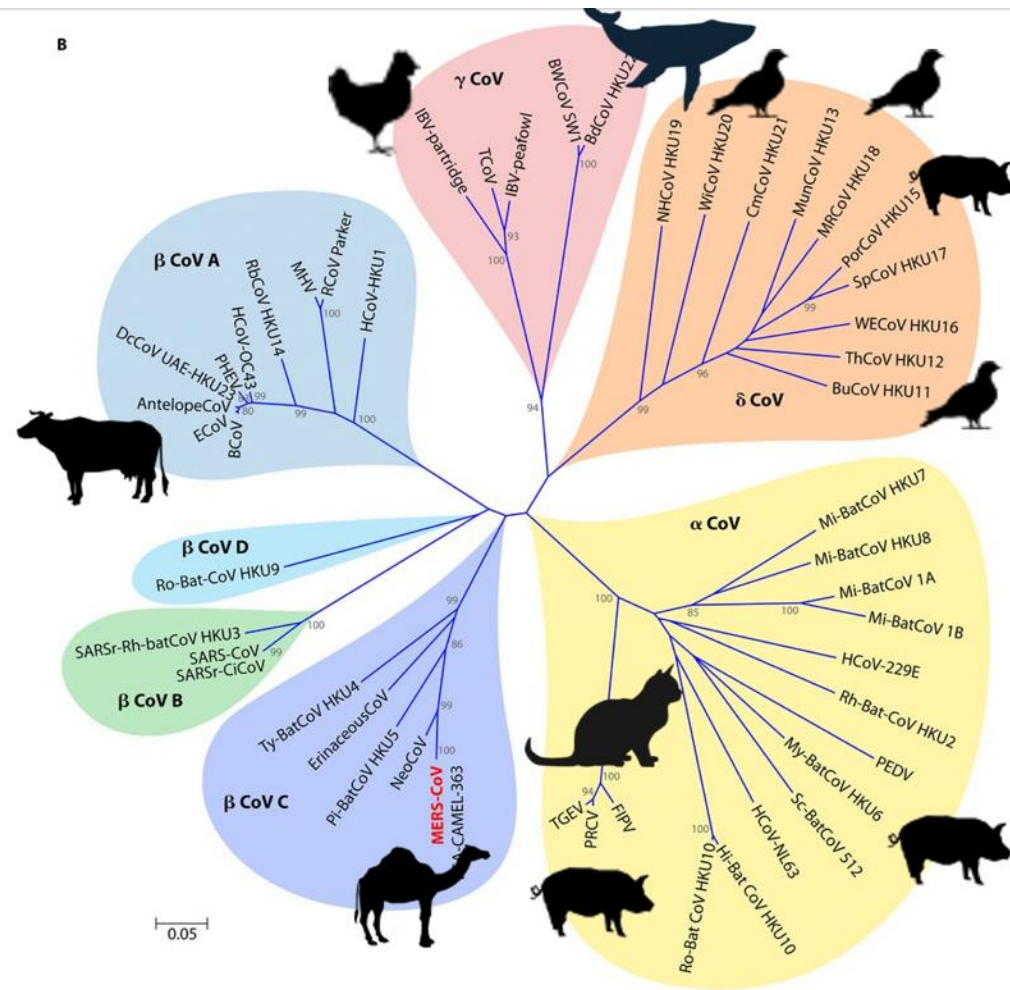
- Zoonotic disease emergence
- Pathogen distribution
- Health disparities
- Food and water safety & security
- Endangered species & habitat conservation
- Poverty alleviation
- Loss of biodiversity
- Environmental contamination
- Diagnostic limitations

# Coronaviruses are Global

Global distribution evidence of multi-species infection and host-jumping

## MAJOR ANIMAL PATHOGENS

- Pigs – Transmissible gastroenteritis virus, Porcine epidemic diarrheal virus
- Cats – Feline Infectious Peritonitis virus (antiviral GS-441524)
- Chickens – Infectious bronchitis virus
- Cattle – Bovine coronavirus complex
- Many other species...





# Coronaviruses are Global

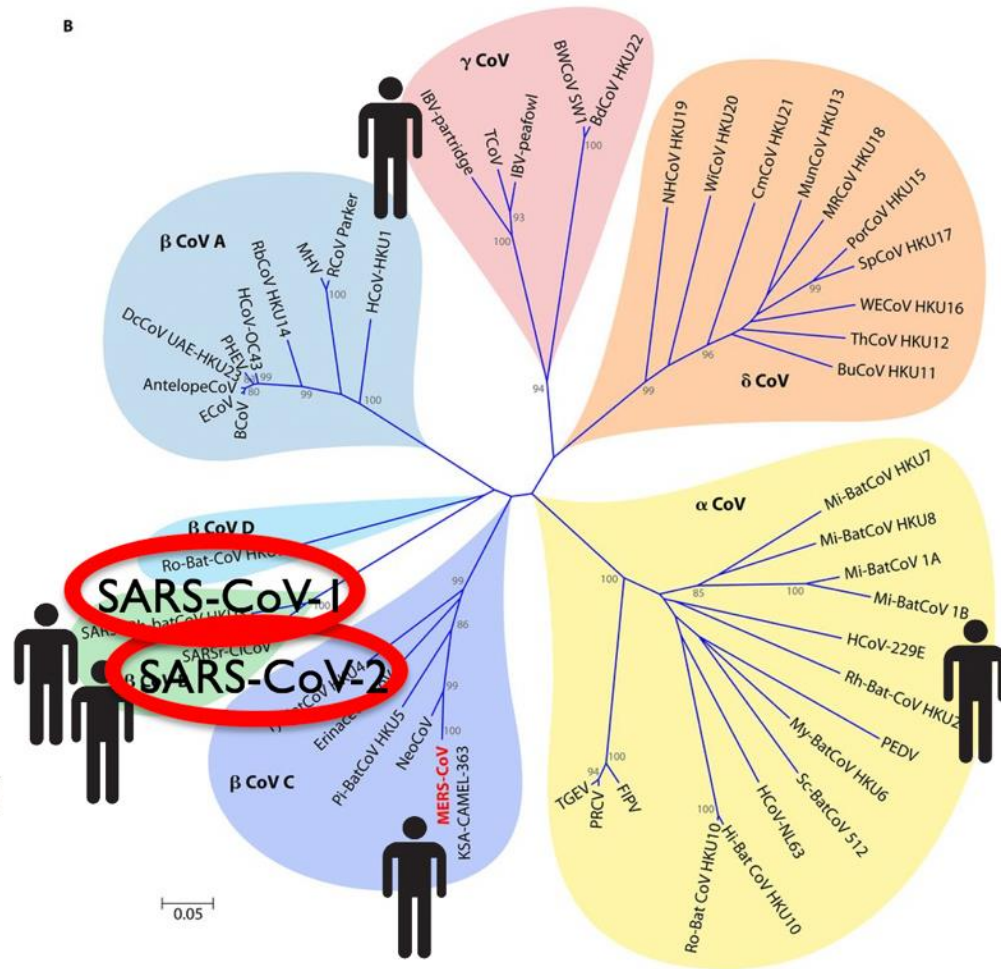
## Global distribution evidence of multi-species infection and host-jumping

## HUMANS

- $\alpha/\beta 1$  Several mild respiratory viruses
- $\beta 2b$  2003 SARS-CoV-1 (bats, civet cats, ?)
- $\beta 2b$  2012 MERS-CoV (bats, camels)
- $\beta 2b$  2019 SARS-CoV-2/COVID19 (bats?, ??)

**Unknown if SARS-CoV2 can infect and cause disease other domesticated species**

***Recommended that persons sick should avoid contact with pets and other domesticated animals***

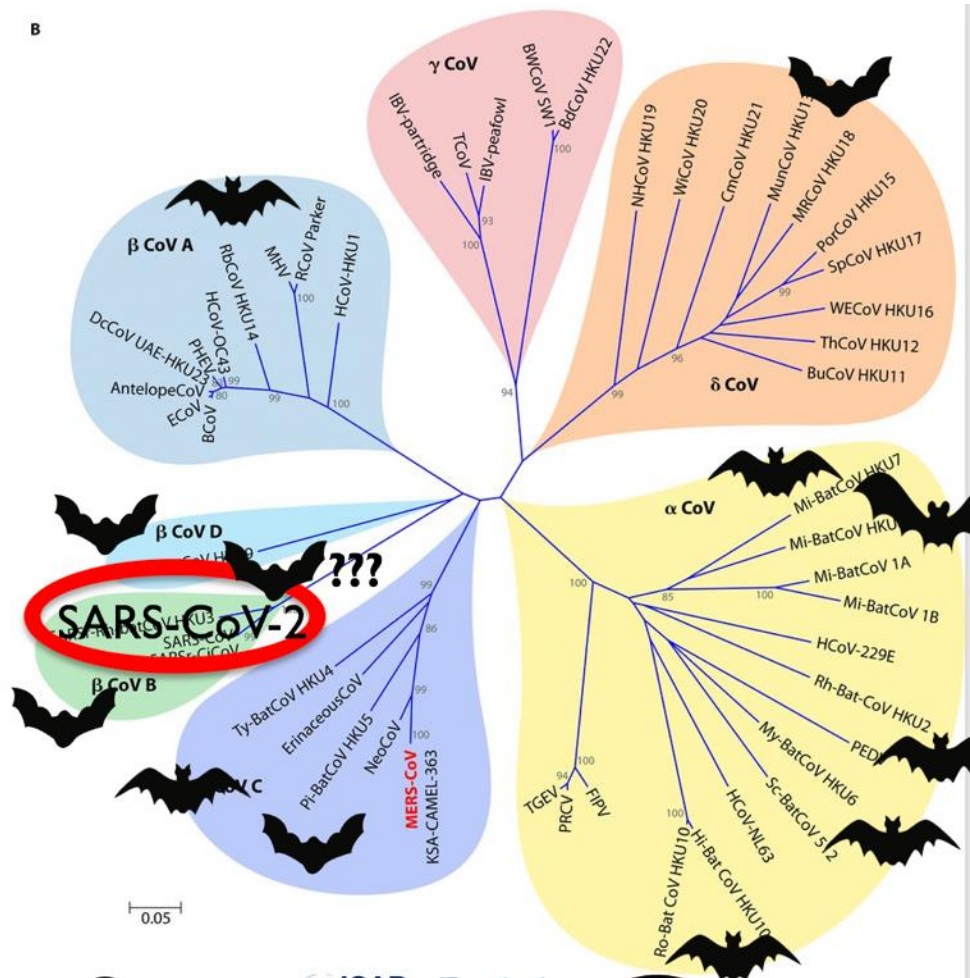


# Coronaviruses are Global

## Bats have the largest number of known coronaviruses

- SARS-CoV-2 may be bat-borne but that is not yet known

Spillover of many emerging viruses from wildlife to people is driven by bat and human contact (bushmeat, guano harvesting, land use change)





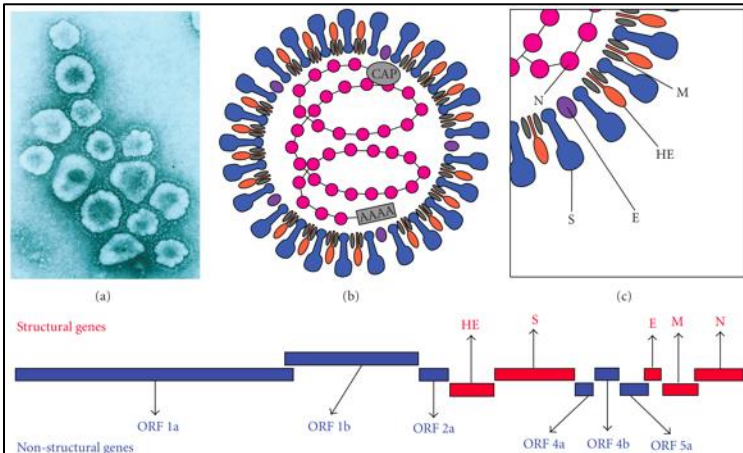


HOST

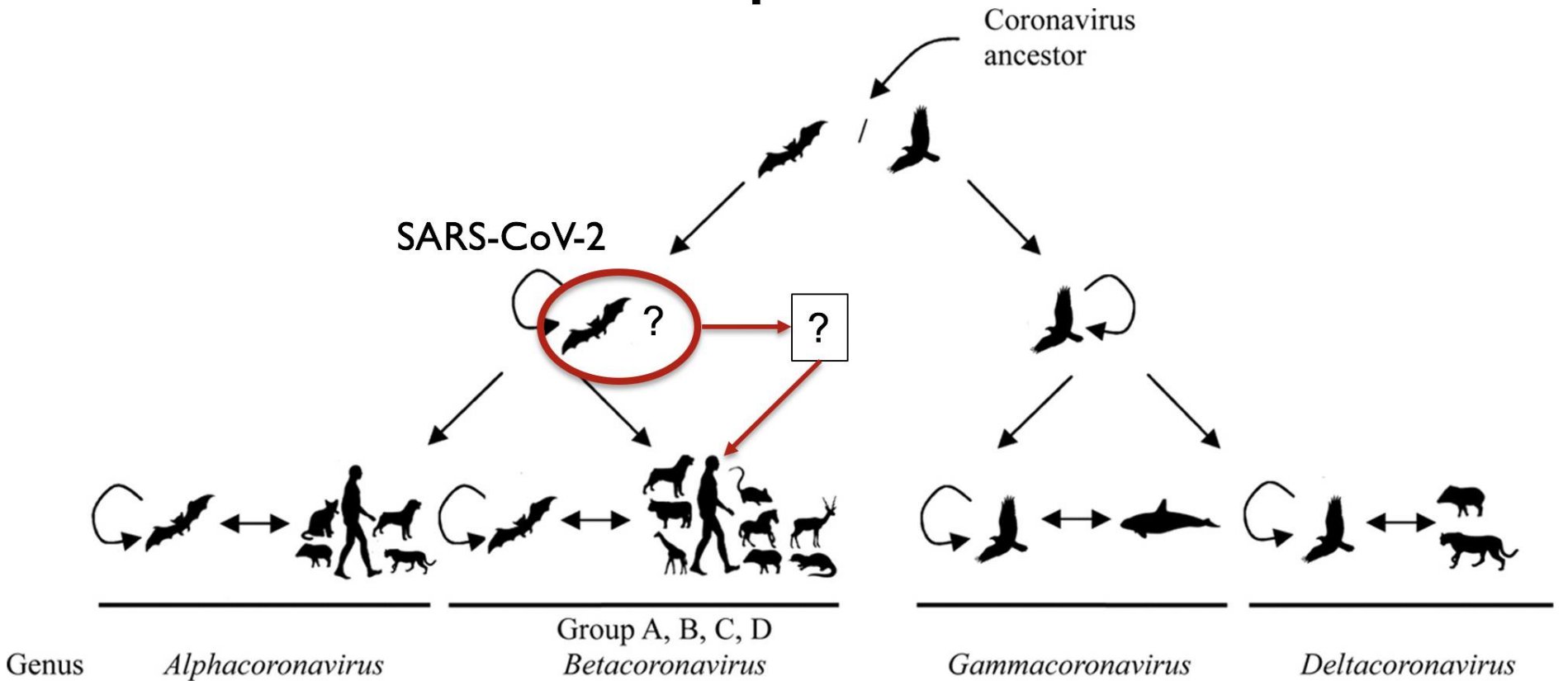
DISEASE?

PATHOGEN

ENVIRONMENT



# Coronavirus Evolution and Spillover

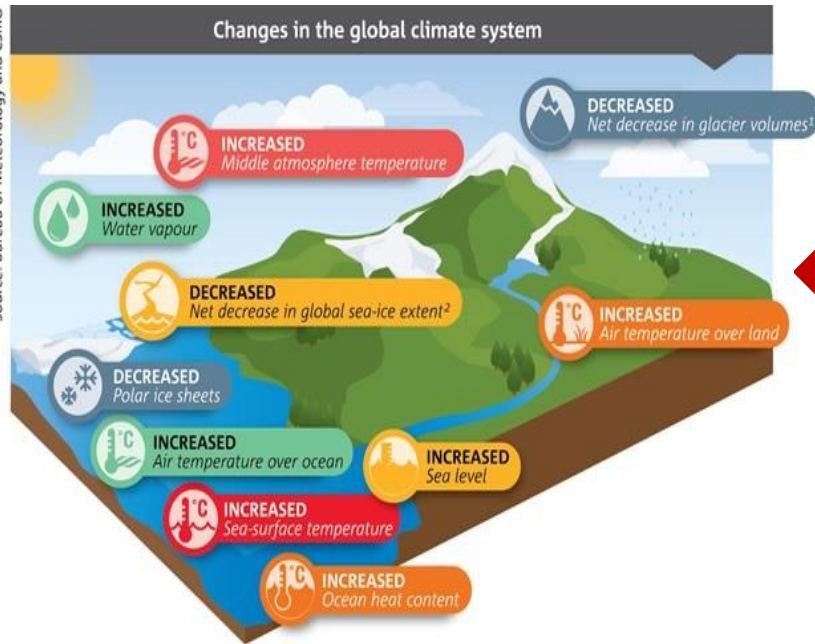


Patrick C. Y. Woo et al. *J. Virol.* 2012; doi:10.1128/JVI.06540-11



# Land use change & population density drive viral spillover events...

## Climate



## Population Growth



# Drivers in Emerging Infectious Diseases



**Globalization**

**Changing Ecosystems**

**Human Demographics & Behavior**

**Markets & Trade**

**Migration & Conflict**

**Poverty & Social Inequality**

**Microbial Adaptation**

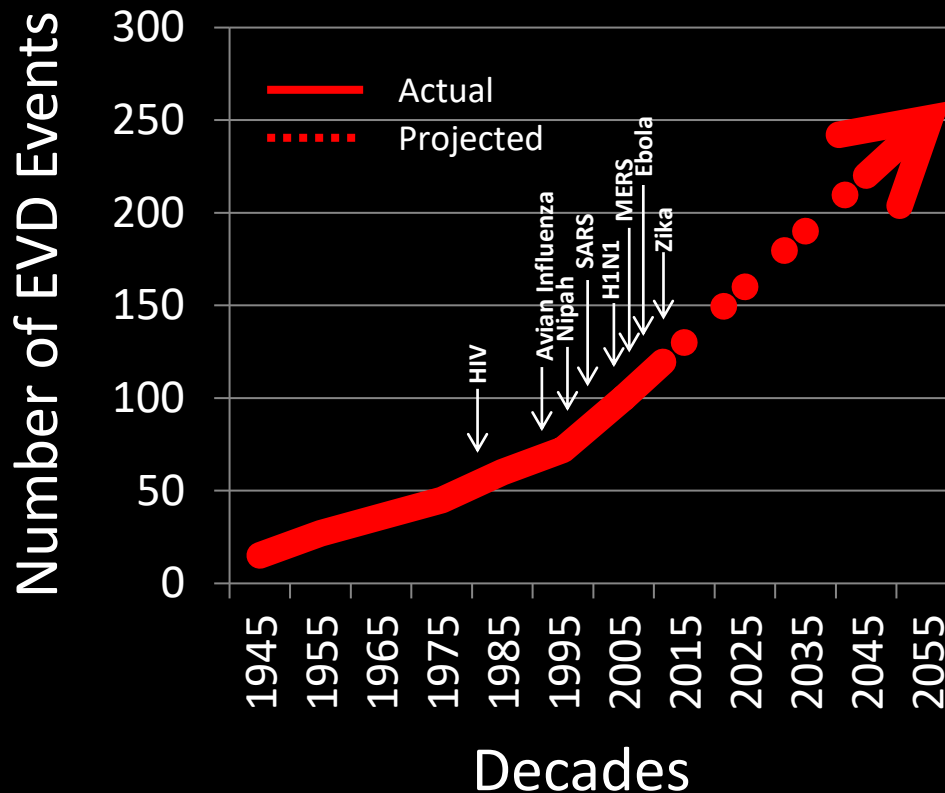
**and more...**



# Global travel & trade can turn local epidemics into pandemics



# The threat from emerging viruses is increasing



Each year, approx. **3 new Viral Diseases** emerge

Driven by

- Population expansion (1.6 billion in 1900 to 11.5 billion people in 2100)
- Increased encroachment into wildlife habitat which accelerates the “spillover” from wildlife to humans





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*One Health Institute*

# PREDICT



**EcoHealth Alliance**



**METABIOTA**



Smithsonian  
Institution

**The Ministries of Health, Agriculture & Environment and  
Implementing University and NGO Partners in 35 Countries**



**THE CENTER FOR  
INFECTION AND IMMUNITY**  
**COLUMBIA UNIVERSITY**  
IN THE CITY OF NEW YORK



**HealthMap**  
Global Health, Local Information



**ProMED**  
mail



**UCSF**

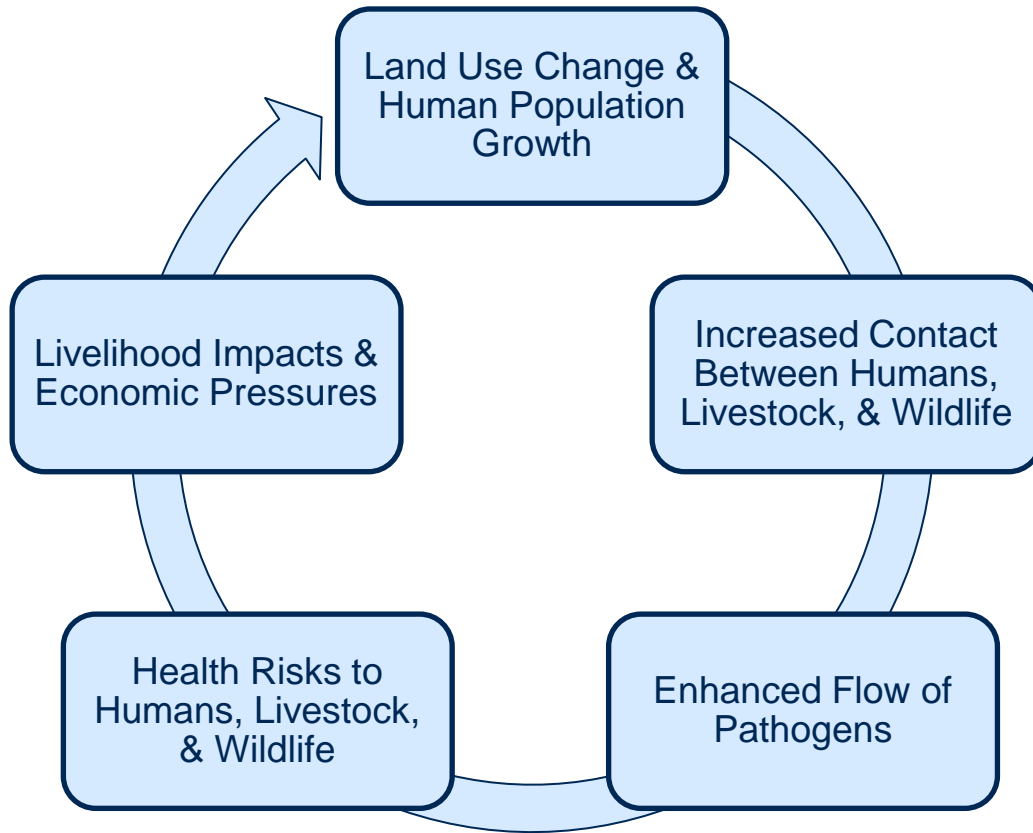


**UCDAVIS**

**VETERINARY MEDICINE**

*One Health Institute*

# One Health Interface



- Majority of emerging infectious diseases (EIDs) in people are of animal origin (zoonotic)
- 75% of emerging zoonoses have wildlife origins
- Human activities at the interface linked to EIDs (Nipah virus, SARS, Ebola)
- Annual population growth among highest in buffers to protected areas near wildlife



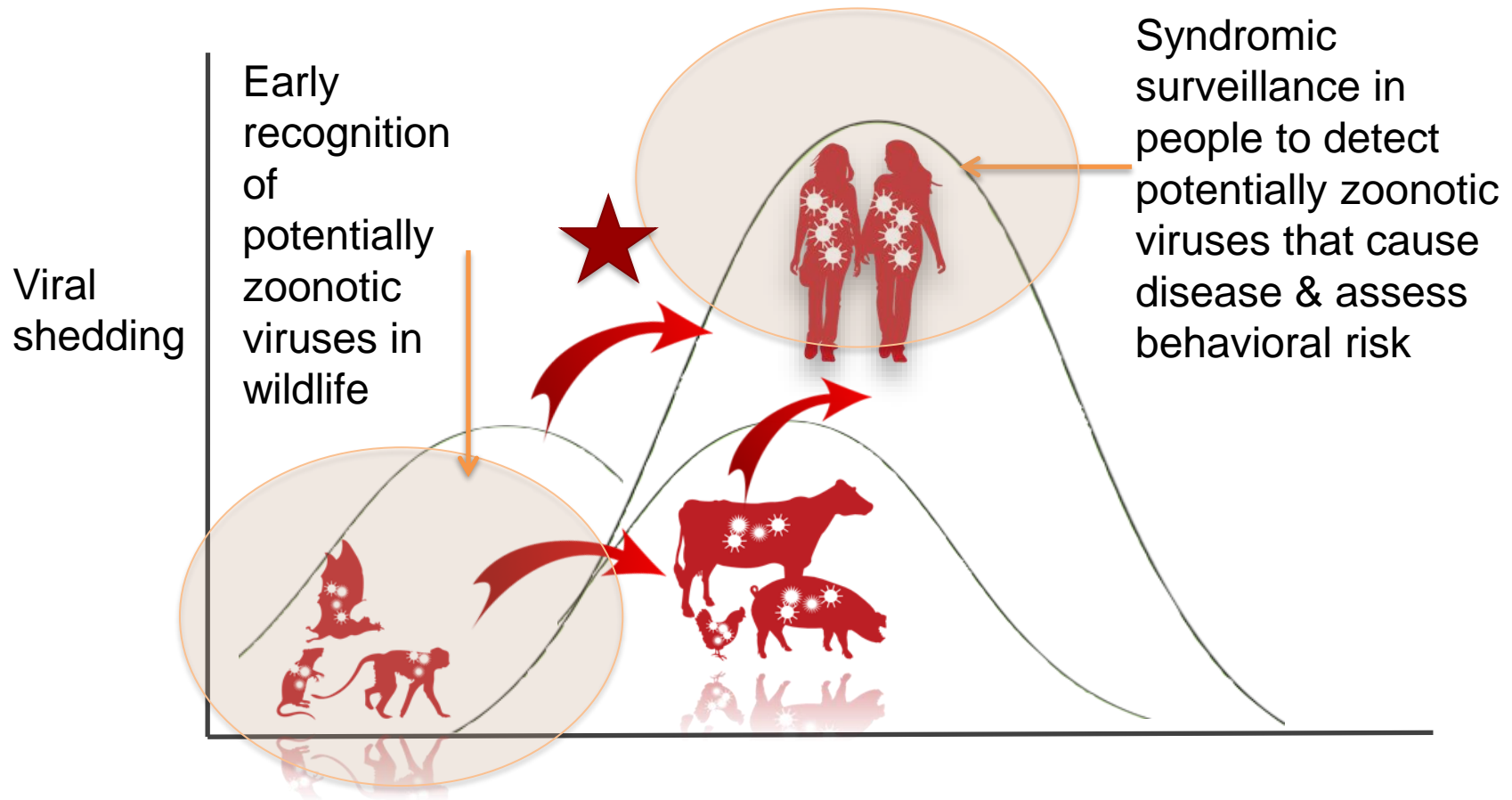
# Targeted, Risk-based Surveillance

- **Primates**
- **Bats**
- **Rodents**
- **Birds**
- **Suids**
- **Carnivores**
- **Ungulates**



# PREDICT Surveillance Strategy

*Target = zoonotic viruses that causes disease in animals & people*





# High Risk Interfaces



# Bat Guano Farms



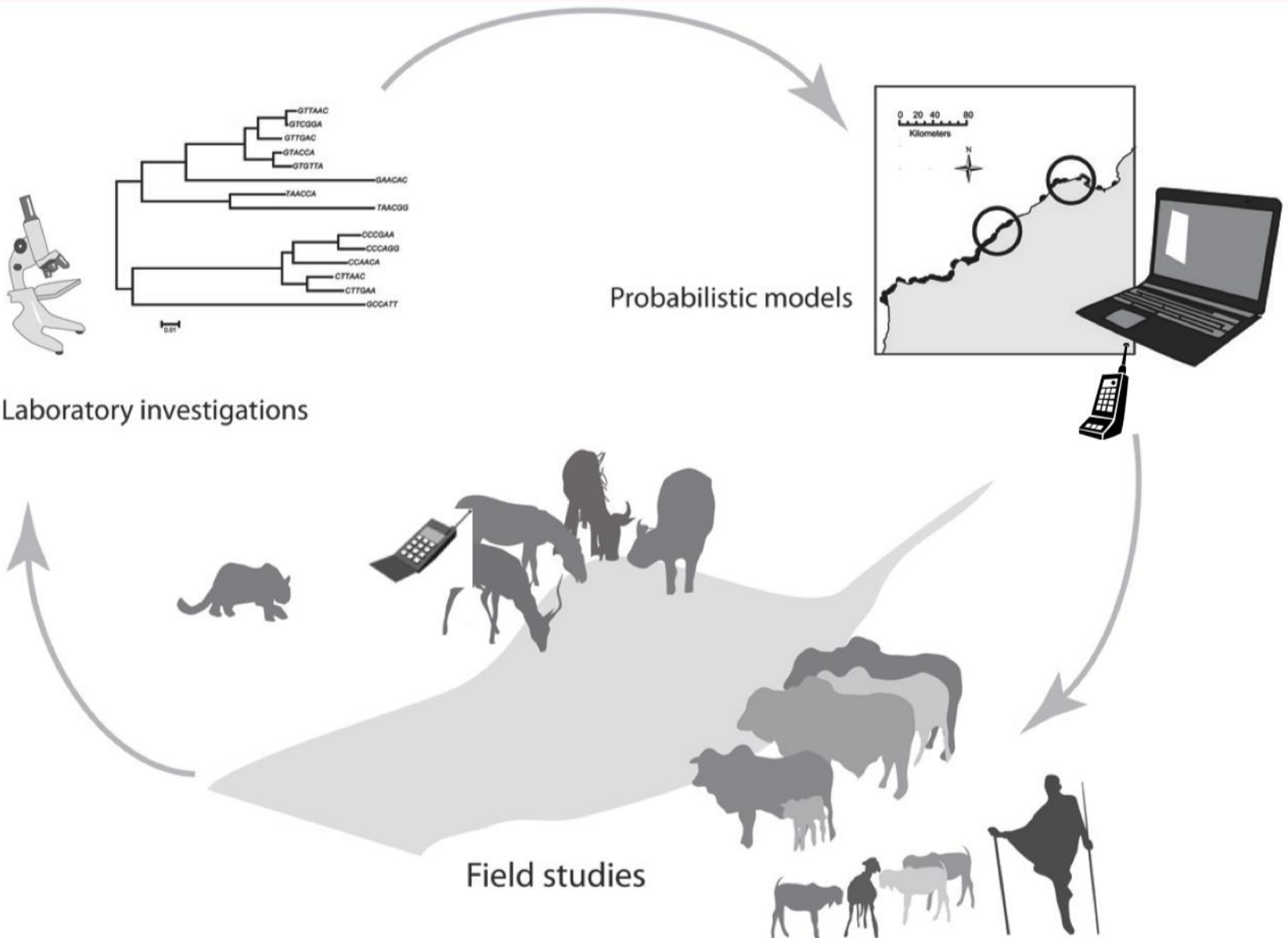
Vietnam, Cambodia & Thailand





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# PREDICT



# Developed & Operationalized Diagnostic Platform



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**PREDICT**

ONE HEALTH  
**OneUCDAVIS**

# PREDICT OVERVIEW



**DEVELOPED** the One Health Workforce by training more than 6,000 people in over 30 countries.



**STRENGTHENED** laboratory systems and zoonotic disease detection capabilities in over 60 labs around the world.



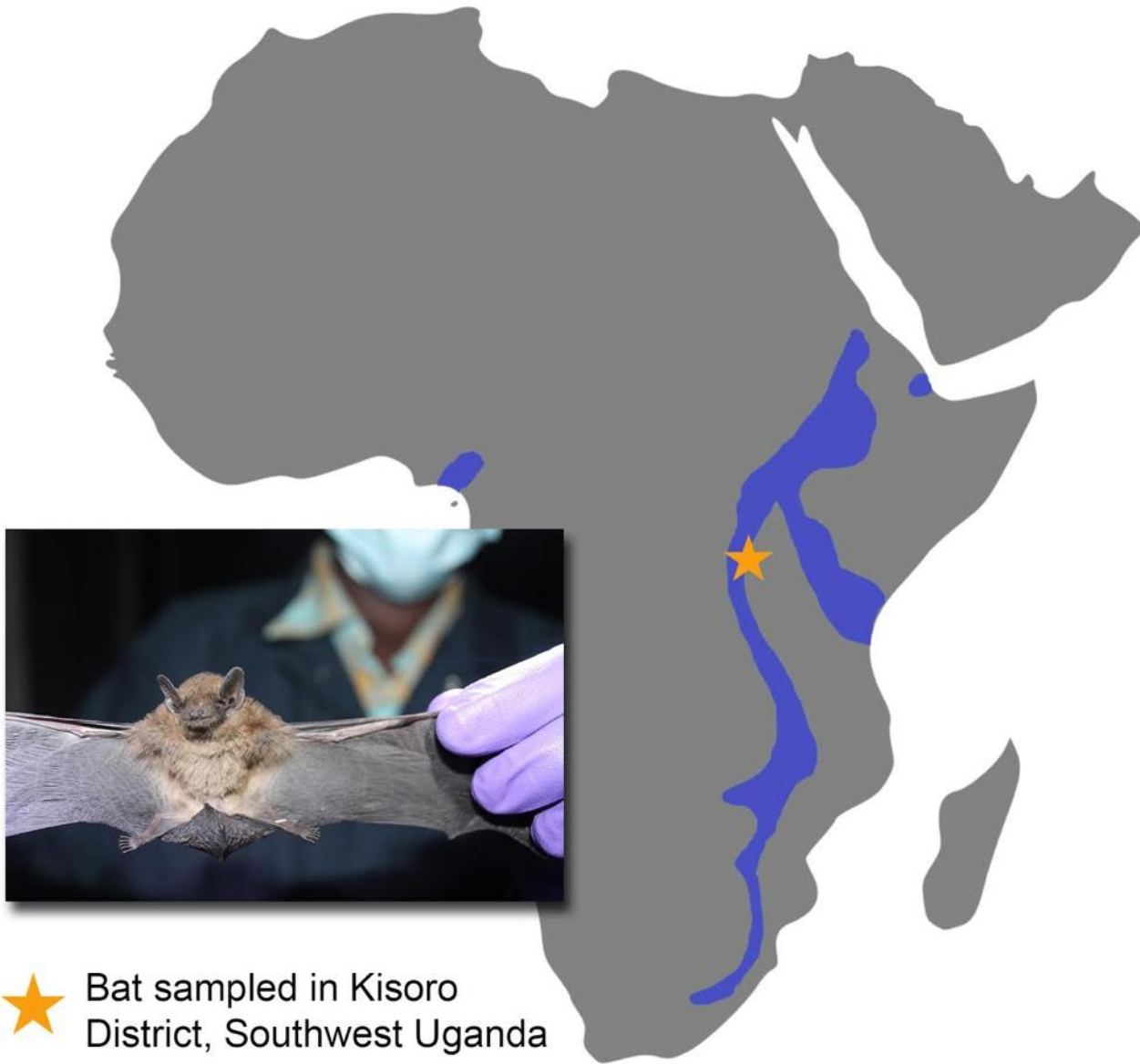
**OPERATIONALIZED** One Health surveillance and sampled over 163K animals and people, helping minimize the spillover of zoonotic disease threats from animals into human populations.



**DETECTED** over 1,100 unique viruses, including zoonotic diseases of public health concern such as Bombali ebolavirus, Zaire ebolavirus, Marburg virus, and MERS- and SARS-like coronaviruses.



# Novel MERS-like Corona Virus from Uganda



★ Bat sampled in Kisoro District, Southwest Uganda

● Distribution of *Pipistrellus hesperidus*

## Bats Are Natural Reservoirs of SARS-Like Coronaviruses

Wendong Li,<sup>1,2</sup> Zhengli Shi,<sup>2\*</sup> Meng Yu,<sup>3</sup> Wuze Ren,<sup>2</sup> Craig Smith,<sup>4</sup> Jonathan H. Epstein,<sup>5</sup> Hanzhong Wang,<sup>2</sup> Gary Cramer,<sup>3</sup> Zhihong Hu,<sup>2</sup> Huajun Zhang,<sup>2</sup> Jianhong Zhang,<sup>2</sup> Jennifer McEachern,<sup>3</sup> Hume Field,<sup>4</sup> Peter Daszak,<sup>5</sup> Bryan T. Eaton,<sup>3</sup> Shuyi Zhang,<sup>1,6\*</sup> Lin-Fa Wang<sup>3\*</sup>

Severe acute respiratory syndrome (SARS) emerged in 2002 to 2003 in southern China. The origin of its etiological agent, the SARS coronavirus (SARS-CoV), remains elusive. Here we report that species of bats are a natural host of coronaviruses closely related to those responsible for the SARS outbreak. These viruses, termed SARS-like coronaviruses (SL-CoV), display greater genetic variation than SARS-CoV isolated from humans or from civets. The human and civet isolates of SARS-CoV nestle phylogenetically within the spectrum of SL-CoVs, indicating that the virus responsible for the SARS outbreak was a member of this coronavirus group.

survey bats in the search for the natural reservoir of SARS-CoV.

In this study, conducted from March to December of 2004, we sampled 408 bats representing nine species, six genera, and three families, from four locations in China (Guangdong, Guangxi, Hubei, and Tianjin) after trapping them in their native habitat (Table 1). Blood, fecal, and throat swabs were collected; serum samples and cDNA from fecal or throat samples were independently analyzed, double-blind, with different methods in Wuhan and Geelong (14).

Among six genera of bat species surveyed (*Rousettus*, *Cynopterus*, *Myotis*, *Rhinolophus*, *Nyctalus*, and *Miniopterus*), three communal, cave-dwelling species from the genus *Rhinolophus* (horseshoe bats) in the family *Rhinolophidae* demonstrated a high SARS-CoV antibody prevalence: 13 out of 46 bats (28%) in *R. pearsoni* from Guangxi, 2 out of 6 bats (33%) in *R. pusillus* from Guangxi; and 5 out



# COVID-19



## COVID-19 Dashboard

Total Confirmed

**12,169,400**

Confirmed Cases by  
Country/Region/Sovereignty

**3,105,315** US

**1,713,160** Brazil

**767,296** India

**706,240** Russia

**316,448** Peru

**306,216** Chile

**289,154** United Kingdom

**275,003** Mexico

**253,056** Spain

<https://coronavirus.jhu.edu/map.html>

Stage 3

Pandemic emergence

International travel and trade

- HIV/AIDS
- Severe acute respiratory syndrome

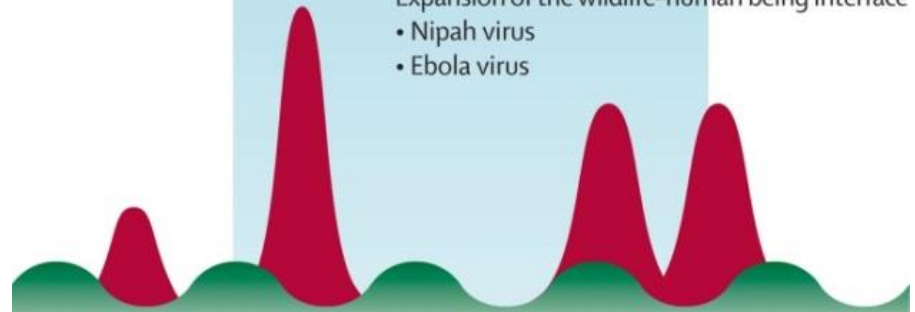


Stage 2

Localised emergence

Expansion of the wildlife–human being interface

- Nipah virus
- Ebola virus

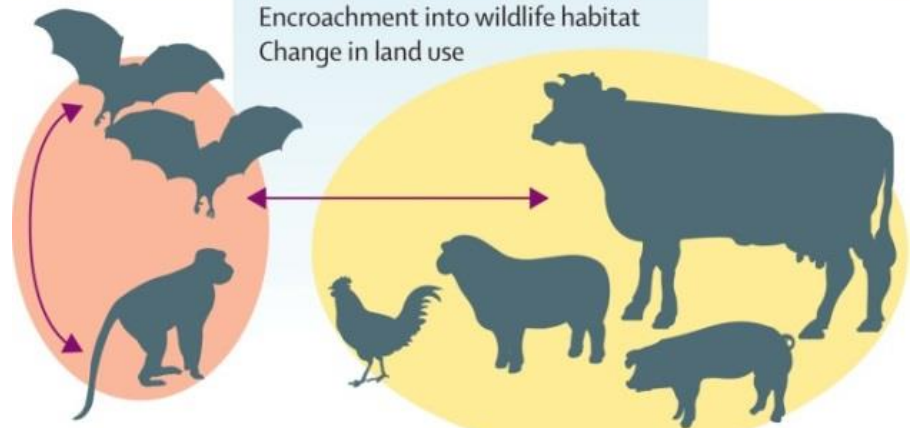


Stages of Emergence

Stage 1

Pre-emergence

Encroachment into wildlife habitat  
Change in land use





# COVID-19 Case Map – July 9, 2020



# COVID-19 What now?



Masks, Good Hygiene & Social  
Distancing



# Questions & Discussion



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