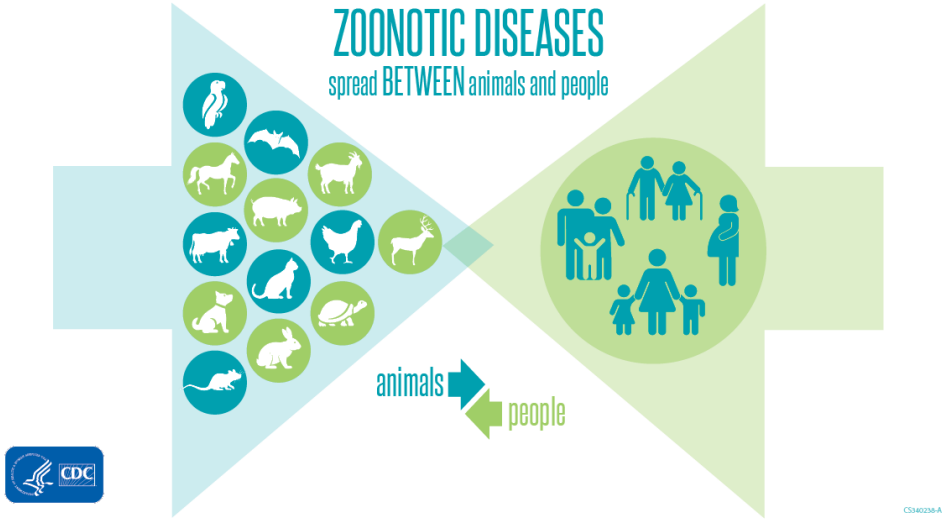
# Human impact on (emerging) infectious diseases – part 2

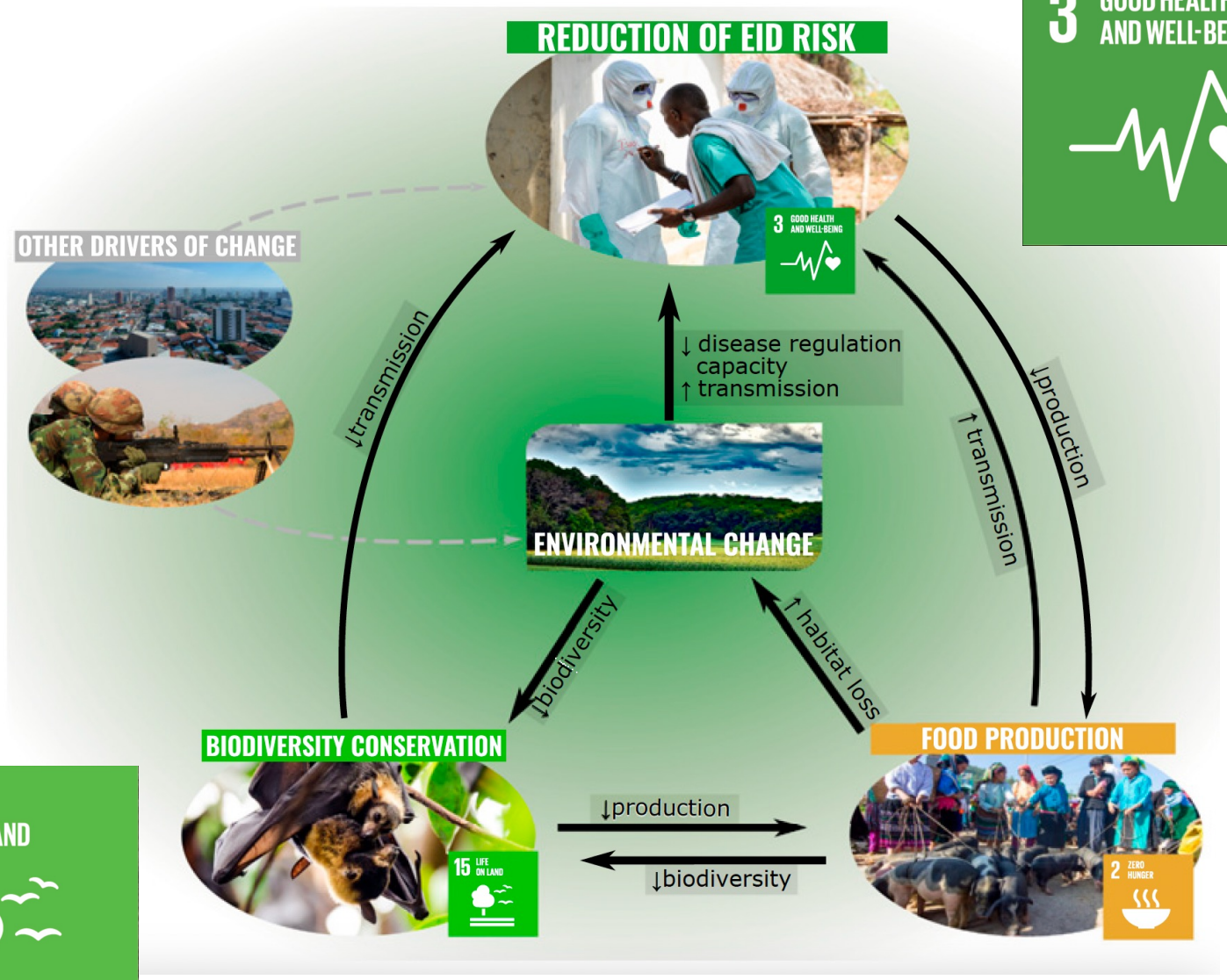
**Lecturer: Prof. Melanie Blokesch**

# Outline of today's lecture

1. **Emerging infectious diseases**
2. **Emerging viruses.**
3. **Specific examples – HIV, Ebola, Zika, Corona viruses.**



# Risk of EIDs in context of Sustainable Development Goals









Di Marco *et al.* (2020) *PNAS*

# Impacts of emerging infectious diseases (EIDs)

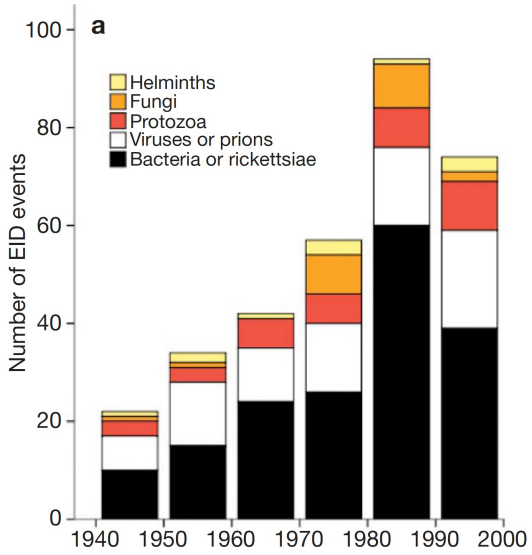
- Cause large-scale mortality and morbidity.
- Disrupt trade and travel networks.
- Stimulate civil unrest.
- Impact the economy => SARS outbreak in 2003, the H1N1 pandemic in 2009, and the West African Ebola outbreak in 2013–2016 each caused more than US $10 billion in economic damages.

**Disease emergence correlates with human population density and wildlife diversity, and is driven by anthropogenic changes such as deforestation and expansion of agricultural land (i.e., land-use change), intensification of livestock production, and increased hunting and trading of wildlife.**

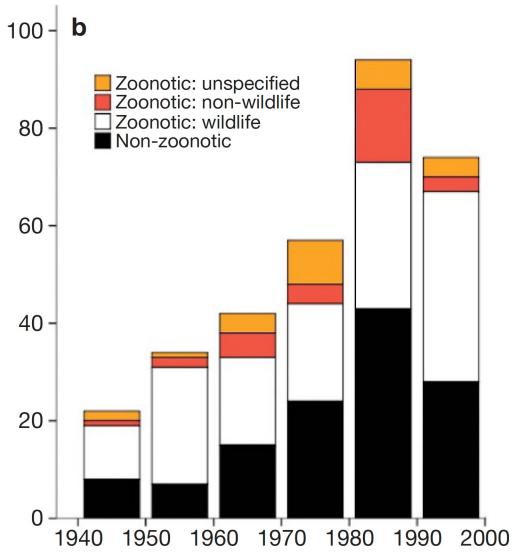
Di Marco *et al.* (2020) *PNAS*

# Global trends in EIDs

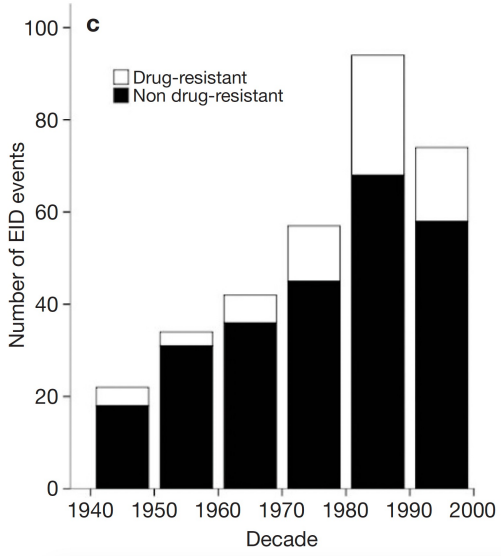
**a**, pathogen type



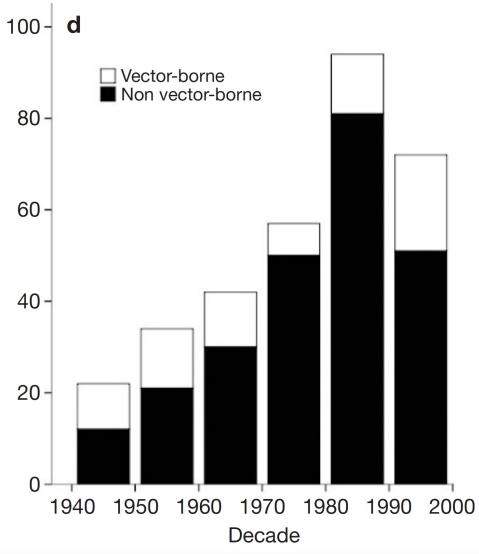

**b**, transmission type




**c**, drug resistance

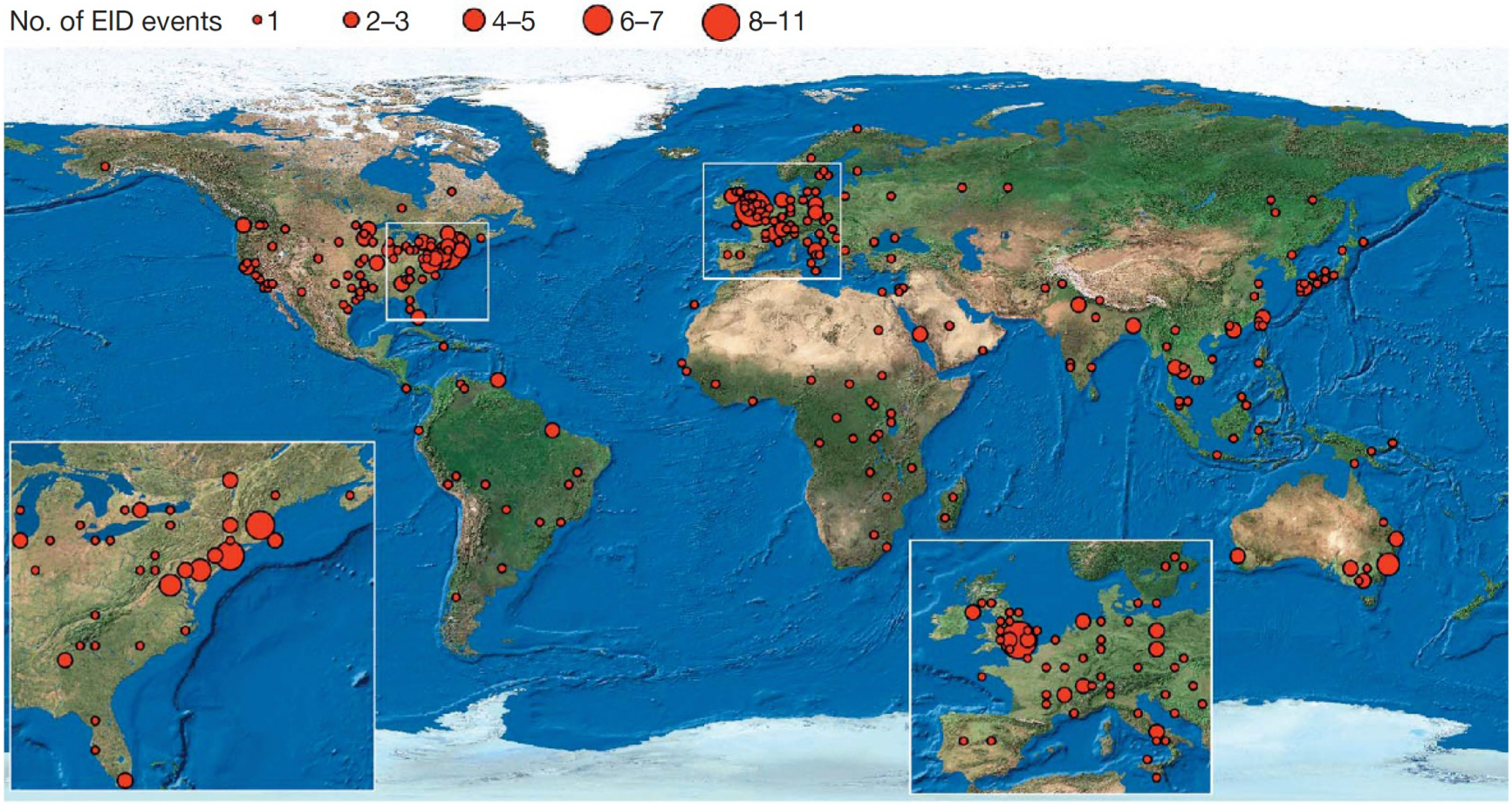



**d**, transmission mode




Jones *et al.* (2008) *Nature*

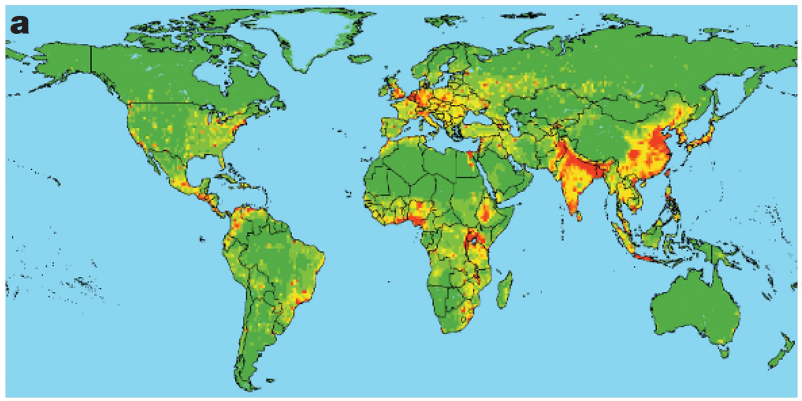
# Richness map of origins of EID (1940-2004)



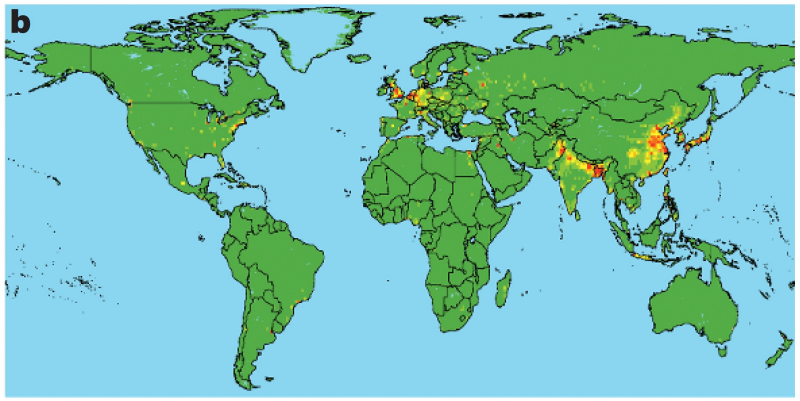

Jones *et al.* (2008) *Nature*

# Distribution of relative risk of an EID event

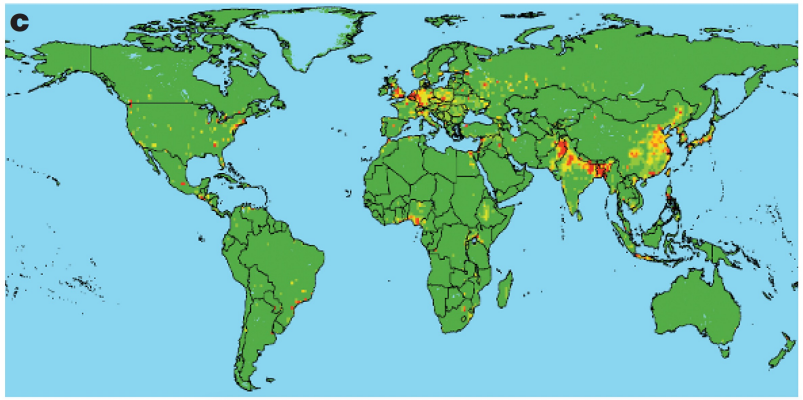
**a**, zoonotic pathogens from wildlife



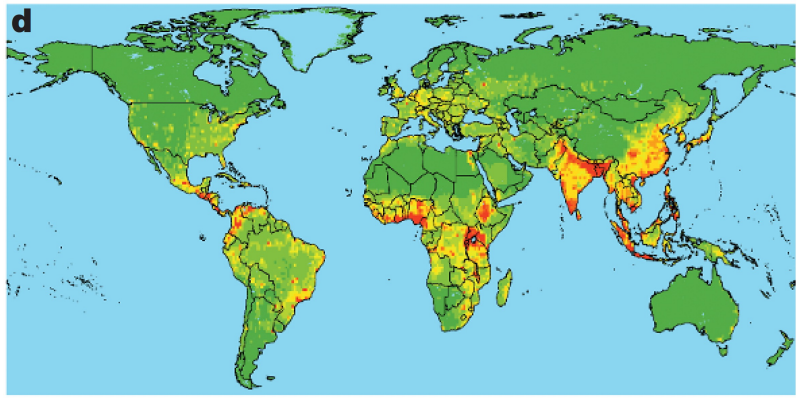

**b**, zoonotic pathogens from non-wildlife




**c**, drug-resistant pathogens




**d**, vector-borne pathogens




Jones *et al.* (2008) *Nature*

# Potential biases in study

- How to define ‘emerging’?
- Closely related pathogens sharing characteristics (impacts statistical analyses).
- Reporting bias.

**Once reporting bias is accounted for => in general, most emerging infections are found where there are most people.**

**“We must expect more infectious diseases to emerge in the near future”**

Woolhouse (2008) *Nature*

# Emerging viruses

- Novel viruses or genetically altered forms of known viruses often cause epidemics that can be disastrous.
- Numerous factors contribute to the propensity of viruses to emerge as pathogens:
  - High mutation rates.
  - Genetic recombination.
  - Host range expansion.
  - Zoonotic potential.
  - Ability to evade host defenses.

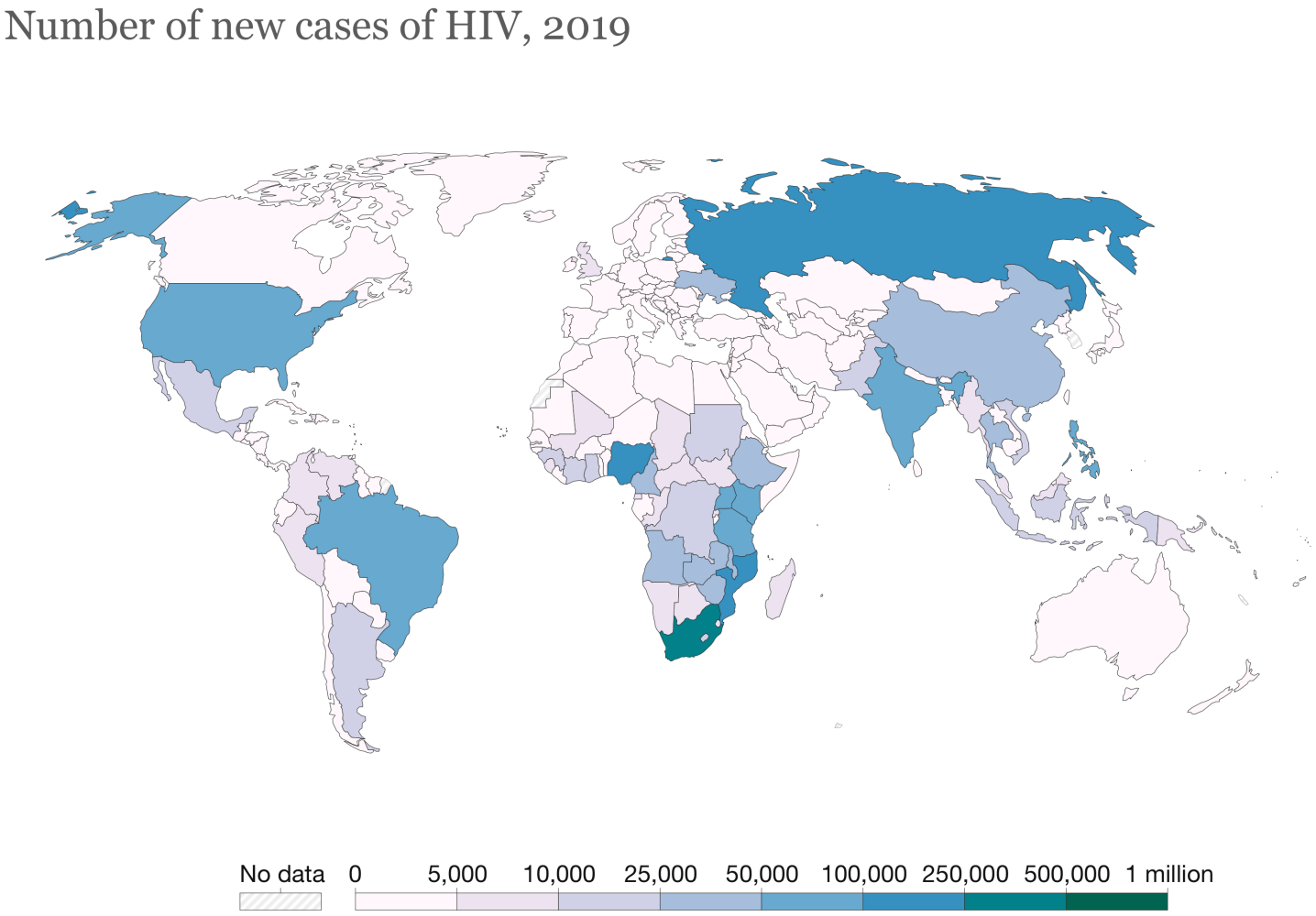
# Epidemic/Pandemic viruses with known host jumps

| virus | host combinations |
|---|---|
| Influenza A virus | avian to human, swine, horse, seal, dog. Swine to human, horse to dog |
| Human immunodeficiency virus | non-human primate to human, two major events |
| Ebola virus | bat to human, outbreaks, some extended epidemics |
| | bat to gorilla (to human) |
| | bat to duiker (to human) |
| MERS coronavirus | camel to human, mostly spillover, some outbreaks |
| SARS coronavirus | bat to palm civet to human, global spread but controlled |
| Nipah virus | bat to swine epidemic, spillover to humans |
| Canine parvovirus (CPV) | carnivore to dog pandemic |
| Zika virus | primate to human, adaptation to mosquito vector and humans resulted in epidemic |

Wasik *et al.* (2019) *Phil. Trans. R. Soc. B*

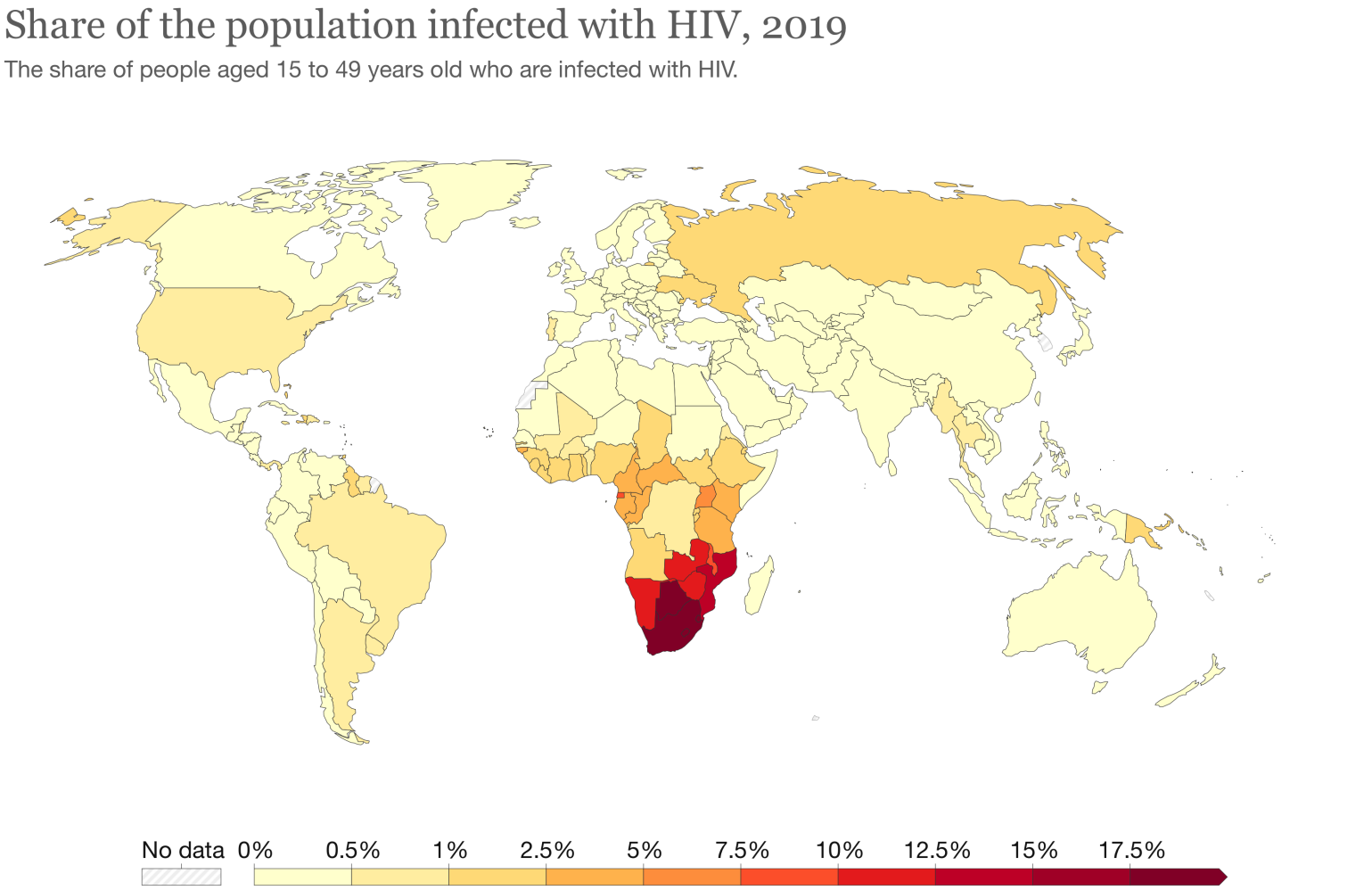
# Human immunodeficiency virus (HIV)

# HIV/AIDS by the numbers



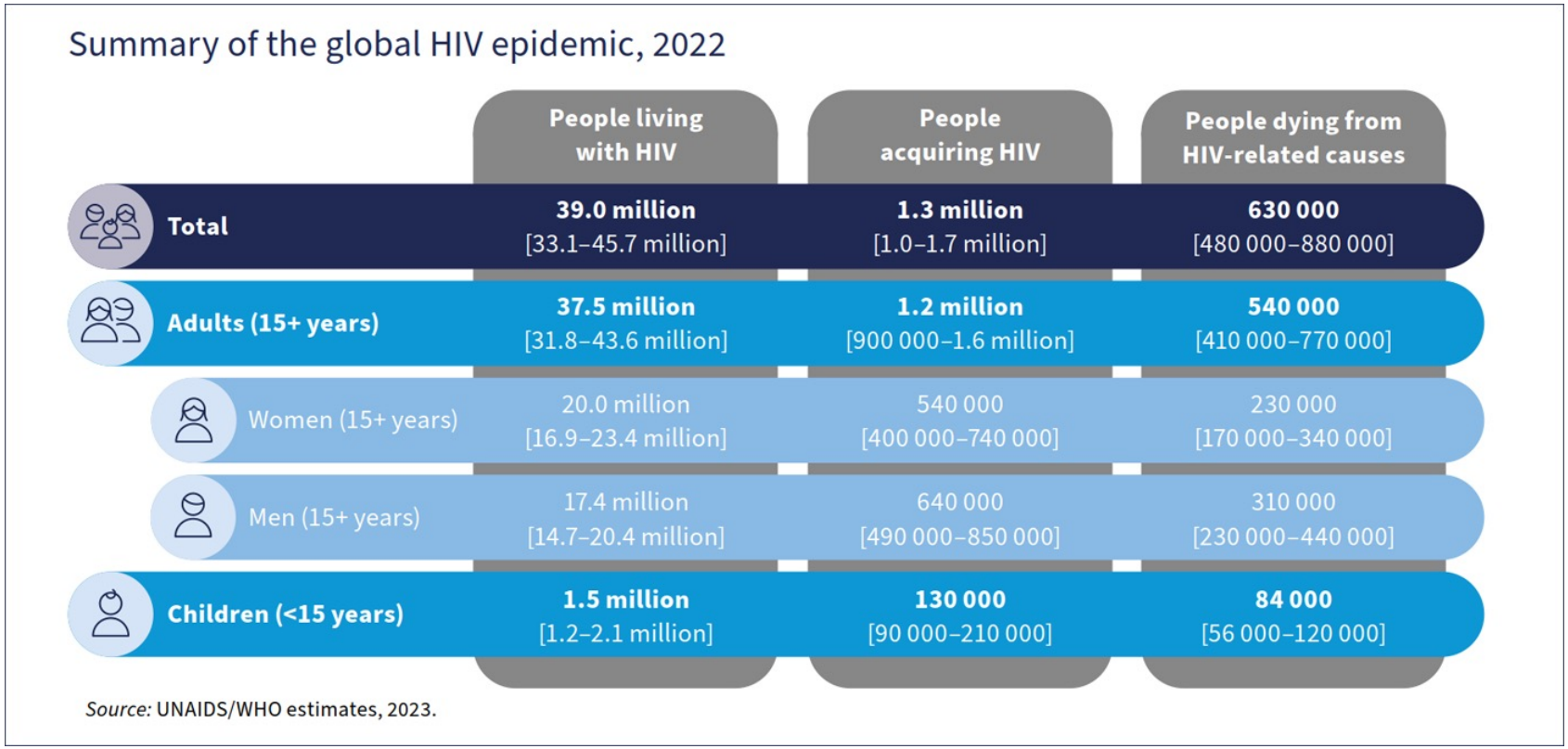

*Our World in Data*

# HIV/AIDS by the numbers




*Our World in Data*

# HIV/AIDS by the numbers




**Prevalence of HIV among adults**

**0.7%**

of adults aged 15–49 years worldwide are living with HIV in 2022

**Number of new HIV infections**

**1.3 million**

people were newly infected worldwide in 2022

**People living with HIV**

**3.2%**

of adults in the WHO African Region were living with HIV in 2022, accounting for two-thirds of the people living with HIV worldwide

*UN AIDS*

# Origins of HIV

FIGURE 1. ***Pan troglodytes:*** **The Primate Source of HIV-1**

Hahn (2005) *THE PRN NOTEBOOK*

# Occurrence of common chimpanzee (*Pan troglodytes*)

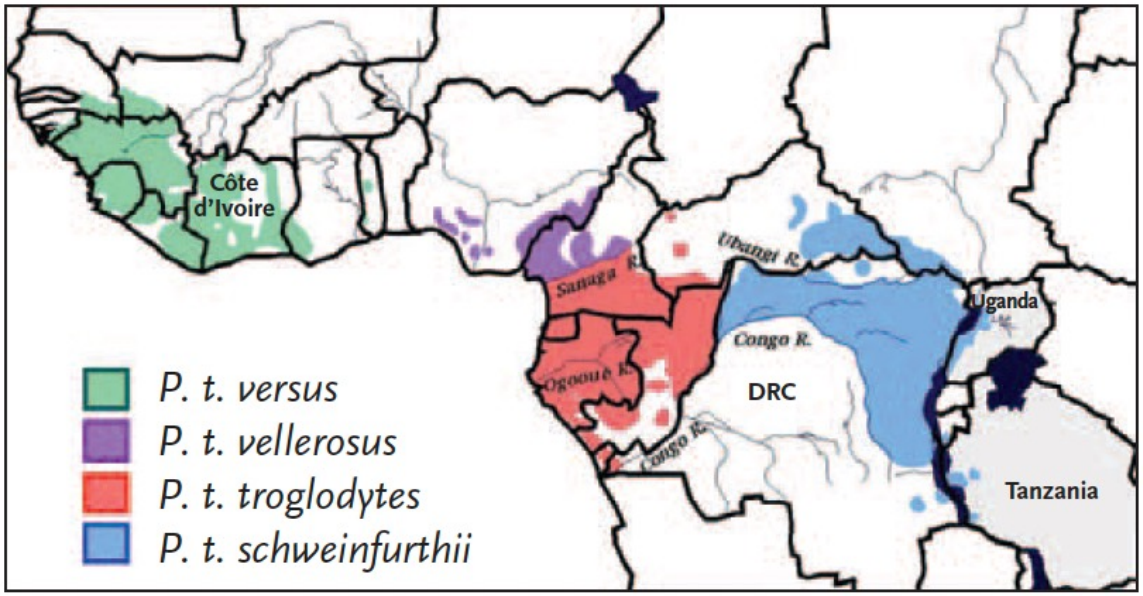



FIGURE 2. ***Pan Troglodytes* Subspecies**

Hahn (2005) *THE PRN NOTEBOOK*

# Exposure to primate blood – bushmeat trade

FIGURE 4. **Bushmeat in Pointe Noire, Democratic Republic of Congo**

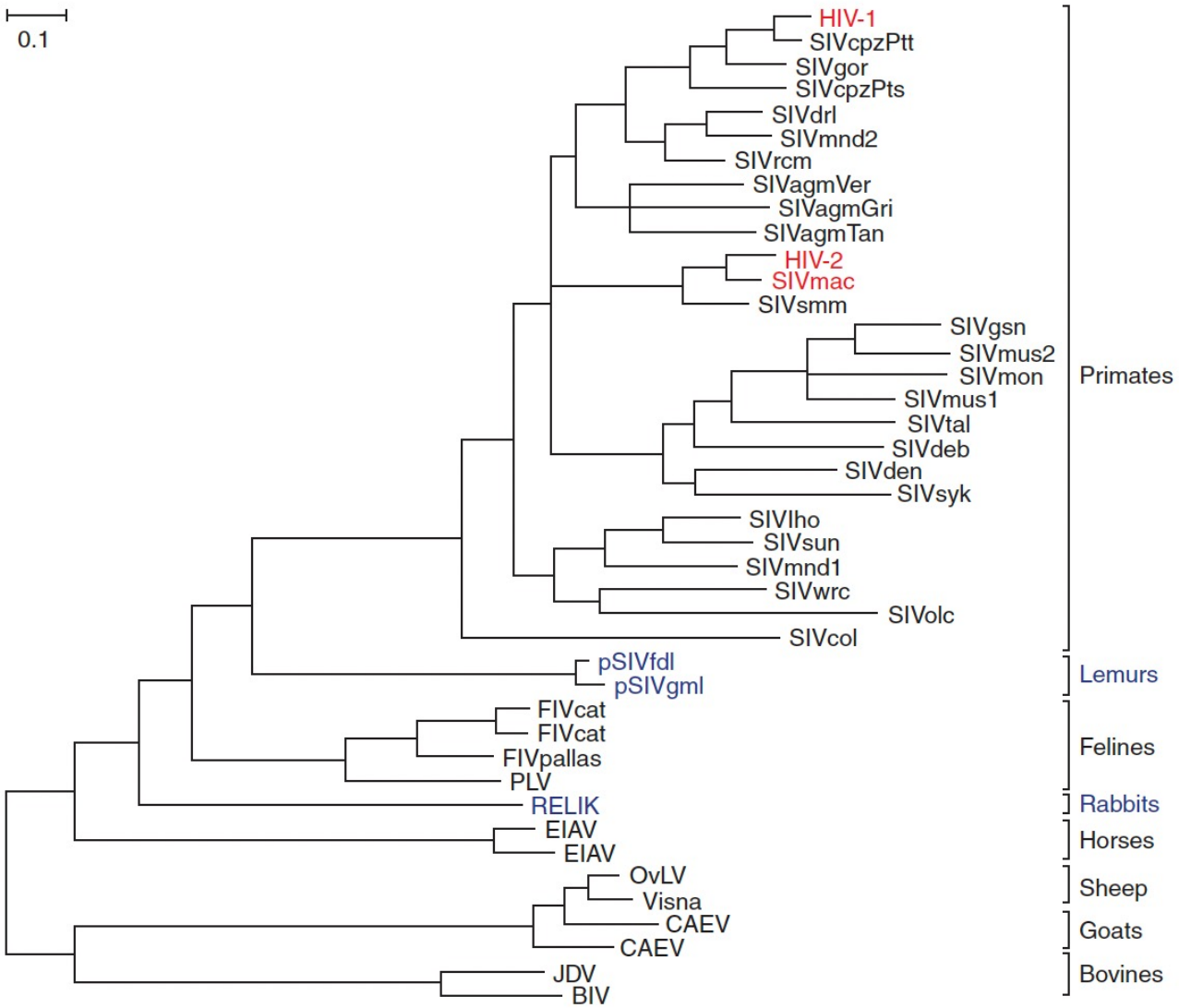
Hahn (2005) *THE PRN NOTEBOOK*

# Origins of HIV and the AIDS Pandemic

- Acquired immunodeficiency syndrome (AIDS) of humans is caused by two lentiviruses – HIV-1 & HIV-2
- HIV-1 & HIV-2 result of multiple cross-species transmissions of simian immunodeficiency viruses (SIVs) naturally infecting African primates.
- Most transfer resulted in limited spread.
- One transmission event from chimpanzees in south-eastern Cameroon gave rise to HIV-1 main (M) group - the principal cause of the AIDS pandemic.
- Tracing genetic changes that occurred SIVs (monkeys) -> to apes -> to humans provides framework to examine requirements of successful host switches and zoonotic risk.

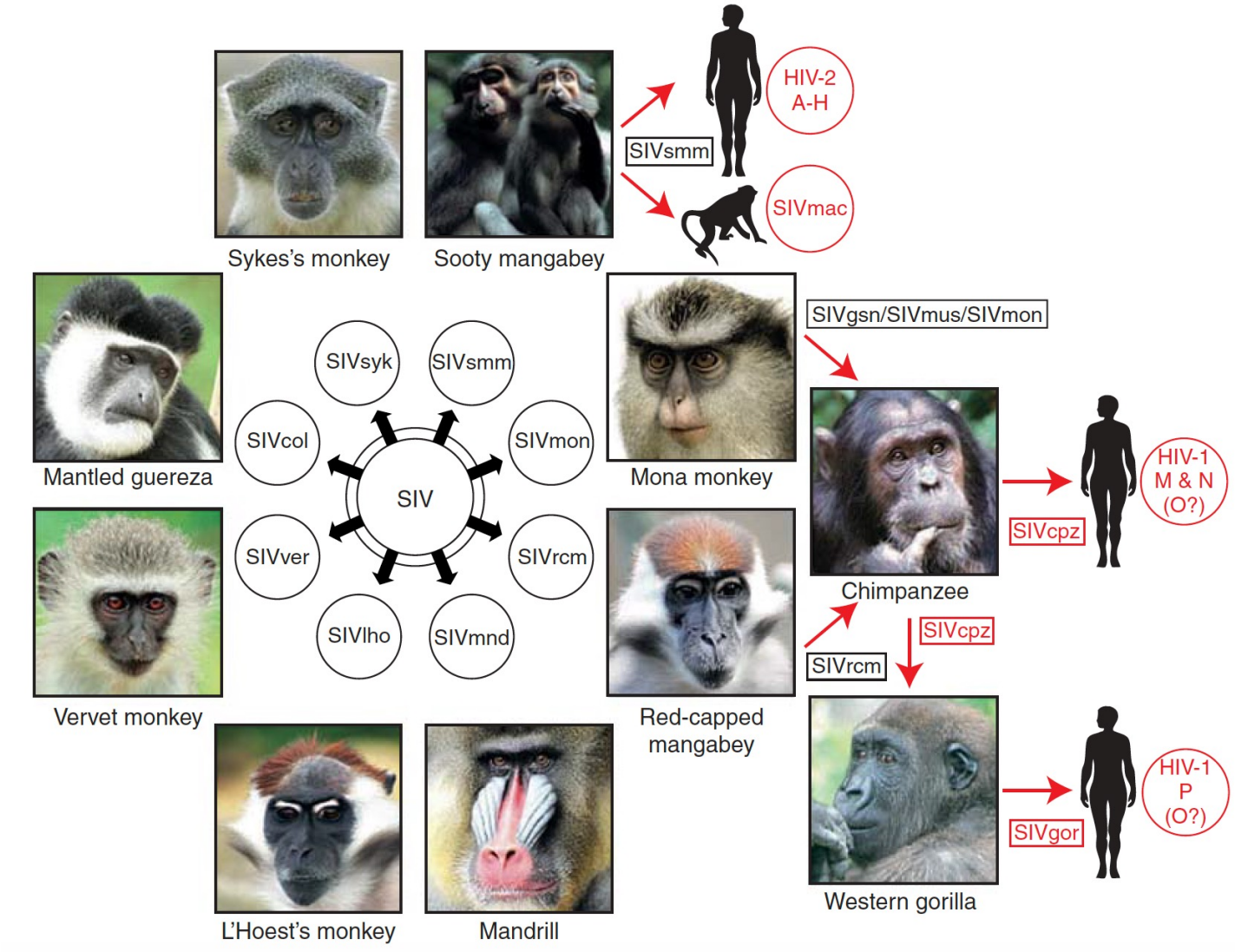
Sharp and Hahn (2011) *Cold Spring Harb. Perspect. Med.*

# Phylogeny of lentiviruses



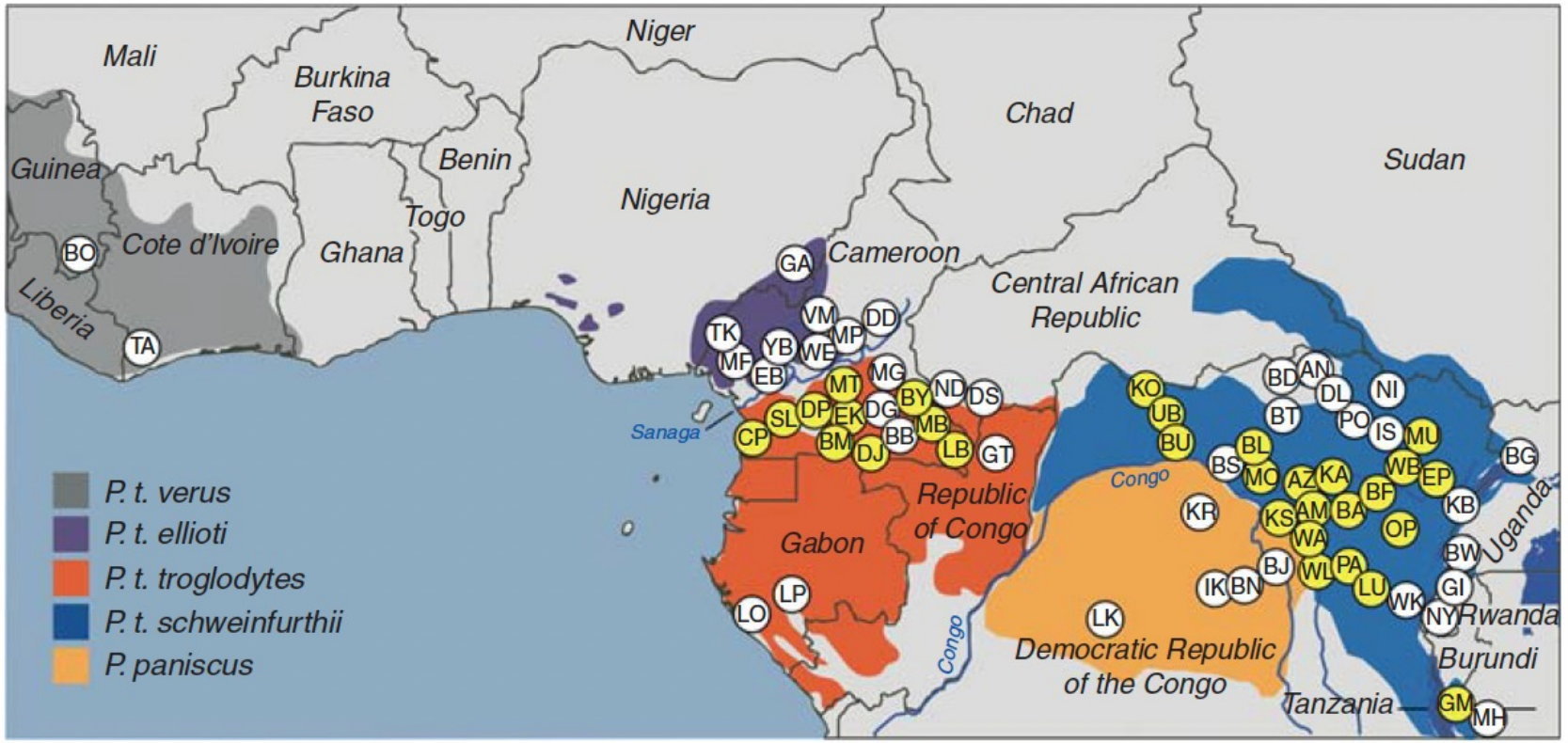

Sharp and Hahn (2011) *Cold Spring Harb. Perspect. Med.*

# Origins of HIV



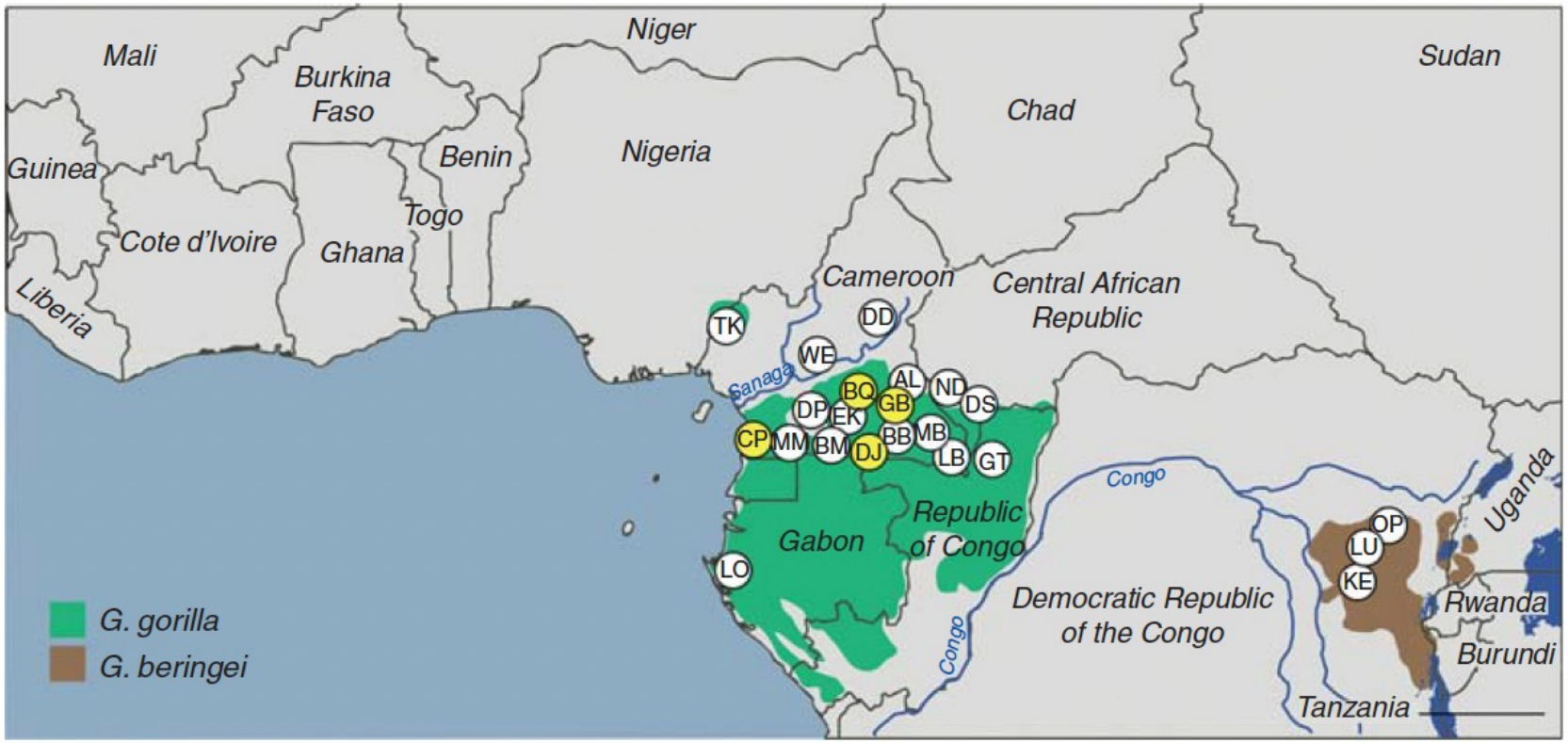

Sharp and Hahn (2011) *Cold Spring Harb. Perspect. Med.*

# Distribution of SIVcpz infections



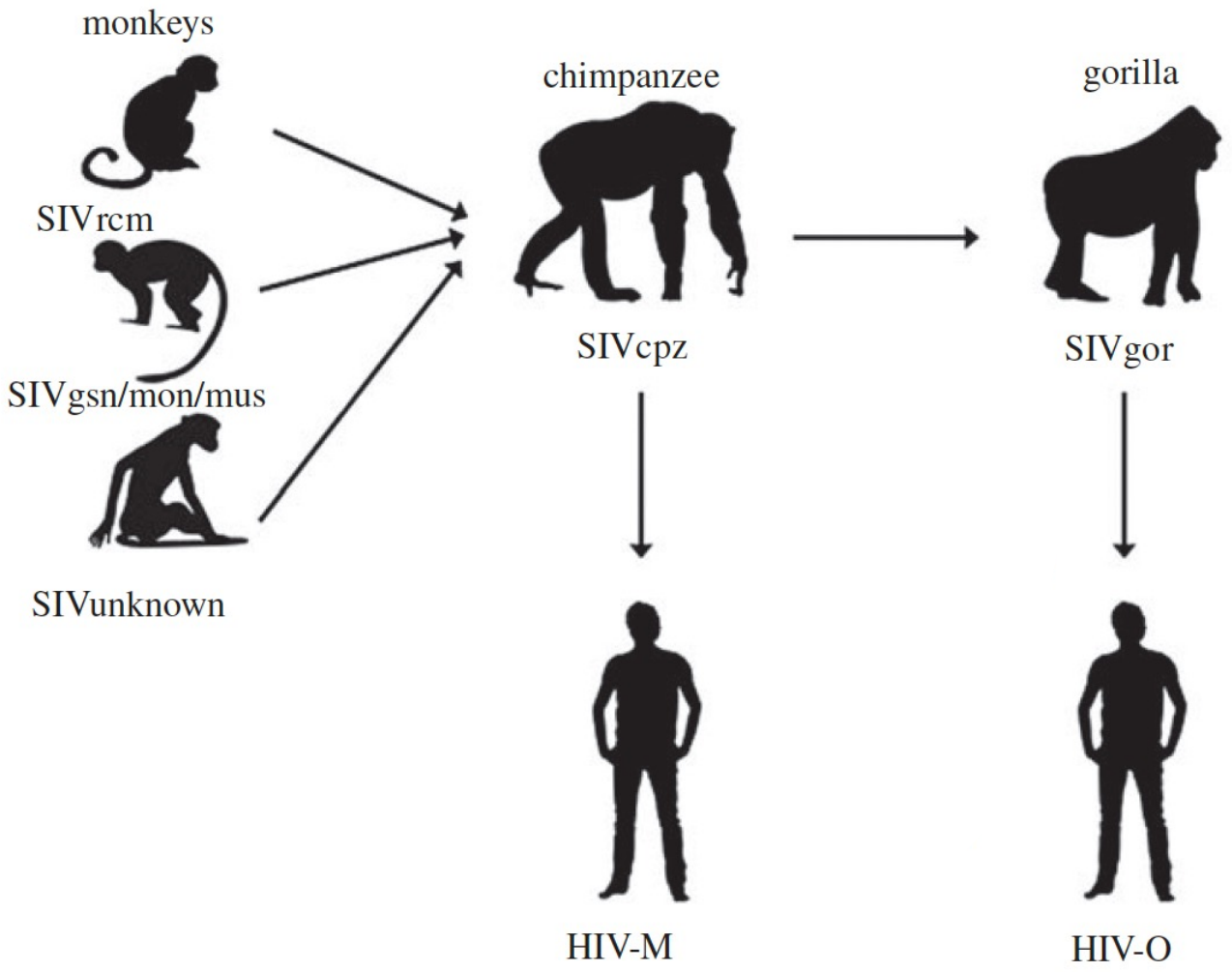

Sharp and Hahn (2011) *Cold Spring Harb. Perspect. Med.*

# Distribution of SIVgor infections




Sharp and Hahn (2011) *Cold Spring Harb. Perspect. Med.*

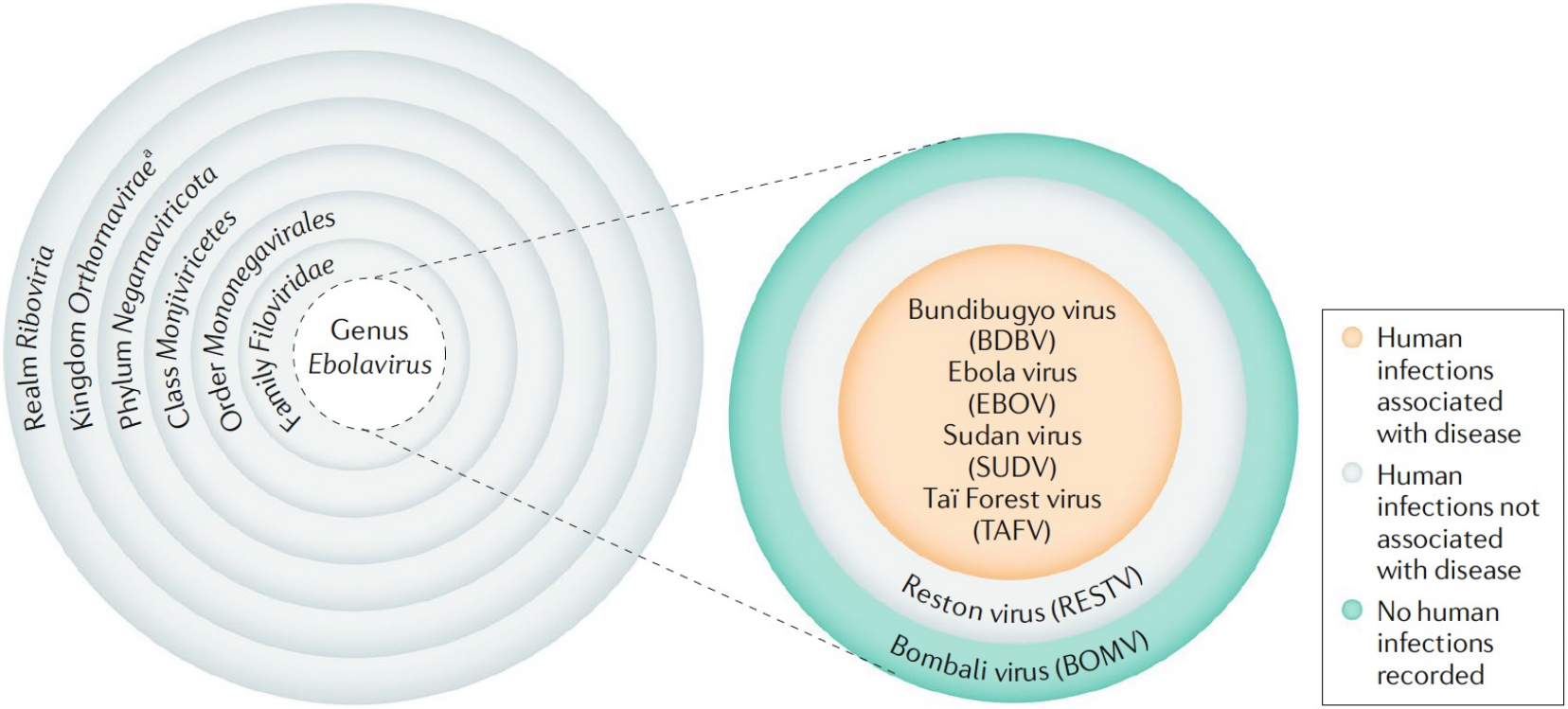
# HIV strains and their emergence in humans




Wasik *et al*. (2019) *Phil. Trans. R. Soc. B*

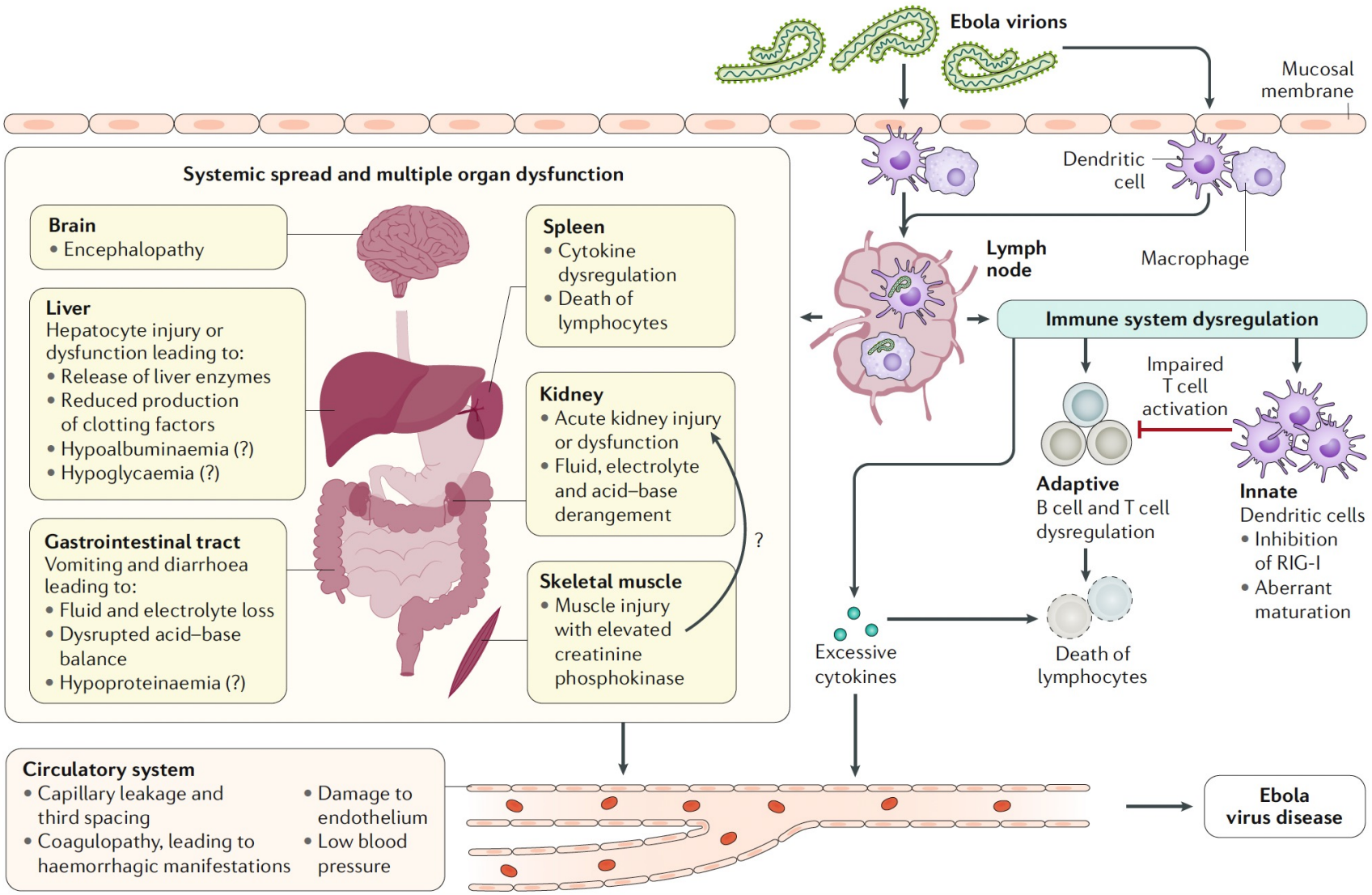
# Ebola virus

# Filovirus taxonomy



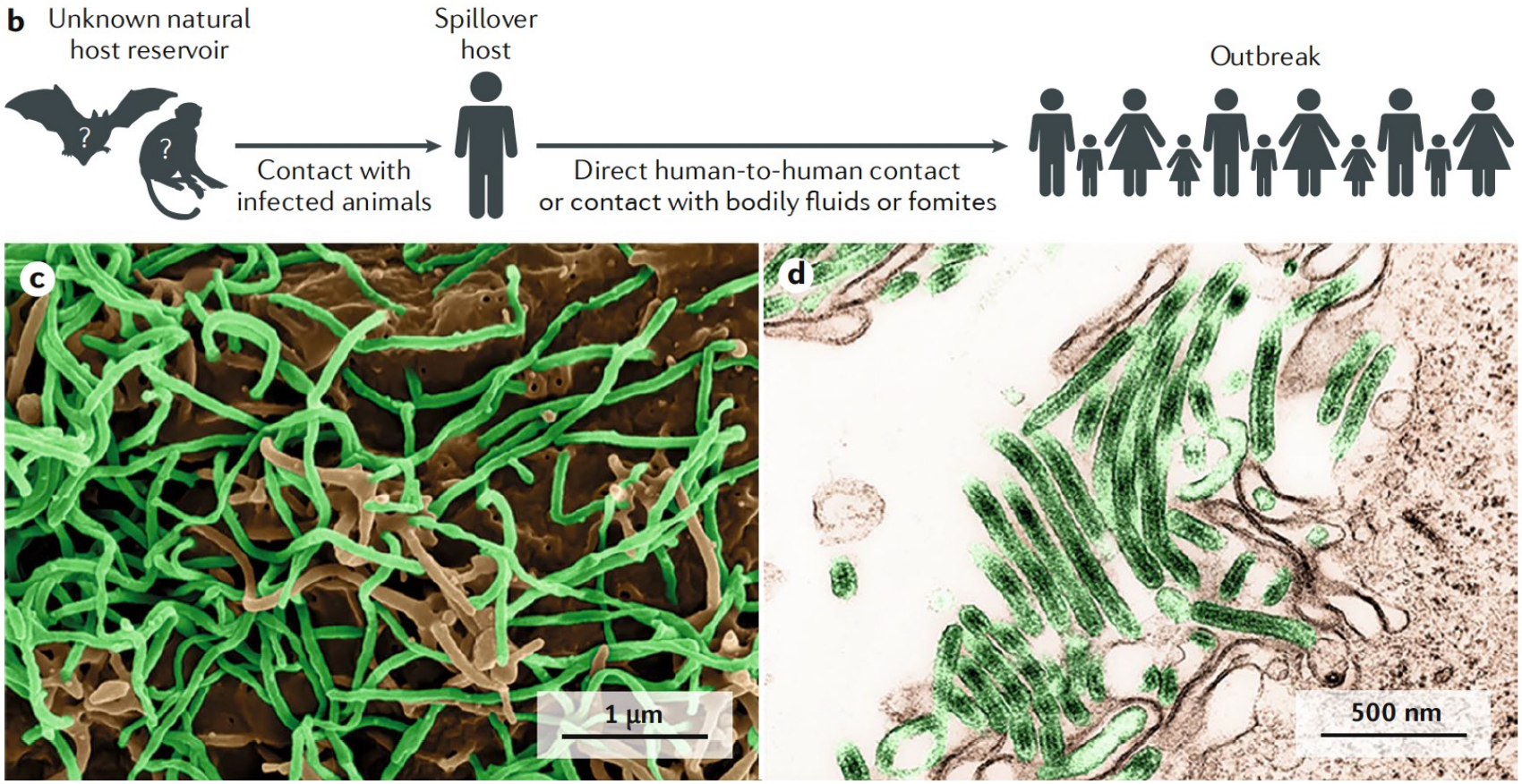

Jacob *et al.* (2020) *Nat. Dis. Primers*

# Ebola pathogenesis




Jacob *et al.* (2020) *Nat. Dis. Primers*

# Ebola virus transmission




Jacob *et al.* (2020) *Nat. Dis. Primers*

# Ebola discovery and outbreaks

- Ebola virus (EBOV) discovered in 1976 in Democratic Republic of the Congo (DRC; then Zaire).
- At least 17 Ebola virus disease outbreaks originated in Gabon, Guinea, the Republic of the Congo or Zaire/DRC.
- Estimated 33,604 EBOV infections in humans, including 14,742 deaths (average CFR 43.8%).

Jacob *et al.* (2020) *Nat. Dis. Primers*

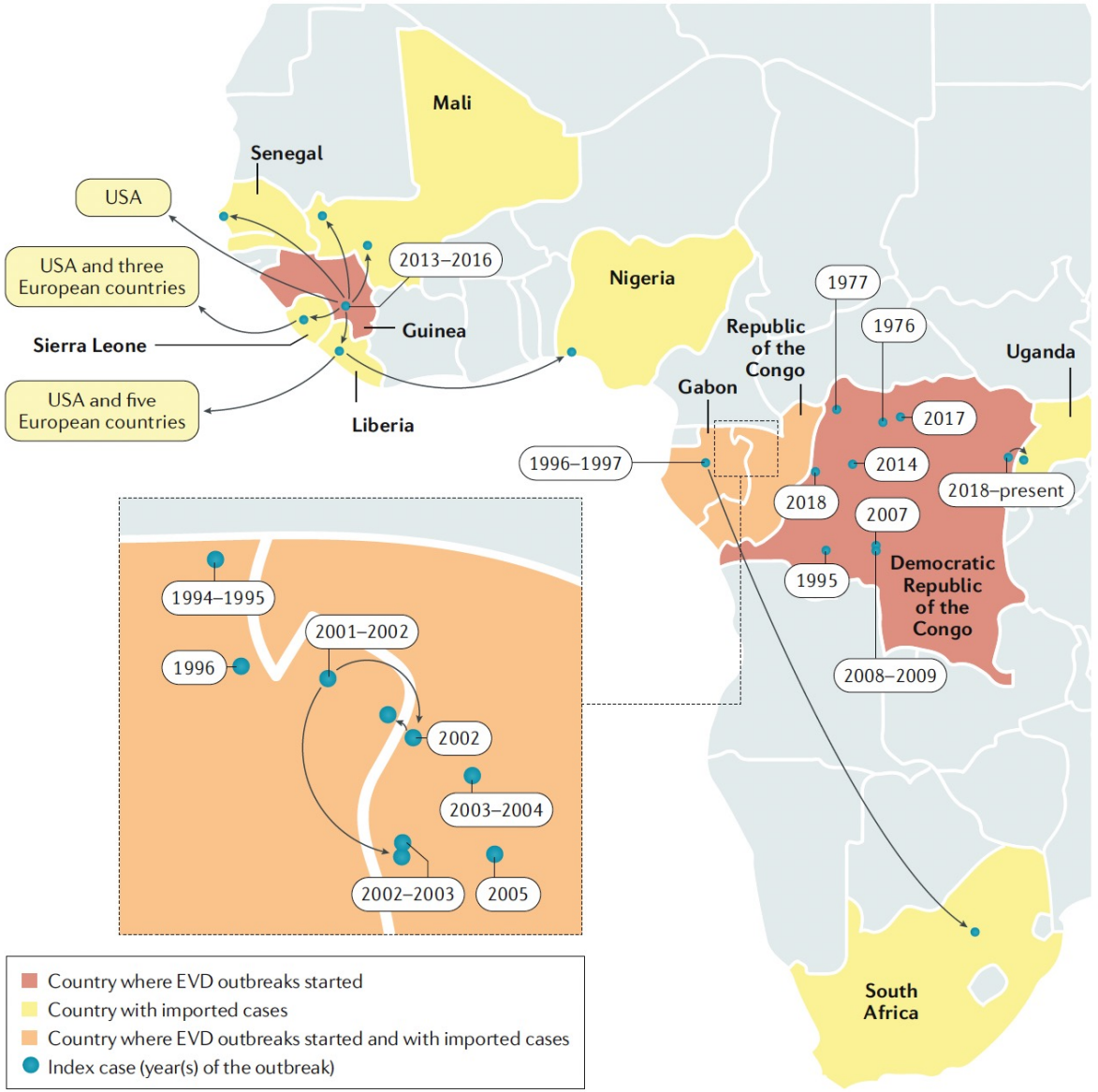
# Ebola virus disease outbreaks

Table 1 | **Ebola virus disease outbreaks statistics**

| Country (year) | Case–fatality rate (%) | Number of cases |
|---|---|---|
| COD (then Zaire) (1976) | 88.1 | 318 |
| COD (then Zaire) (1977) | 100.0 | 1 |
| Gabon (1994–1995) | 61.5 | 52 |
| COD (then Zaire) (1995) | 77.3 | 317 |
| Russia[a] (1996) | 100.0 | 1 |
| Gabon (1996) | 67.7 | 31 |
| Gabon, also exported to South Africa (1996–1997) | 74.2 | 62 |
| Gabon, COG (2001–2002) | 78.2 | 124 |
| COG, also exported to Gabon (2002) | 90.9 | 11 |
| COG (2002–2003) | 89.5 | 143 |
| COG (2003–2004) | 82.9 | 35 |
| Russia[a] (2004) | 100.0 | 1 |
| COG (2005) | 81.8 | 11 |
| COD (2007) | 70.5 | 264 |
| COD (2008–2009) | 46.9 | 32 |
| Guinea, also exported to Liberia, Mali, Senegal, Sierra Leone and USA; from Liberia, cases were exported to France, Germany, Netherlands, Nigeria, Norway, Spain and USA and, from Sierra Leone, to Italy, UK, Switzerland and USA (2013–2016) | 39.5 | 28,652 |
| COD (2014) | 71.0 | 69 |
| COD (2017) | 50.0 | 8 |
| COD (2018) | 61.1 | 54 |
| COD, also exported to Uganda (2018 to present) | 66.3 | 3,324 |

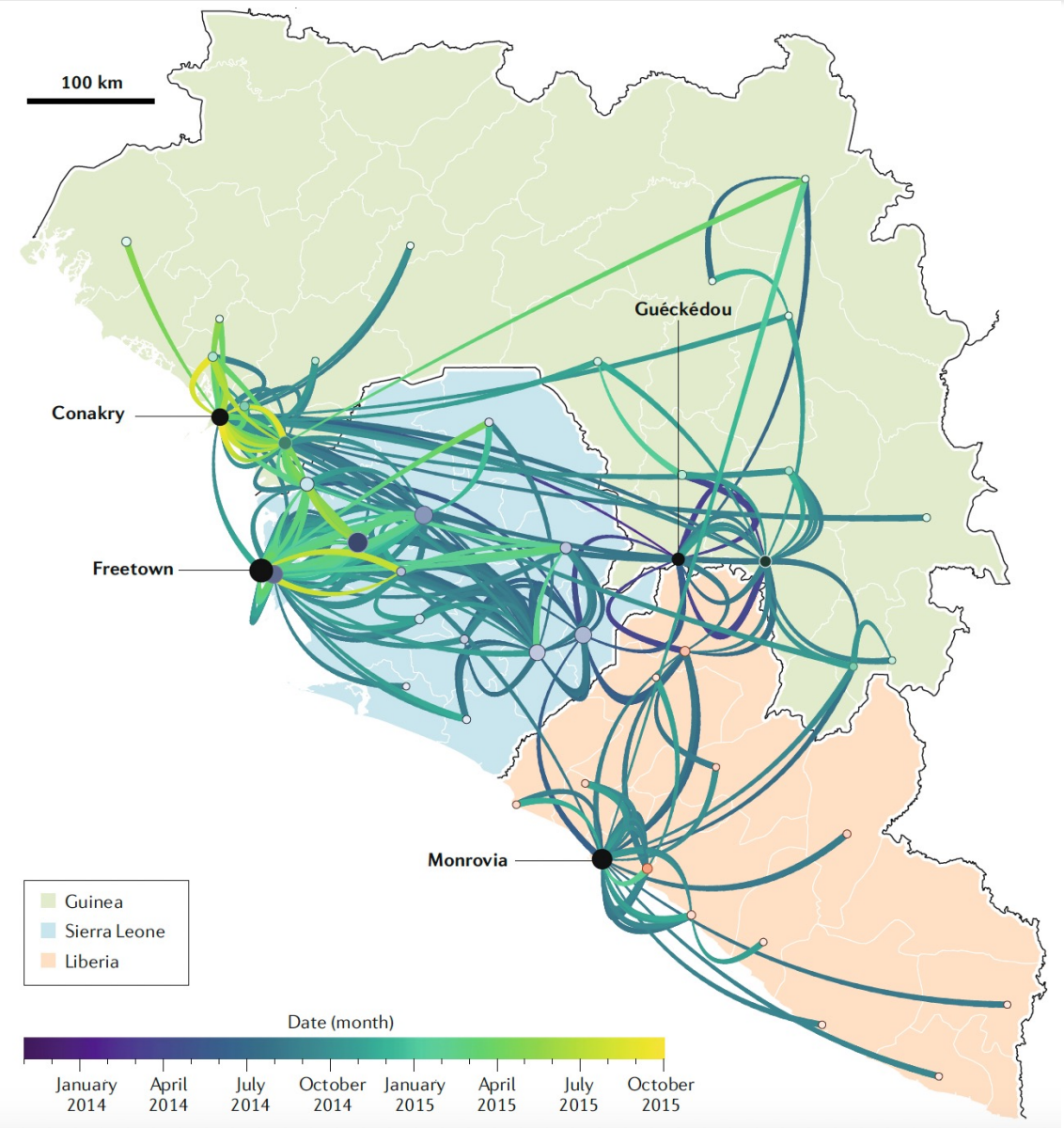
Jacob *et al.* (2020) *Nat. Dis. Primers*

# Ebola virus disease outbreaks



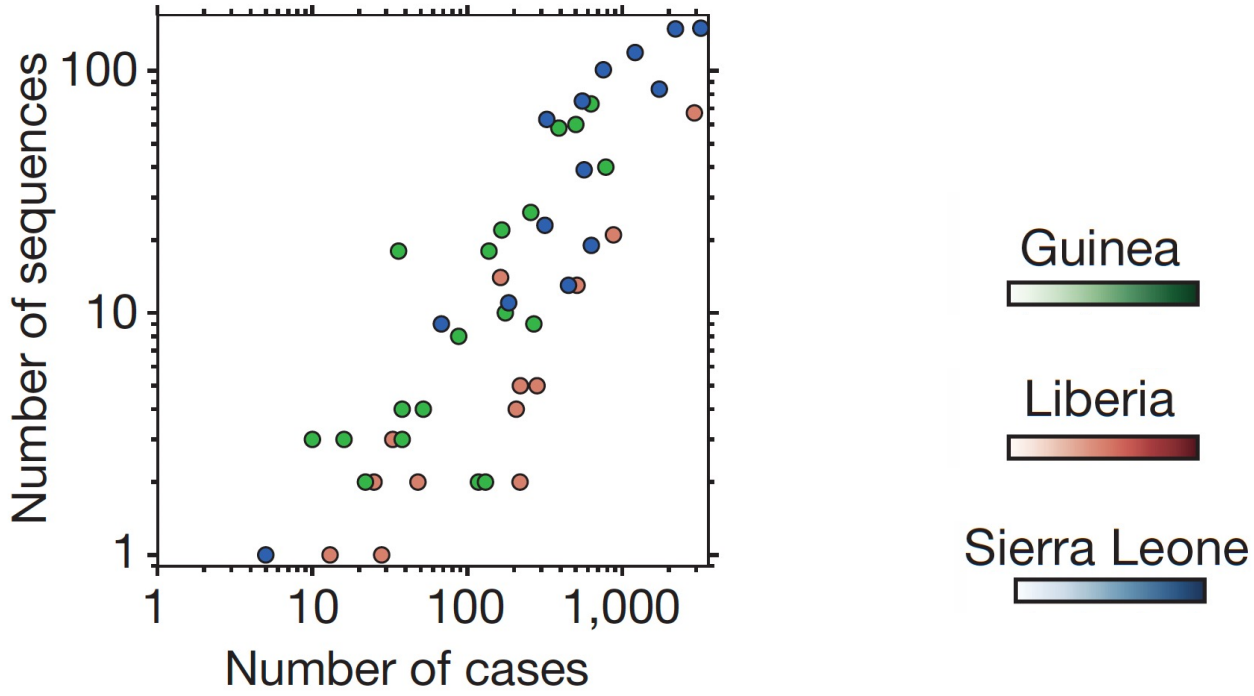

Jacob *et al.* (2020) *Nat. Dis. Primers*

# Ebola outbreak 2013-2016



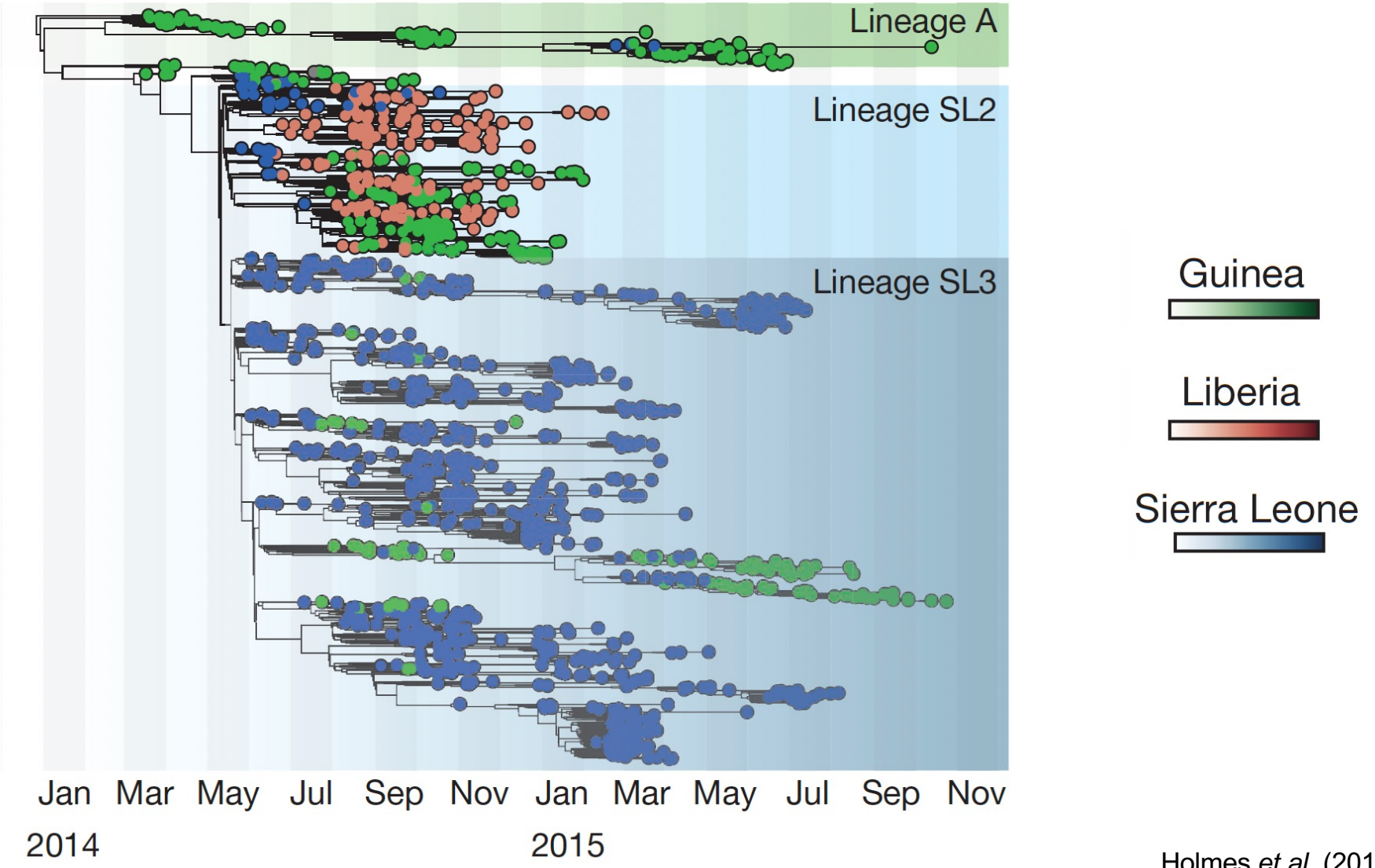

Jacob *et al.* (2020) *Nat. Dis. Primers*

# Ebola outbreak 2013-2016



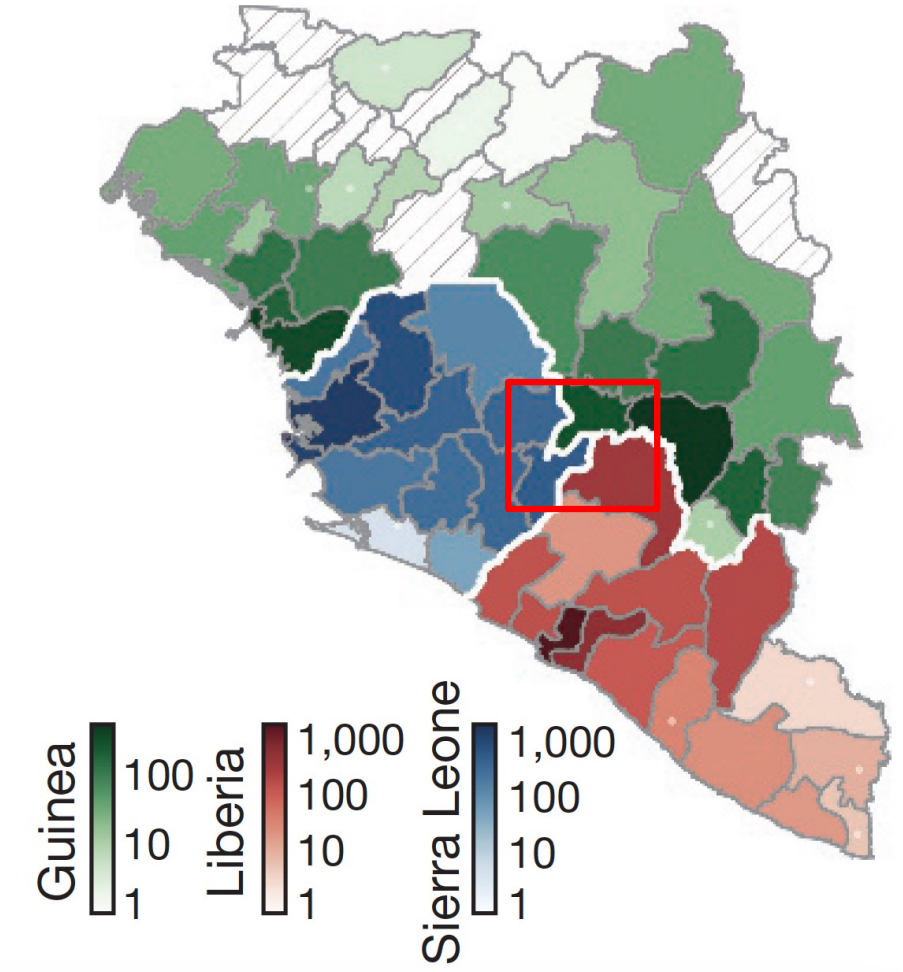

Holmes *et al.* (2016) *Nature*

# Ebola outbreak 2013-2016



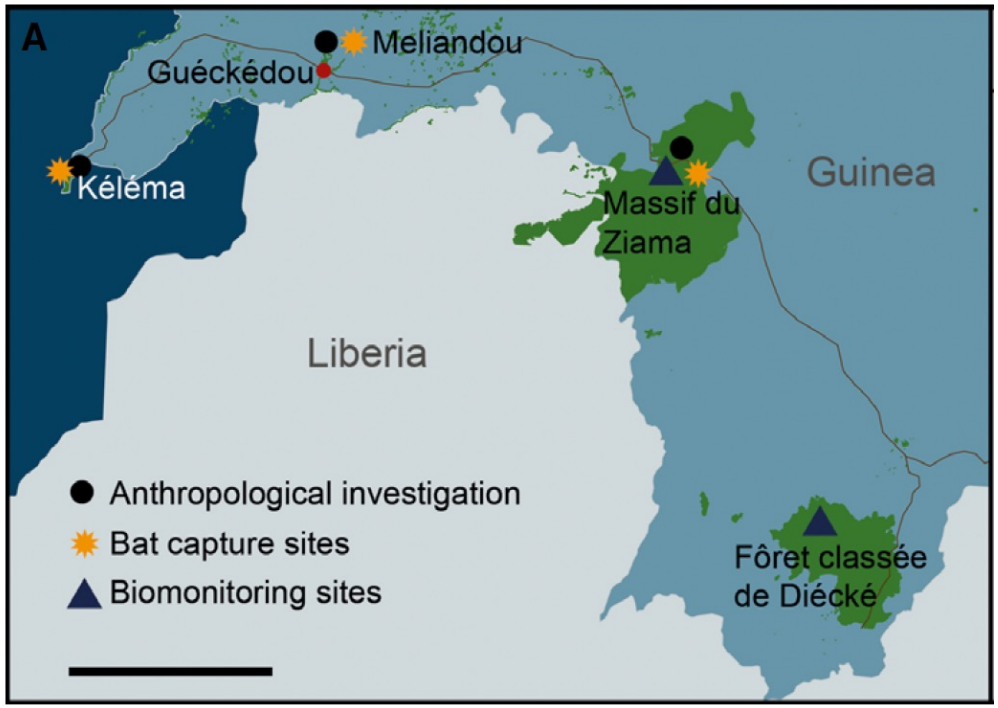

Holmes *et al.* (2016) *Nature*

# Ebola outbreak 2013-2016 – sequencing efforts




Holmes *et al.* (2016) *Nature*

# Ebola sampling and investigation locations




Marí Saéz *et al.* (2015) *EMBO Mol. Med.*

# Ebola sampling and investigation locations

It's widely believed that "patient zero" for the world's deadliest Ebola outbreak was a two-year old boy from the remote village of Meliandou, Guinea. Like many children in his farmland town, the boy would play around and catch bats in the large hollow Cola trees that surrounded his small neighborhood. But in December 2013, the boy fell sick to a mysterious illness that would eventually kill him, and then spread to his family and neighbors. Months later, the disease, identified as Ebola, raced across West Africa, infecting 20,000 people and killing more than 7,800.

*The Atlantic*, 2014

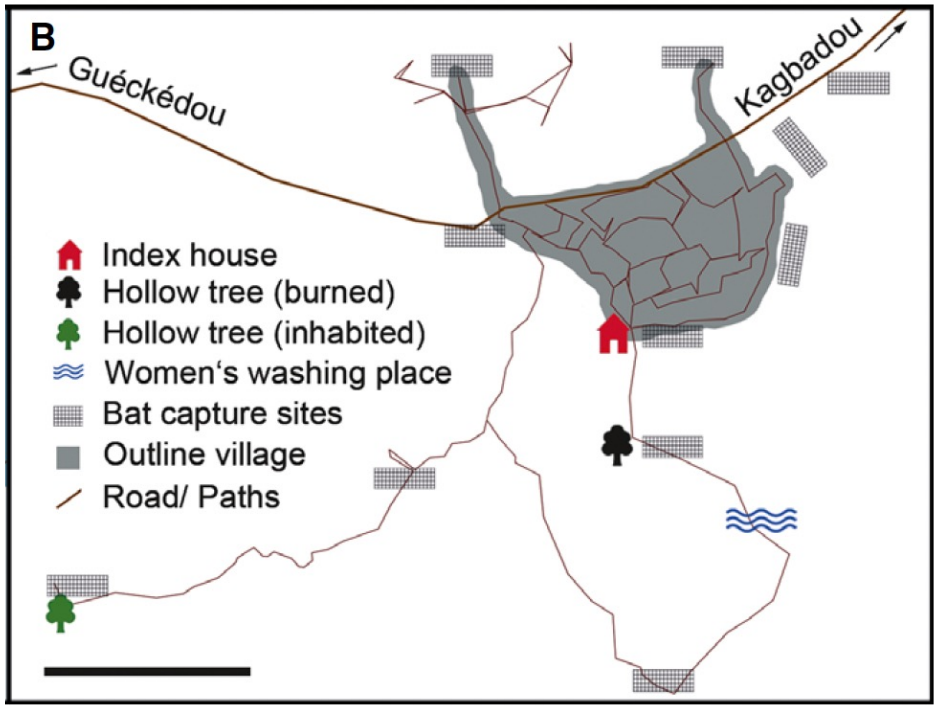
# Ebola sampling and investigation locations


**Meliandou**

**burnt hollow tree**

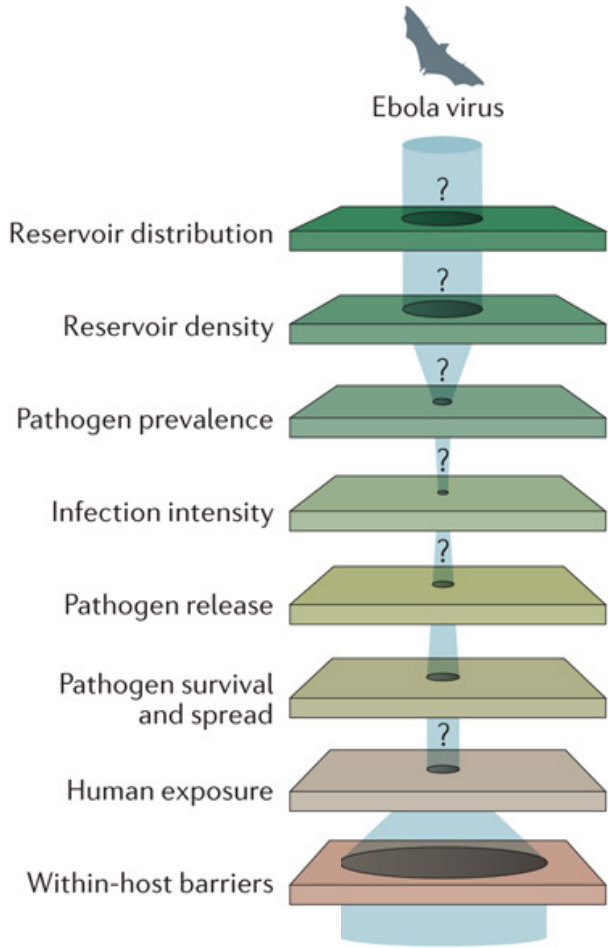
Marí Saéz *et al.* (2015) *EMBO Mol. Med.*

# Ebola sampling and investigation locations




Marí Saéz *et al.* (2015) *EMBO Mol. Med.*

# Bottlenecks to spillover - Ebola




- Not been isolated from bats – definitive reservoir unknown.
- Pathogen released through excretion or slaughter => environmental survival for a week.
- Zoonotic exposure = bottleneck => human interaction with bats, bushmeat, carcasses of other species.

**Once exposed, within-host barriers to Ebola viruses extremely low!**

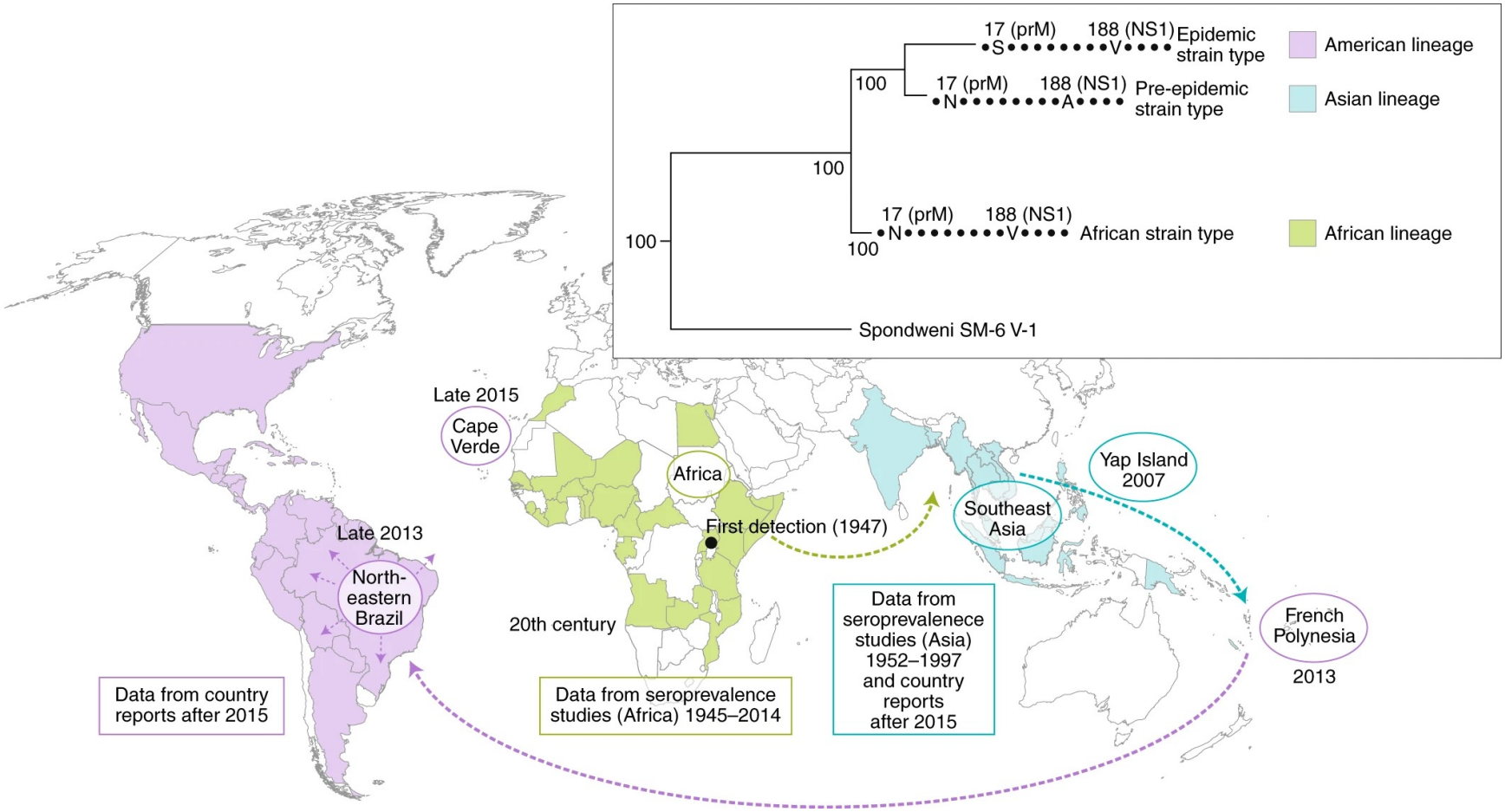
Plowright *et al.* (2017) *Nat. Rev. Microbiol.*

# Zika virus

# Zika virus

- Zika virus was first discovered in 1947 in a rhesus monkey in the Zika Forest of Uganda.
- First human cases of Zika identified in 1952 in Uganda and the United Republic of Tanzania.
- Virus remained confined to Africa and Asia for decades, with sporadic cases reported in these regions.
- First major outbreak occurred in Micronesia in 2007. Subsequently, outbreaks were reported in other Pacific islands.
- Zika virus reached the Americas in 2015, with Brazil experiencing a large outbreak that drew international attention.
- Rapid spread of Zika led the World Health Organization (WHO) to declare it a Public Health Emergency of International Concern in 2016.

# Emergence and evolution of Zika virus




Gutiérrez-Bugallo *et al.* (2019) *Nat. Ecol. Evol.*

# Zika virus disease

- Transmission: Virus is transmitted through *Aedes* mosquitoes, particularly *Aedes aegypti* and *Aedes albopictus*.

- Symptoms: fever, rash, joint pain, and conjunctivitis. Mostly mild and short-lived.

- Birth defects: Association with congenital disabilities, including microcephaly and other neurological complications in infants born to mothers infected during pregnancy.

- Preventive measures:
  - controlling mosquito populations
  - using insect repellents
  - wearing protective clothing
  - implementing safe sex practices (to avoid sexual transmission).

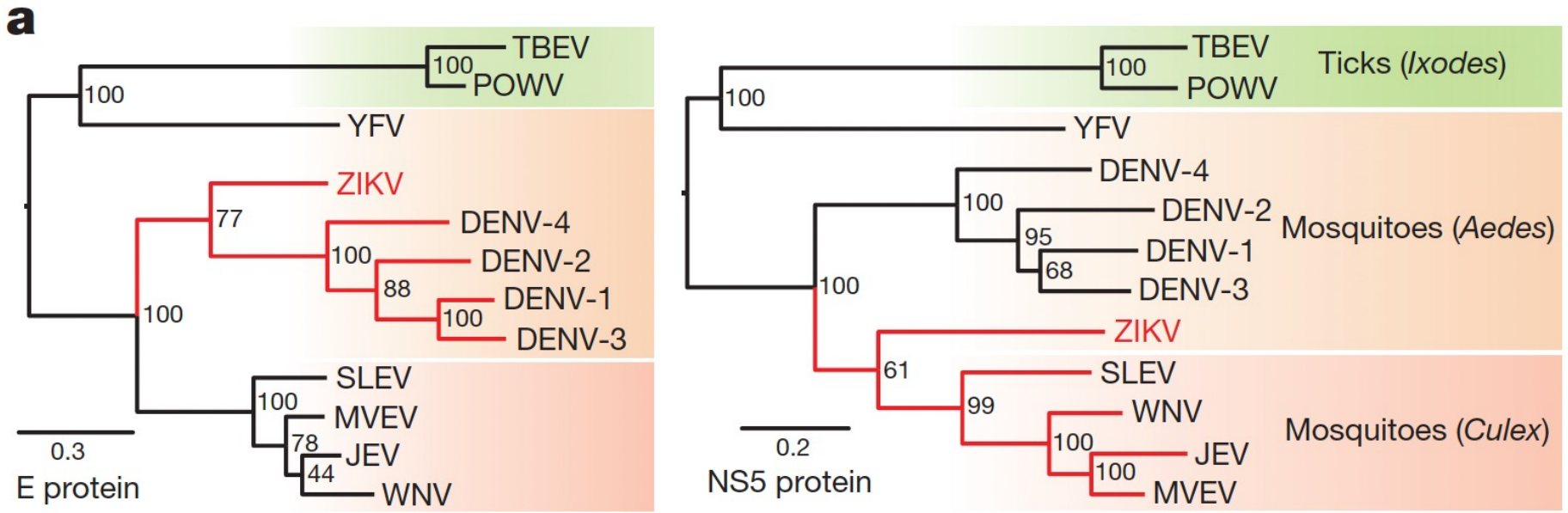
# Vector-borne diseases

Example of diseases transmitted to humans or other animals by blood-feeding arthropods such as mosquitoes, ticks, and fleas:

- Malaria
- Zika virus disease
- Dengue fever
- Chikungunya
- Yellow fever
- West Nile virus
- Lyme disease
- Japanese encephalitis
- Rift Valley fever
- Leishmaniasis
- Typhus
- Chagas disease
- Tularemia
- Onchocerciasis (River blindness)
- Filariasis

# Zika virus is closely related to Dengue virus

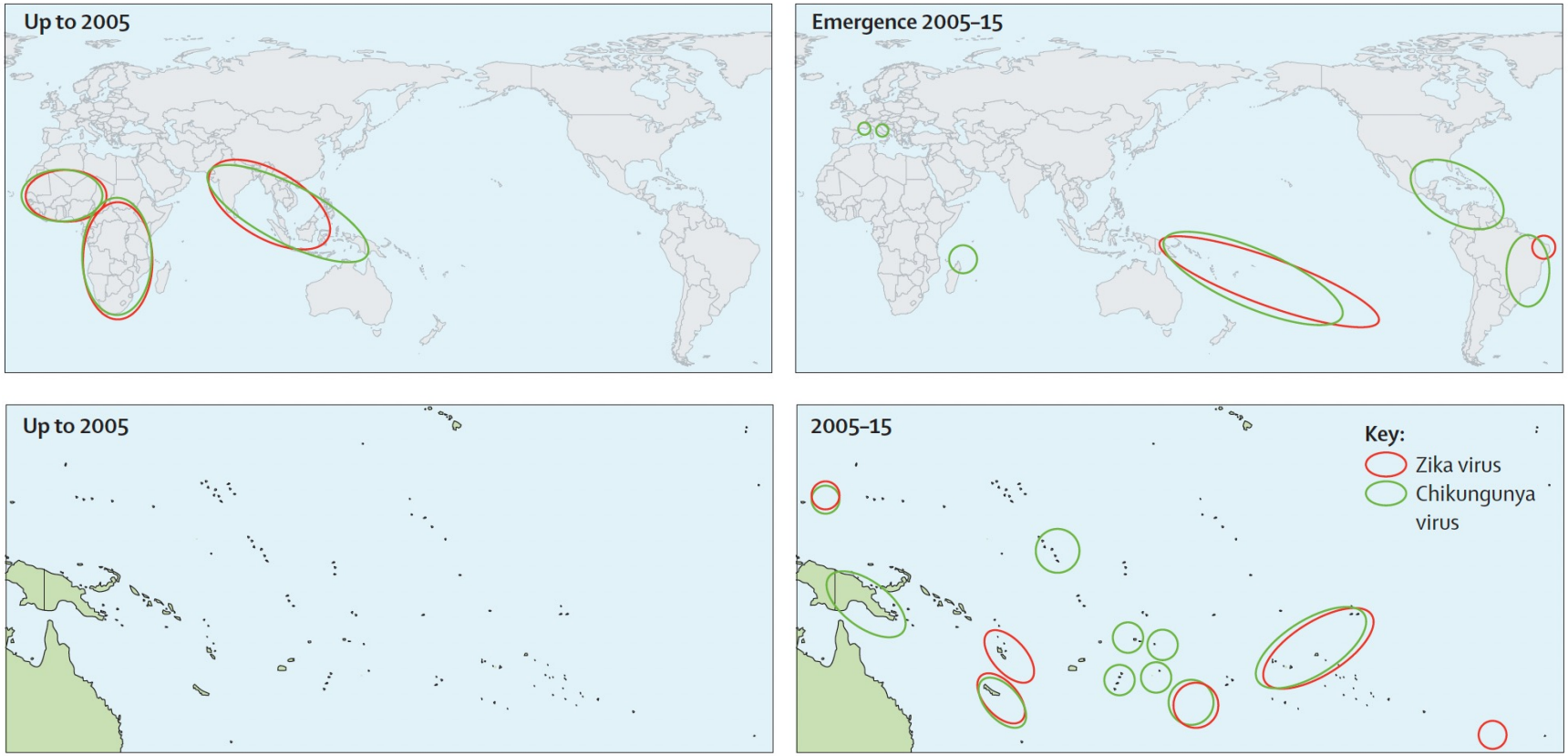
## Phylogenetic trees of the main human pathogenic flaviviruses




Barba-Spaeth *et al.* (2016) *Nature*

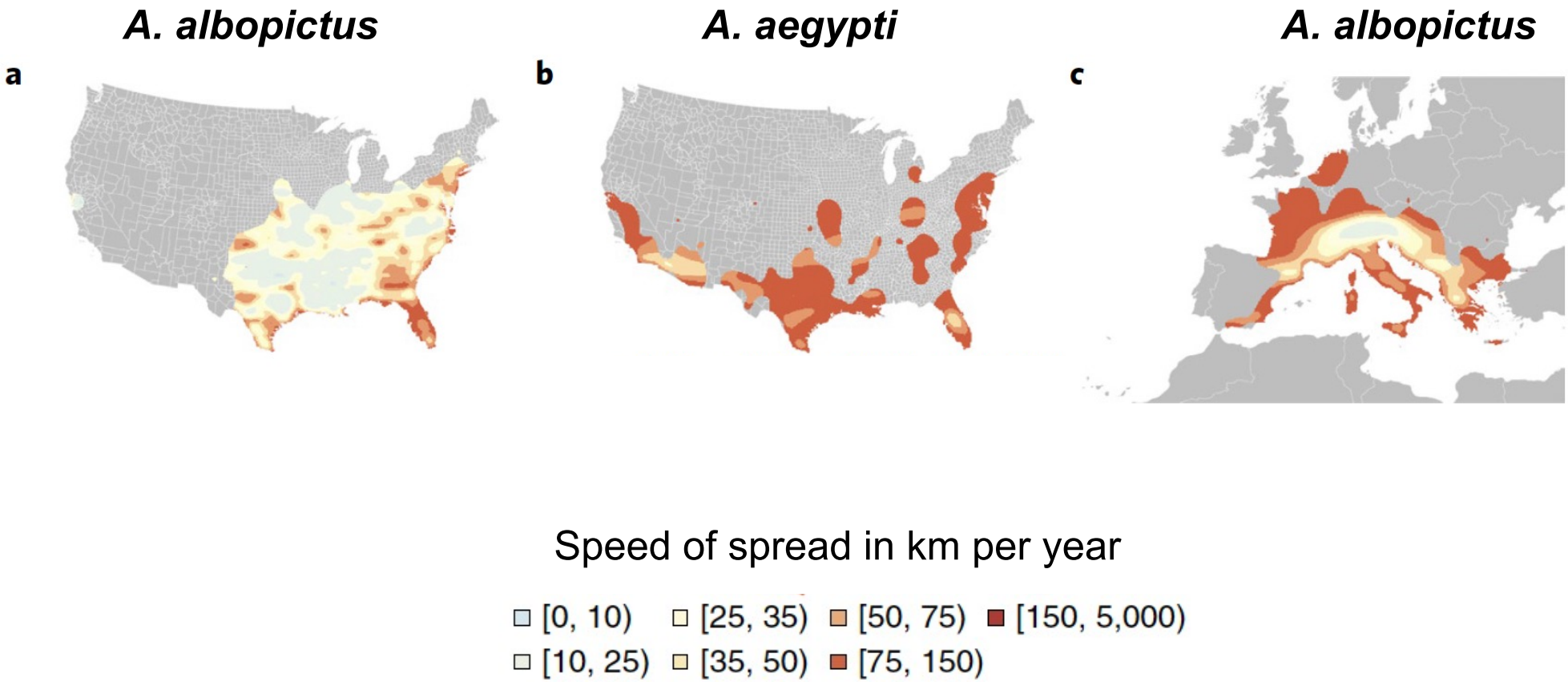
# Vector-borne diseases

## Zika virus: following the path of dengue and chikungunya?




Musso *et al.* (2015) *Lancet*

# Reconstruction of *A. albopictus* and *A. aegypti* spread

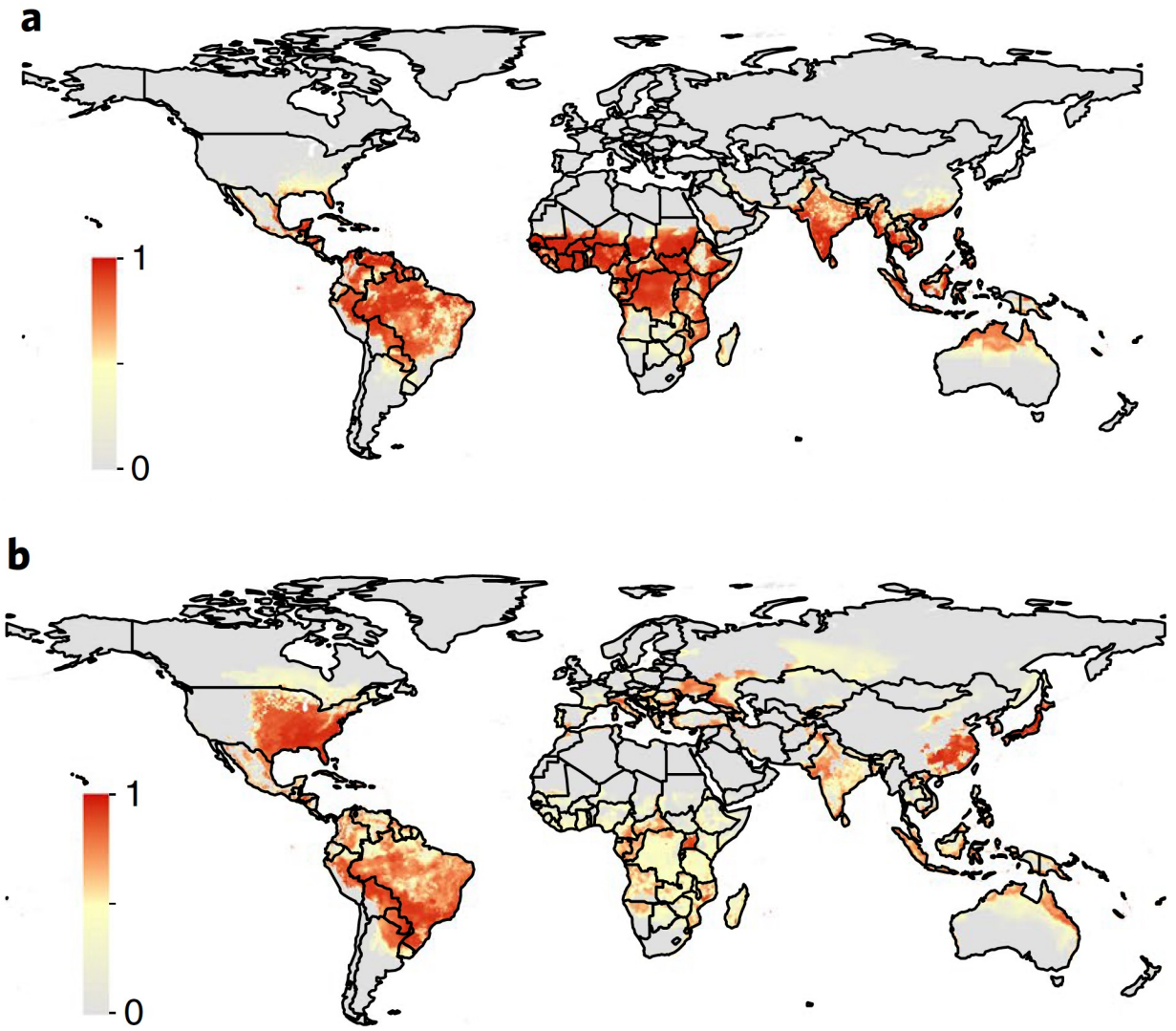



Kraemer *et al.* (2019) *Nat. Microbiol.*

# Predicted geographical distribution by 2050

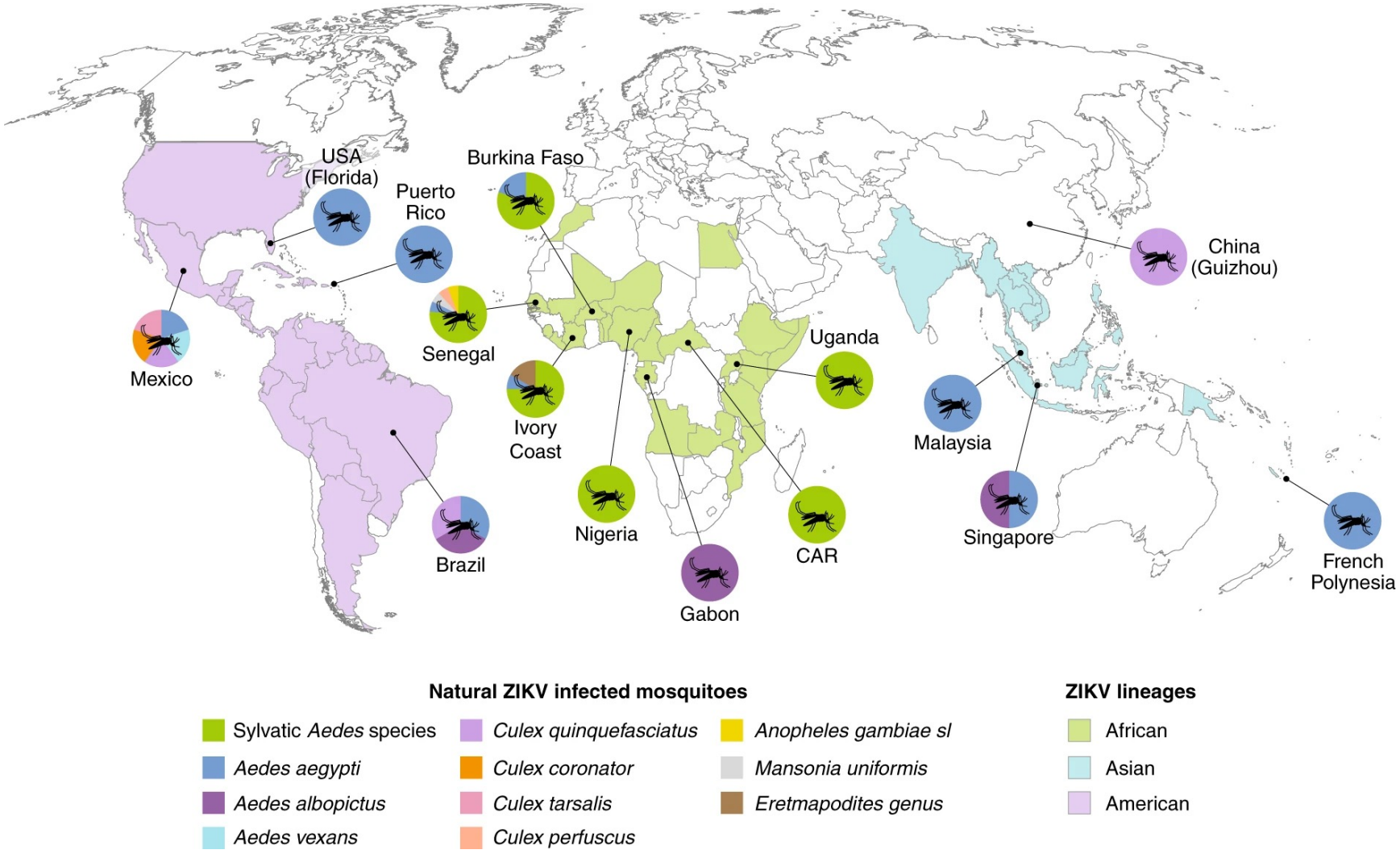
***A. aegypti***

***A. albopictus***



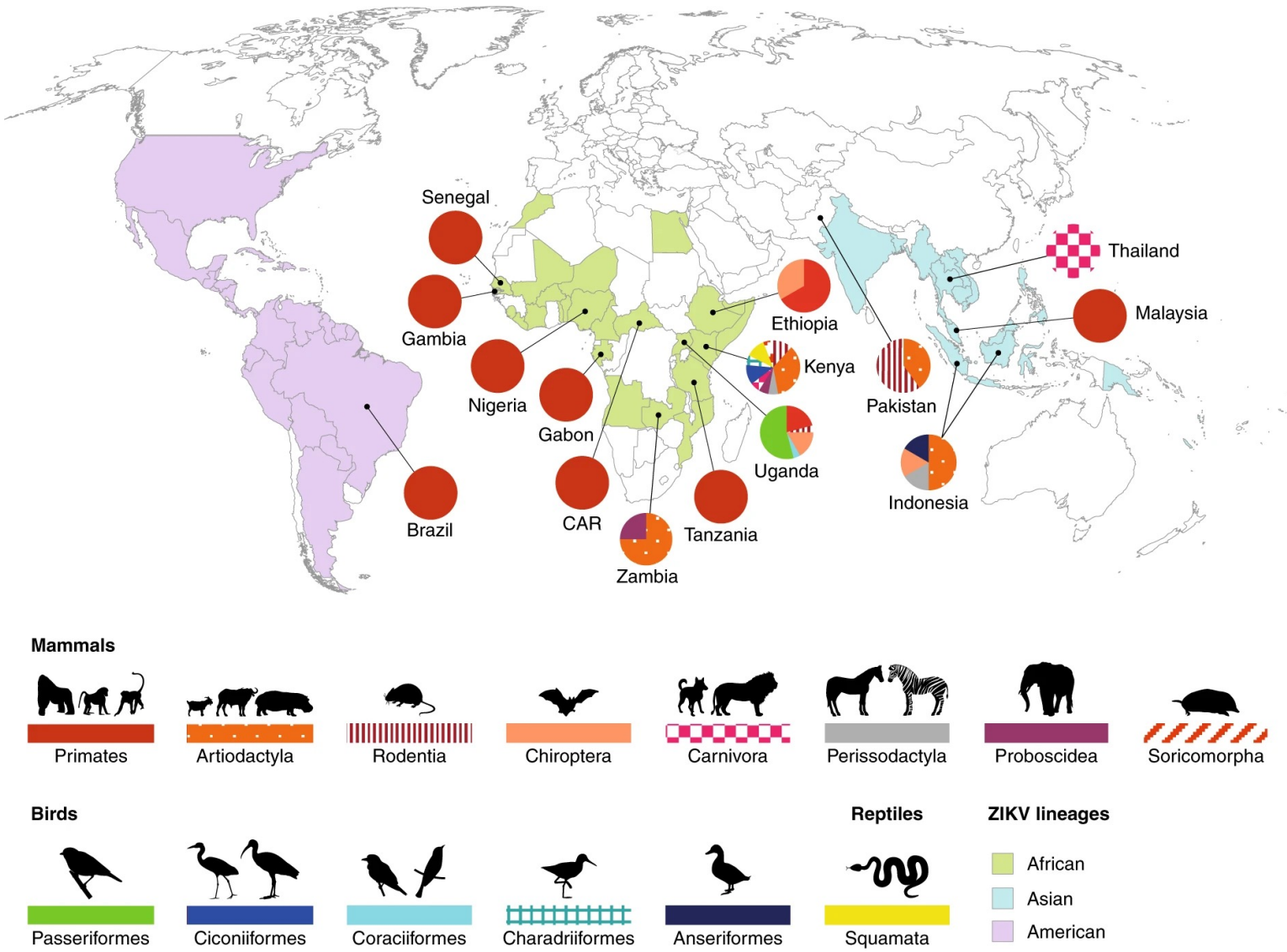

Kraemer *et al.* (2019) *Nat. Microbiol.*

# Distribution of vectors naturally infected with Zika virus



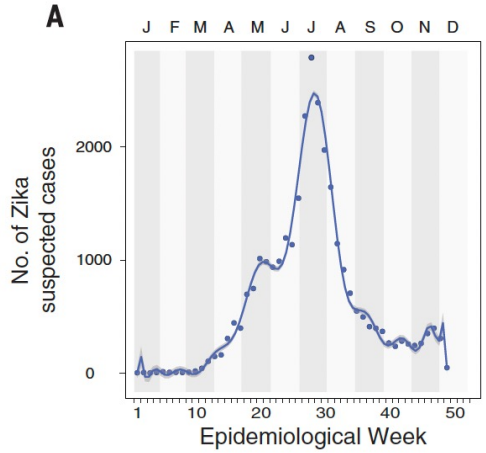

Gutiérrez-Bugallo *et al.* (2019) *Nat. Ecol. Evol.*

# Distribution of hosts reported as susceptible to Zika virus

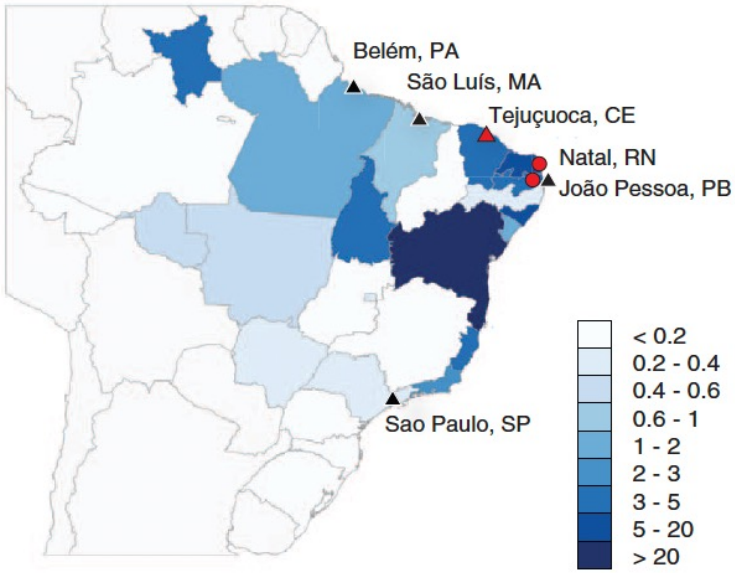



Gutiérrez-Bugallo *et al.* (2019) *Nat. Ecol. Evol.*

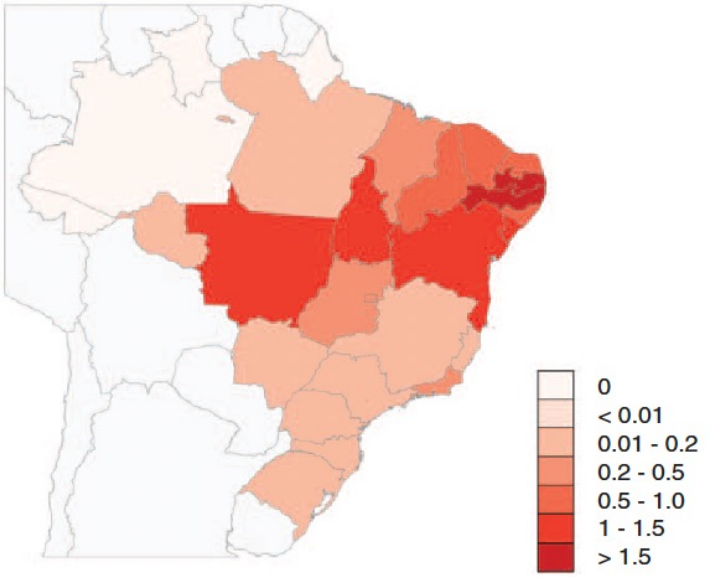
# Zika virus and microcephaly cases in Brazil in 2015




## ZIKV cases

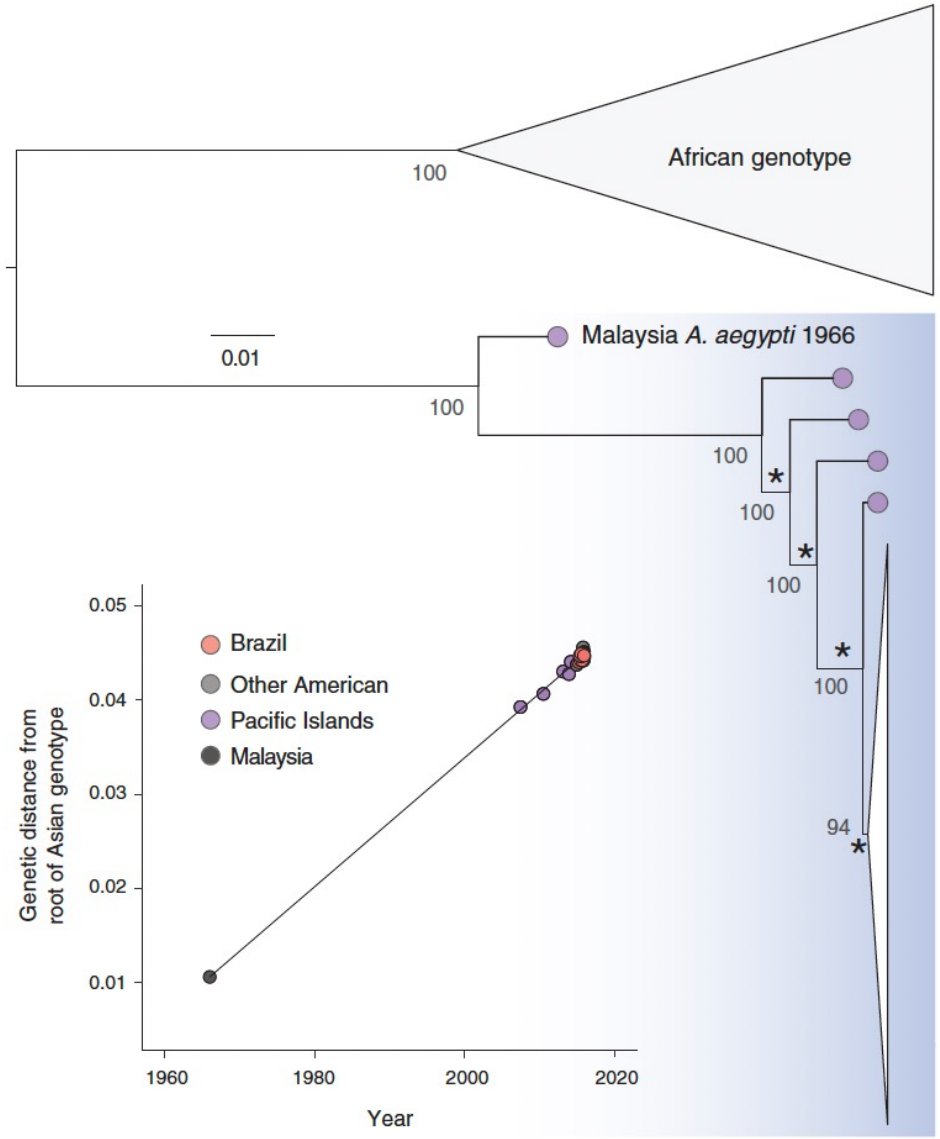



## microcephaly cases



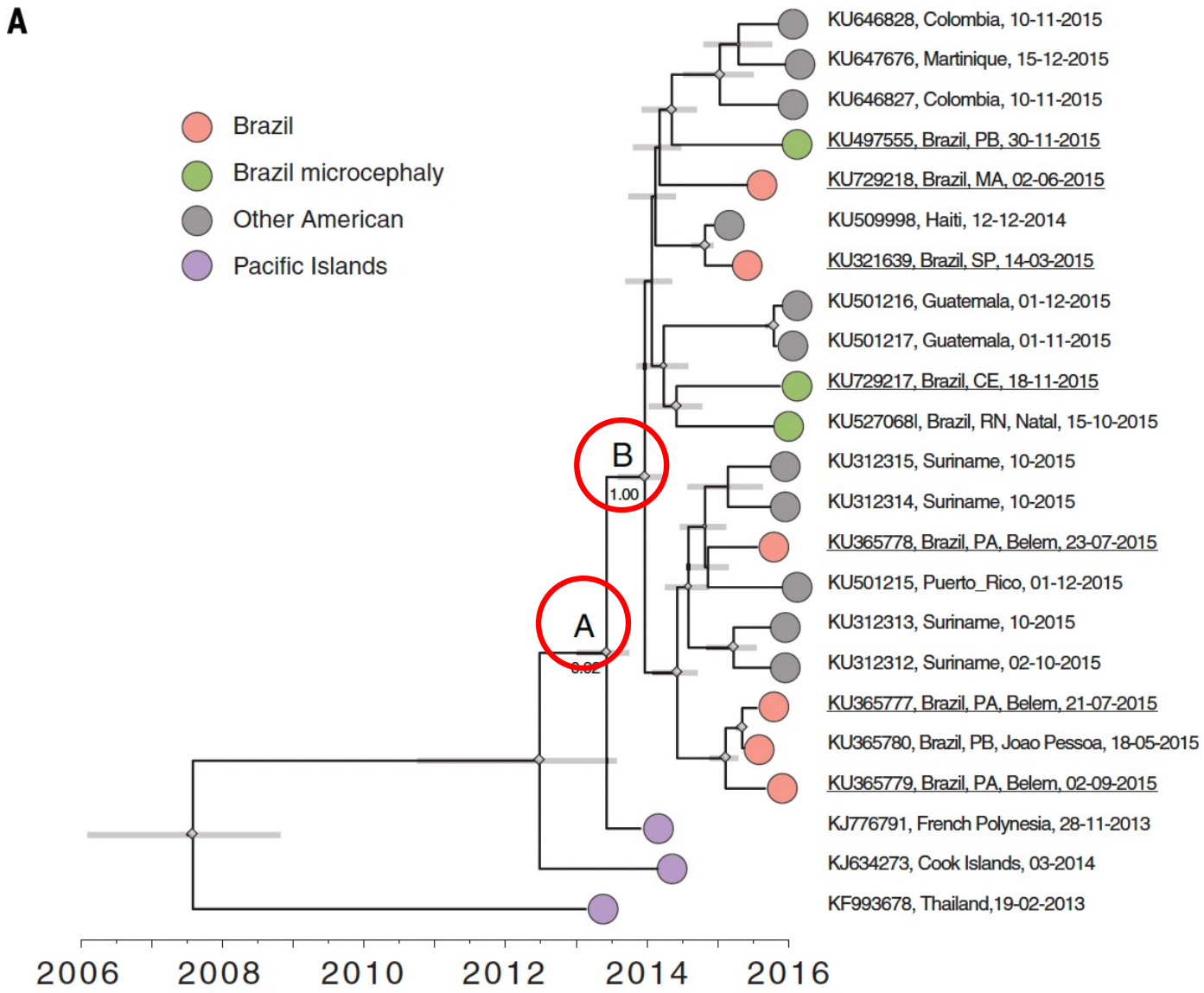

Faria *et al.* (2016) *Science*

# Phylogeny of ZIKV



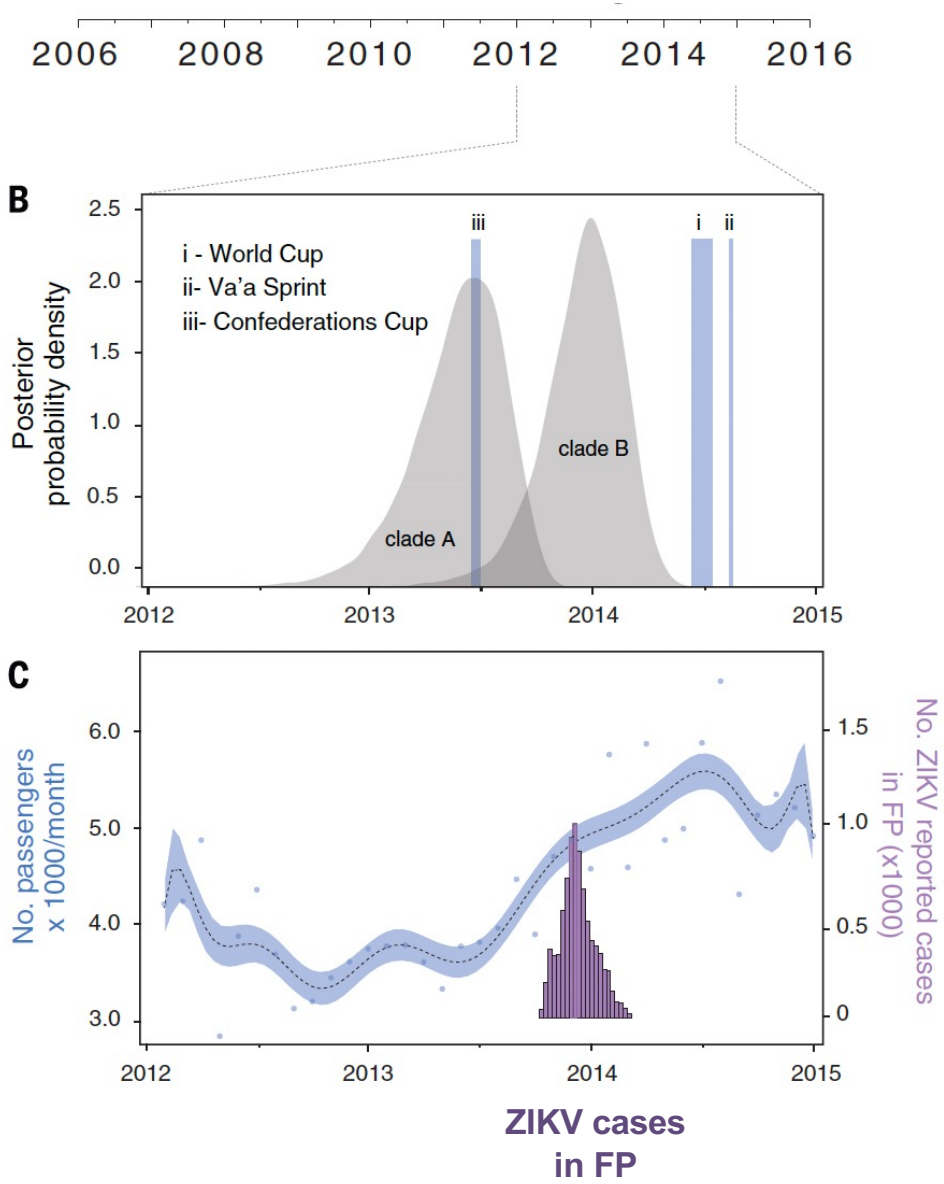

Faria *et al.* (2016) *Science*

# Introduction of ZIKV to the Americas



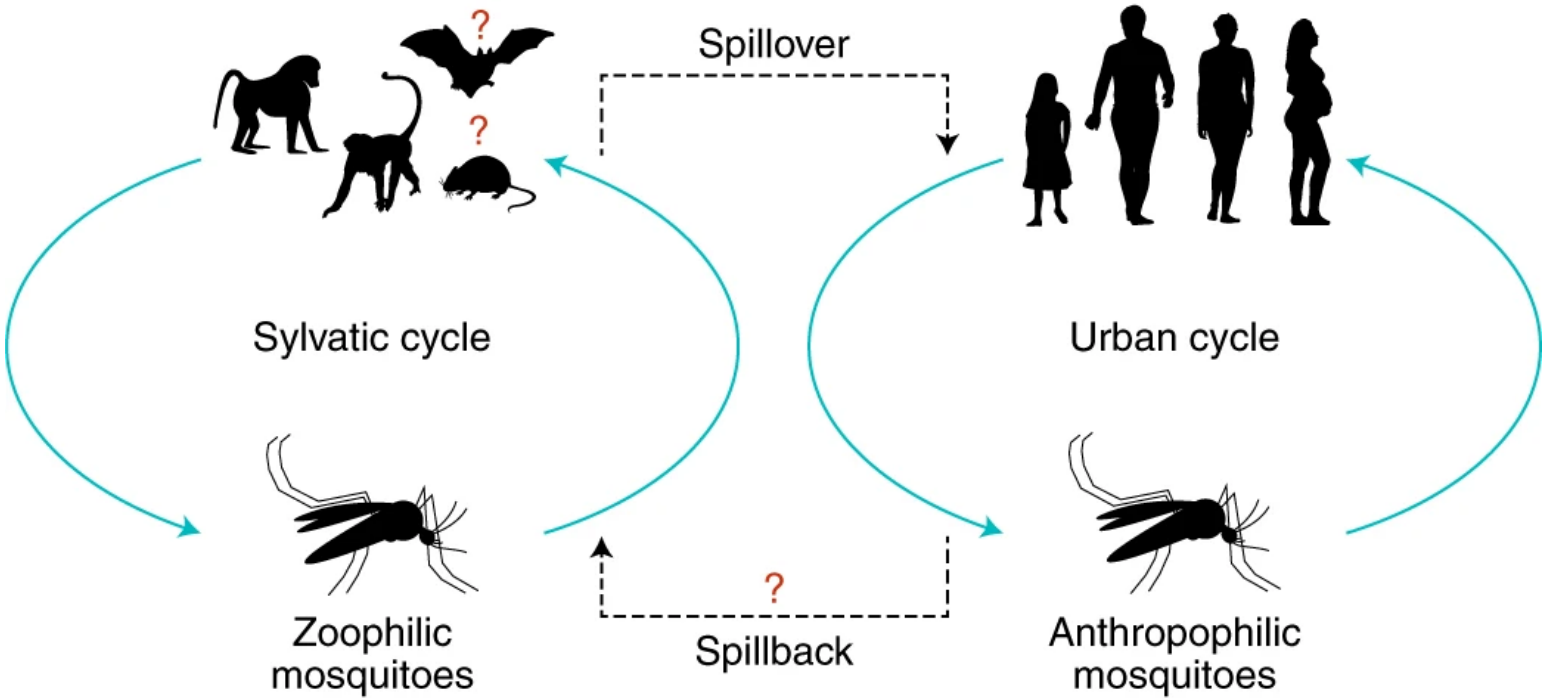

Faria *et al.* (2016) *Science*

# Introduction of ZIKV to the Americas




Faria *et al.* (2016) *Science*

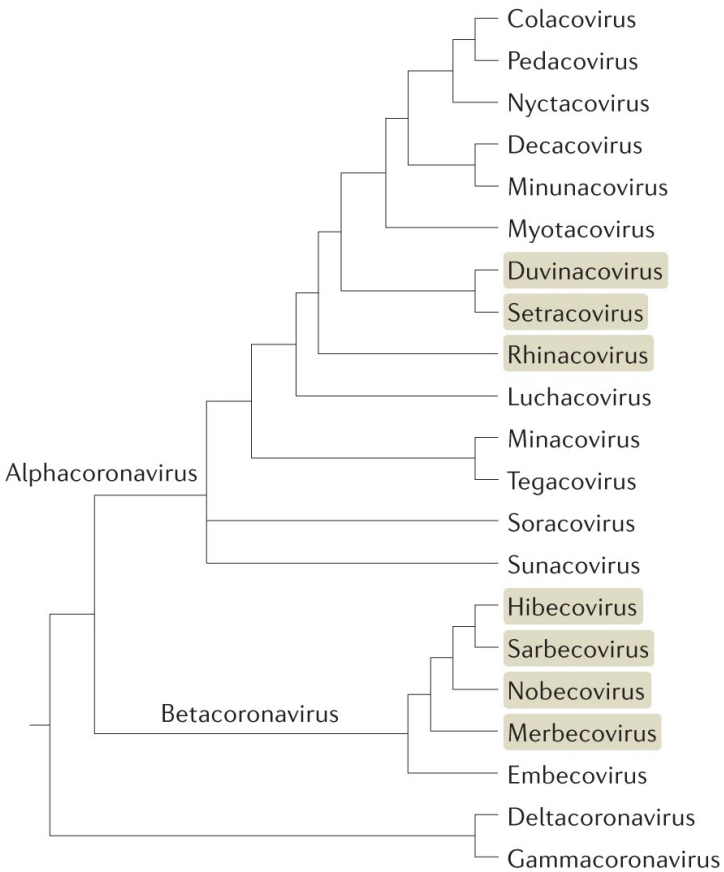
# Zika virus vector-borne transmission




Gutiérrez-Bugallo *et al.* (2019) *Nat. Ecol. Evol.*

# Corona viruses – MERS, SARS, SARS-CoV2

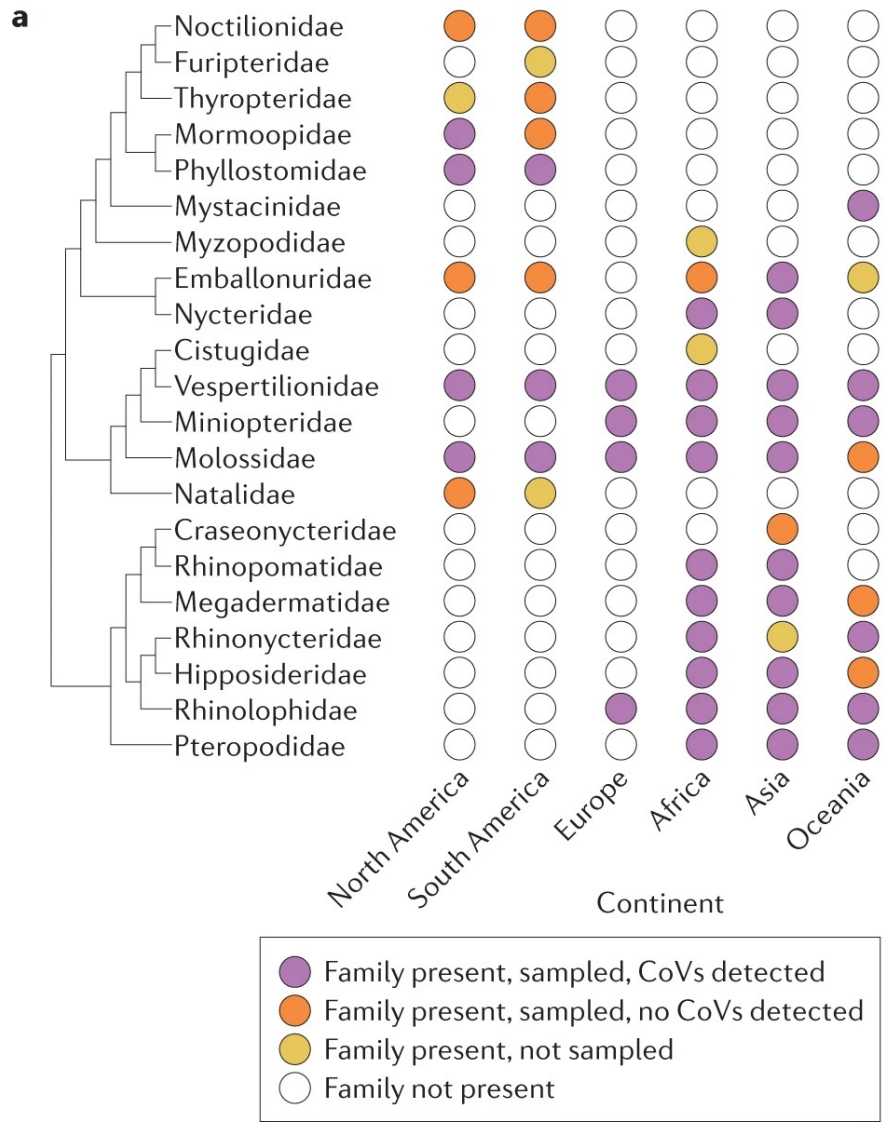
# Coronavirus taxonomy and host distribution




| Genus/subgenus | Notable virus species | Hosts species |
|---|---|---|
| **Alphacoronavirus** | | |
| Colacovirus | Myl-CoV | Bats (Vespertilionidae) |
| Pedacovirus | PEDV | Bats (Vespertilionidae), pigs |
| Nyctacovirus | | Bats (Vespertilionidae) |
| Decacovirus | | Bats (Hipposideridae, Rhinolophidae) |
| Minunacovirus | | Bats (Miniopteridae) |
| Myotacovirus | | Bats (Vespertilionidae) |
| Duvinacovirus | HCoV-229E | Bats (Hipposideridae), dromedary camels, alpacas, humans |
| Setracovirus | HCoV-NL63 | Bats (Rhinonycteridae), humans |
| Rhinacovirus | SADS-CoV | Bats (Rhinolophidae), pigs |
| Luchacovirus | | Rodents (Muridae, Cricetidae) |
| Minacovirus | | Ferrets, minks |
| Tegacovirus | CCoV, FCoV, TGEV | Cats, dogs, pigs |
| Soracovirus | | Shrews (*Suncus murinus*) |
| Sunacovirus | | Shrews (*Sorex araneus*) |
| **Betacoronavirus** | | |
| Hibecovirus | | Bats (Hipposideridae) |
| Sarbecovirus | SARS-CoV, SARS-CoV-2 | Bats (Rhinolophidae), Malayan pangolins, carnivores (Canidae, Felidae, Mustelidae, Viverridae), humans |
| Nobecovirus | | Bats (Pteropodidae) |
| Merbecovirus | MERS-CoV | Bats (Vespertilionidae), dromedary camels, humans |
| Embecovirus | BCoV, CRCoV, HCoV-OC43, HCoV-HKU1, MCoV | Rodents (Muridae, Cricetidae), dogs, rabbits, cattle, horses, pigs, sable antelopes, dromedary camels, giraffes, humans |
| **Deltacoronavirus** | PorCoV-HKU15 | Birds, pigs |
| **Gammacoronavirus** | IBV | Birds, cetaceans |

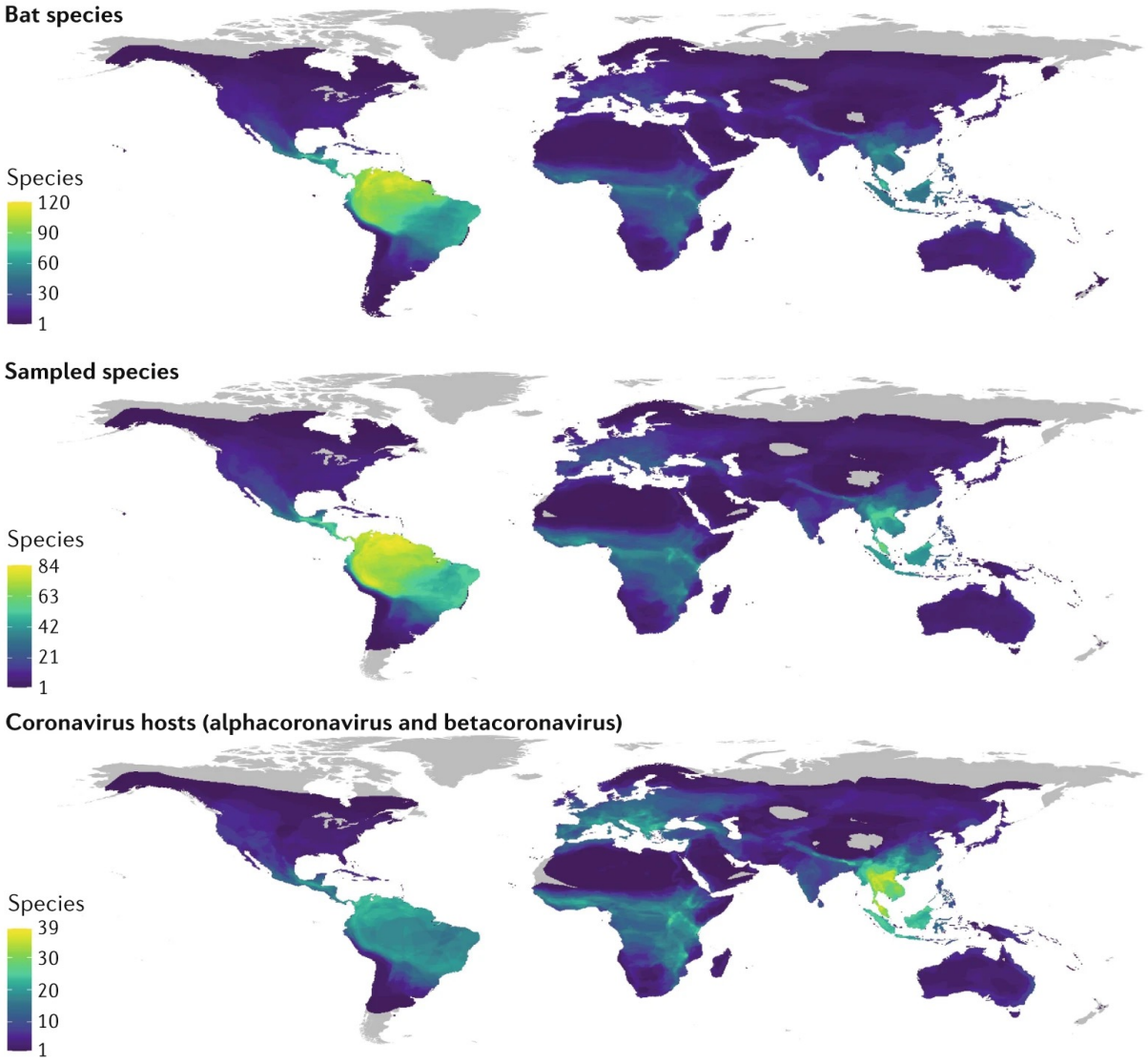
Ruiz-Aravena *et al.* (2021) *Nat. Rev. Microbiol.*

# Distribution of reported bat hosts of coronaviruses



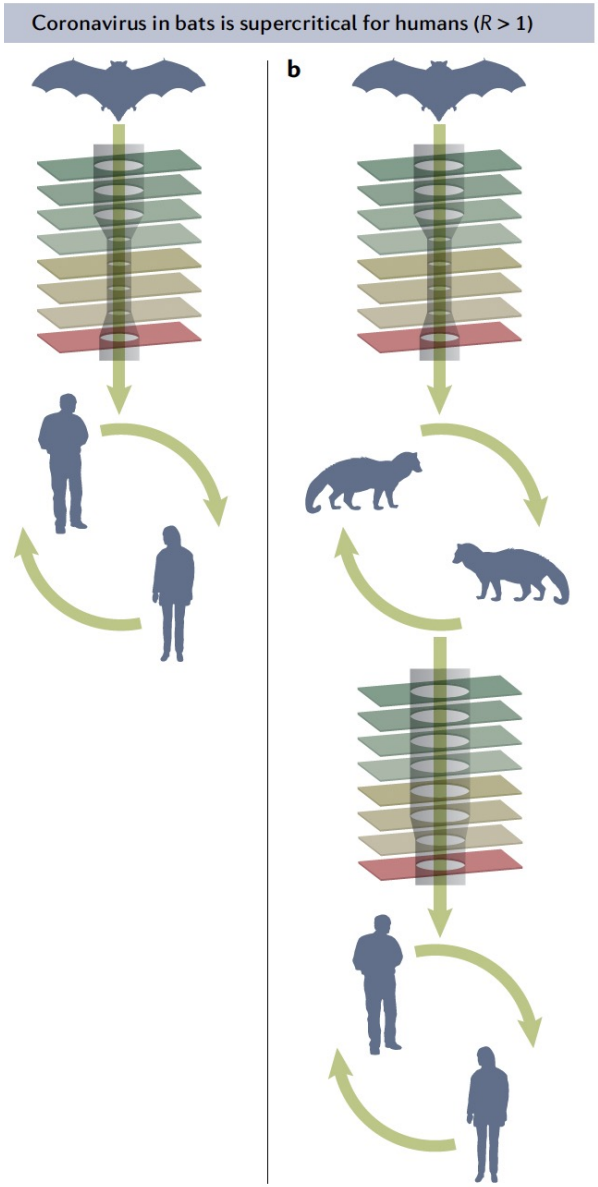

Ruiz-Aravena *et al.* (2021) *Nat. Rev. Microbiol.*

# Geographical distribution of reported bat hosts of CoV



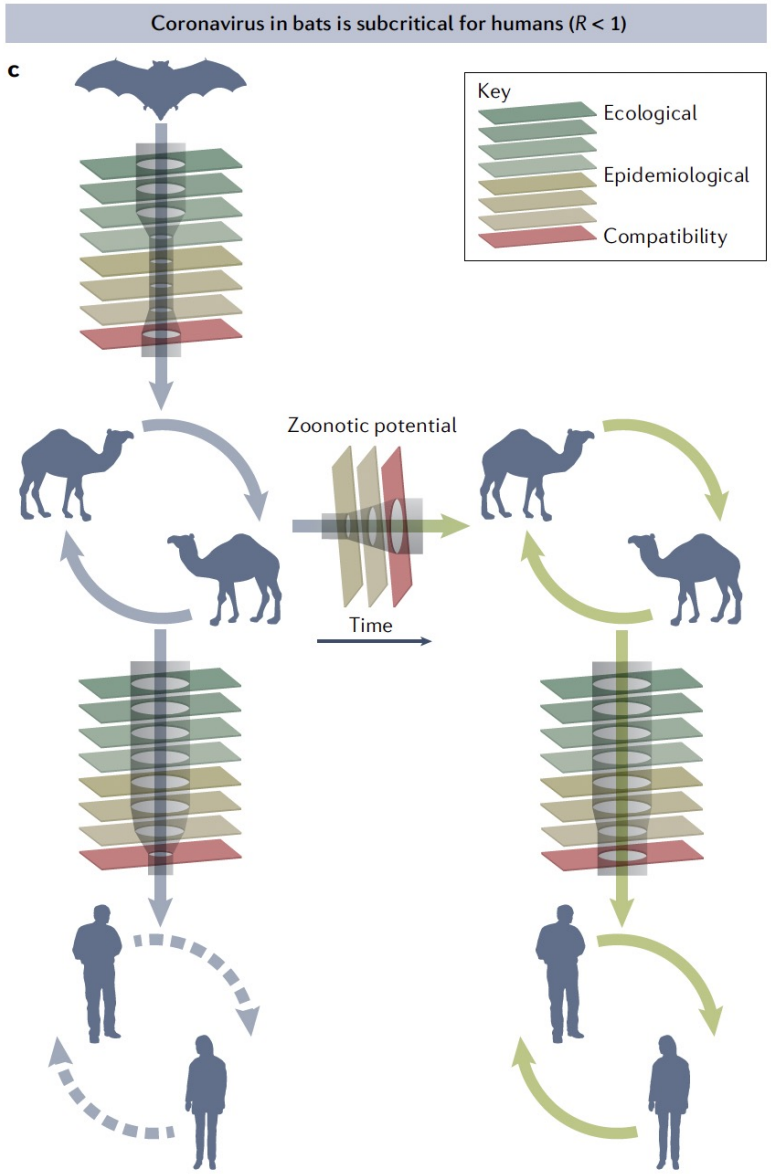

Ruiz-Aravena *et al.* (2021) *Nat. Rev. Microbiol.*

# Pathways to pandemic emergence of bat coronaviruses




Ruiz-Aravena *et al.* (2021) *Nat. Rev. Microbiol.*

# Pathways to pandemic emergence of bat coronaviruses




Ruiz-Aravena *et al.* (2021) *Nat. Rev. Microbiol.*

# SARS: Chronology of the Epidemic

## SARS: Chronology of the Epidemic NOVEMBER 2002 — JULY 2003


**16 November** — First known case of SARS, not identified until much later in Foshan of Guangdong Province, China.

**23 January** — Guangdong Health Bureau sends official document on atypical pneumonia to provincial health bureaus and medical institutions.

**30 January** — Seafood seller in Guangzhou infects more than 50 hospital staff members and 19 relatives, the first known "superspreading event."

**10 February** — World Health Organization's (WHO's) Beijing office receives e-mail warning of a "strange contagious disease" in Guangdong.

**11 February** — Guangdong officials report 305 cases and five deaths of acute respiratory syndrome between 16 November 2002 and 9 February 2003.

**14 February** — The Chinese Ministry of Health informs WHO that the Guangdong outbreak is under control.

**21 February** — A Guangdong physician falls ill in Hong Kong's Metropole Hotel. Other guests carry SARS to Hanoi, Singapore, and Toronto.

**26 February** — A Chinese-American businessman from New York who stayed at the Metropole Hotel is admitted to the French Hospital in Hanoi.

**3 March** — Carlo Urbani examines the Hanoi case and notifies WHO's regional office in Manila of unusual disease.

**7 March** — Health care workers at Hong Kong's Prince of Wales Hospital start falling ill.

Enserink (2013) *Science*

# SARS: Chronology of the Epidemic

**10 March** — Outbreak explodes in Hanoi hospital; at least 22 staff members fall ill with influenzalike symptoms.

**12 March** — WHO issues a rare global alert about a severe form of "atypical pneumonia."

**15 March** — In second alert, WHO names disease SARS, calls it "a worldwide health threat" and issues travel advisories.

**17 March** — WHO sets up network of 11 labs to hunt for the agent causing SARS. Networks for clinicians and epidemiologists will follow.

**24 March** — Scientists in the lab network finger new coronavirus.

**29 March** — WHO's Urbani dies of SARS in Bangkok.

**30 March** — Start of SARS outbreak in Amoy Gardens apartment complex in Hong Kong. More than 300 become infected.


**16 April** — WHO says that macaque study in Rotterdam clinches the case for a new coronavirus as the cause of SARS.

**18 April** — WHO team in Beijing expresses strong concern over inadequate reporting of SARS cases.

**20 April** — Beijing acknowledges 339 previously undisclosed cases. China's minister of health and mayor of Beijing are fired.

Enserink (2013) *Science*

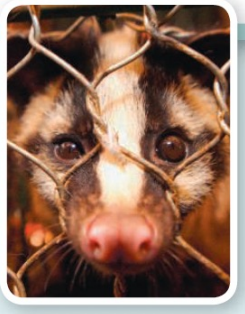
# SARS: Chronology of the Epidemic

**25 April** — Outbreaks in Hanoi, Hong Kong, Singapore, and Toronto show signs of peaking.

**28 April** — Vietnam becomes first country to successfully end SARS outbreak.

**14 May** — Toronto declared SARS-free.

**22 May** — Canada reports new SARS cluster in Toronto.



**23 May** — Scientists announce detection of SARS-like virus in the Himalayan palm civet and raccoon dog.

**31 May** — Singapore declared SARS-free.

**23 June** — Hong Kong declared SARS-free.

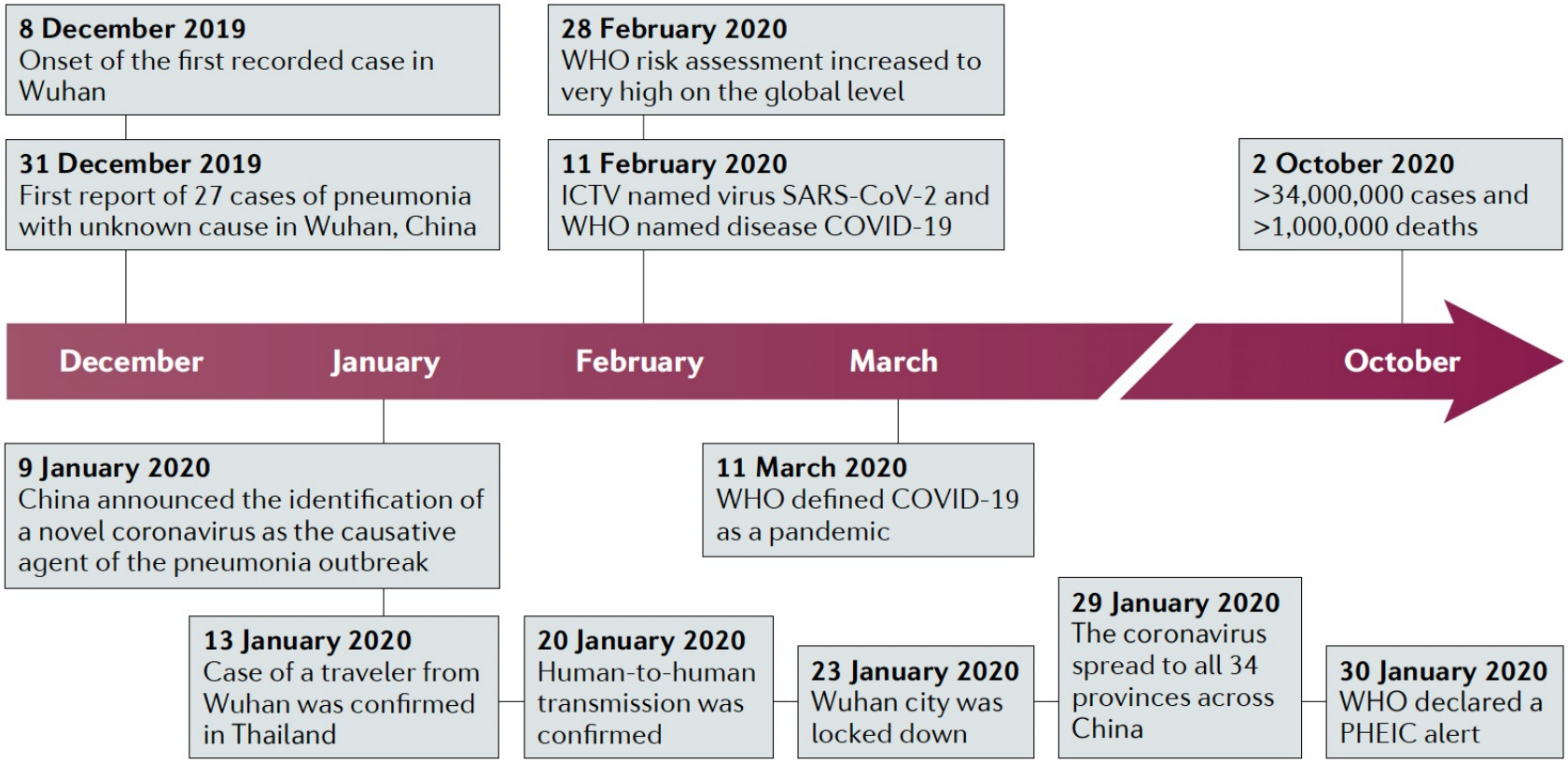
**24 June** — Beijing declared SARS-free.


**2 July** — Toronto declared SARS-free a second time.

**5 July** — Taiwan declared SARS-free. After 8096 cases and 774 deaths, WHO declares the end of the SARS epidemic.

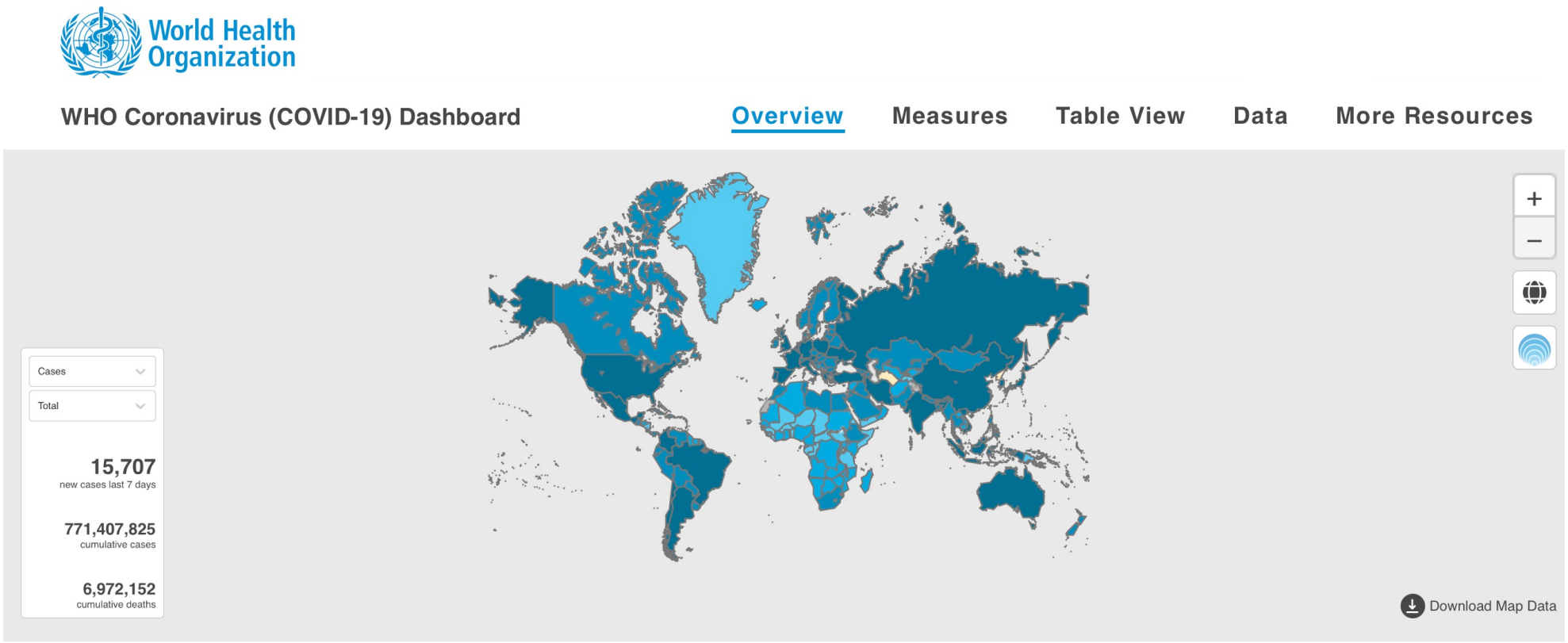
Enserink (2013) *Science*

# Timeline of the key events of the COVID-19 outbreak




Hu *et al.* (2021) *Nat. Rev. Microbiol.*

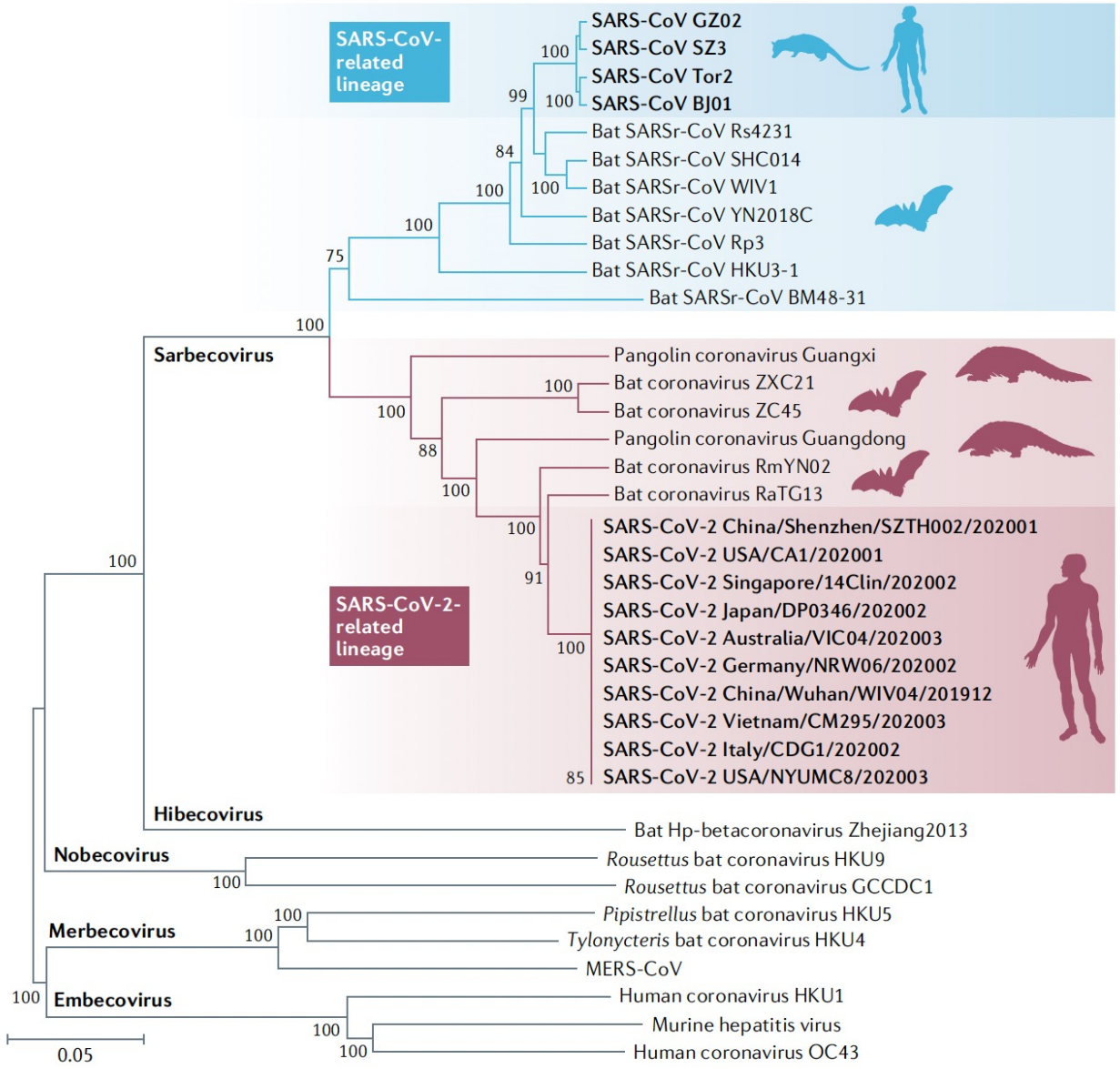
# Phylogenetic tree




**Globally**, as of **4:37pm CEST, 18 October 2023**, there have been **771,407,825 confirmed cases** of COVID-19, including **6,972,152 deaths**, reported to WHO. As of **8 October 2023**, a total of **13,516,282,548 vaccine doses** have been administered.

*WHO*

# Phylogenetic tree




Hu *et al.* (2021) *Nat. Rev. Microbiol.*

# Newest study on virome of small animals

# Virome composition in wild small mammals

- A large number of novel viruses were identified in wild small mammals from China.
- Some were of evolutionary significance or had the ability to jump species boundaries.
- Shrews carried the most viruses in total and in a single animal species.
- Rodents harbored most viruses with the potential be transmitted to new host species.

Chen *et al.* (2023) *Cell*

# Emerging infectious diseases

Infectious zoonotic diseases typically emerge as a result of complex interactions between humans and wild and/or domestic animals

**Around 70% of EIDs, and almost all recent pandemics, originate in animals (the majority in wildlife), and their emergence stems from complex interactions among wild and/or domestic animals and humans.**

Di Marco *et al.* (2020) *PNAS*