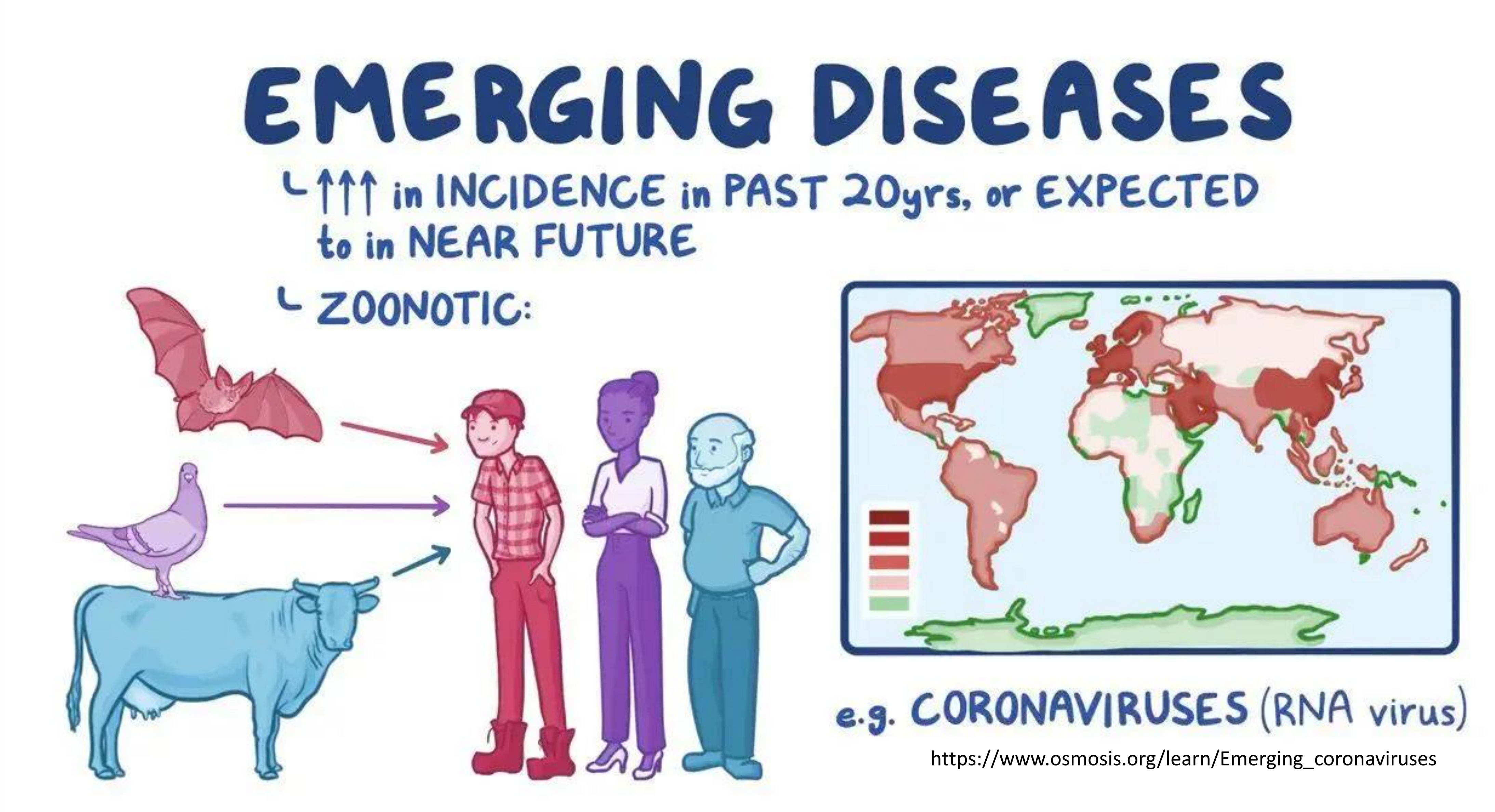
Emerging and re-emerging viruses

Emerging and re-emerging viruses

Key players among the different pathogens that have caused recent epidemics

Emerging viruses are defined as those causing new human infections that had never been encountered earlier

Re-emerging viruses are defined as those causing infections after lying quiescent for many years or even decades…
(new target population, changes in viral biology, etc.)



EMERGING DISEASES

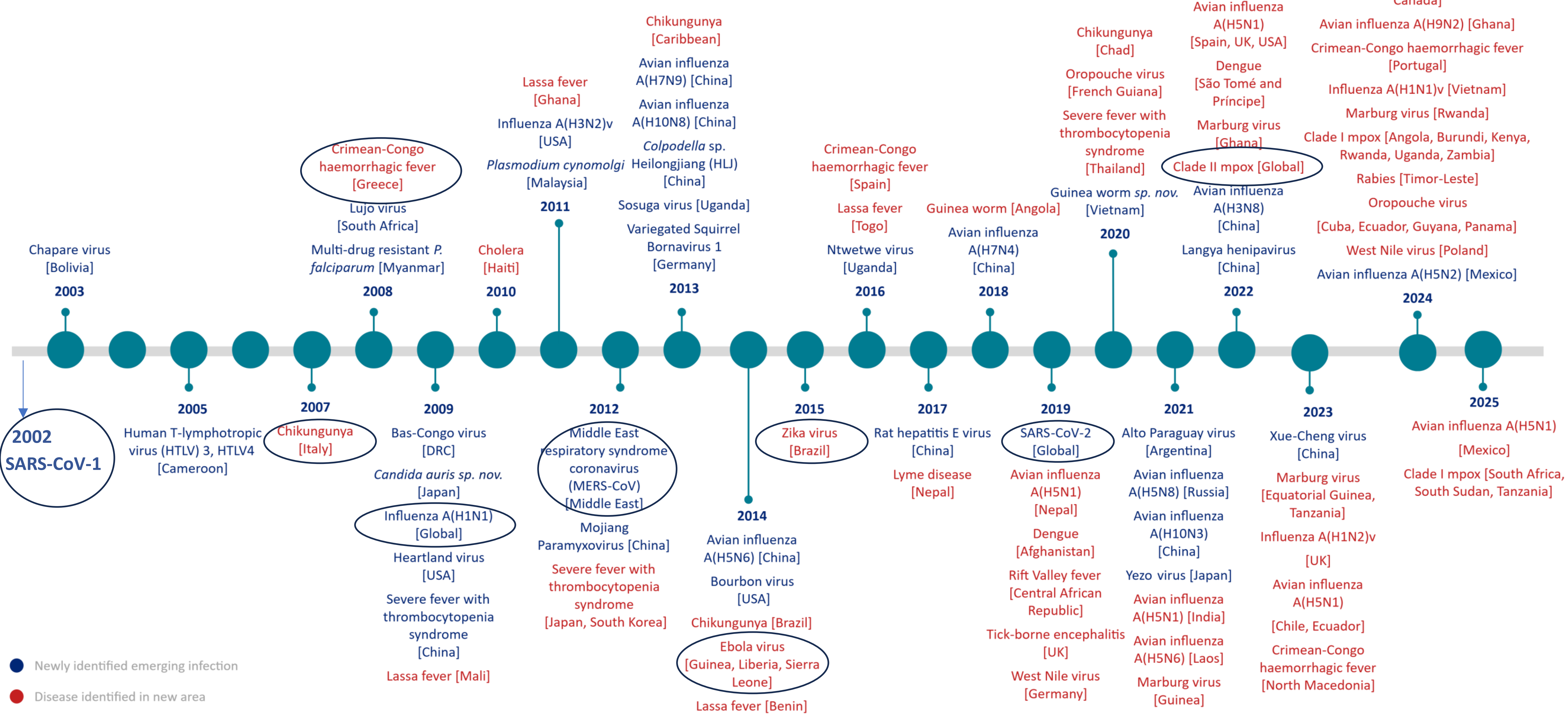
- ↑↑↑ in INCIDENCE in PAST 20yrs, or EXPECTED to in NEAR FUTURE
- ZOONOTIC:

e.g. CORONAVIRUSES (RNA virus)

https://www.osmosis.org/learn/Emerging_coronaviruses

Between 60% and 80% of emerging infections are derived from animal sources

Timeline of emerging infections since 2003



2002
SARS-CoV-1

2003
Chapare virus [Bolivia]

2005
Human T-lymphotropic virus (HTLV) 3, HTLV4 [Cameroon]

2007
Chikungunya [Italy]

2008
Crimean-Congo haemorrhagic fever [Greece]
Lujo virus [South Africa]
Multi-drug resistant *P. falciparum* [Myanmar]

2009
Bas-Congo virus [DRC]
Candida auris sp. nov. [Japan]
Influenza A(H1N1) [Global]
Heartland virus [USA]
Severe fever with thrombocytopenia syndrome [China]
Lassa fever [Mali]

2010
Cholera [Haiti]

2011
Lassa fever [Ghana]
Influenza A(H3N2)v [USA]
Plasmodium cynomolgi [Malaysia]

2012
Middle East respiratory syndrome coronavirus (MERS-CoV) [Middle East]
Mojiang Paramyxovirus [China]
Severe fever with thrombocytopenia syndrome [Japan, South Korea]

2013
Chikungunya [Caribbean]
Avian influenza A(H7N9) [China]
Avian influenza A(H10N8) [China]
Colpodella sp. Heilongjiang (HLJ) [China]
Sosuga virus [Uganda]
Variegated Squirrel Bornavirus 1 [Germany]

2014
Avian influenza A(H5N6) [China]
Bourbon virus [USA]
Chikungunya [Brazil]
Ebola virus [Guinea, Liberia, Sierra Leone]
Lassa fever [Benin]

2015
Zika virus [Brazil]

2016
Crimean-Congo haemorrhagic fever [Spain]
Lassa fever [Togo]
Ntwetwe virus [Uganda]

2017
Rat hepatitis E virus [China]
Lyme disease [Nepal]

2018
Guinea worm [Angola]
Avian influenza A(H7N4) [China]

2019
SARS-CoV-2 [Global]
Avian influenza A(H5N1) [Nepal]
Dengue [Afghanistan]
Rift Valley fever [Central African Republic]
Tick-borne encephalitis [UK]
West Nile virus [Germany]

2020
Chikungunya [Chad]
Oropouche virus [French Guiana]
Severe fever with thrombocytopenia syndrome [Thailand]
Guinea worm *sp. nov.* [Vietnam]

2021
Alto Paraguay virus [Argentina]
Avian influenza A(H5N8) [Russia]
Avian influenza A(H10N3) [China]
Yezo virus [Japan]
Avian influenza A(H5N1) [India]
Avian influenza A(H5N6) [Laos]
Marburg virus [Guinea]

2022
Avian influenza A(H5N1) [Spain, UK, USA]
Dengue [São Tomé and Príncipe]
Marburg virus [Ghana]
Clade II mpox [Global]
Avian influenza A(H3N8) [China]
Langya henipavirus [China]

2023
Xue-Cheng virus [China]
Marburg virus [Equatorial Guinea, Tanzania]
Influenza A(H1N2)v [UK]
Avian influenza A(H5N1) [Chile, Ecuador]
Crimean-Congo haemorrhagic fever [North Macedonia]

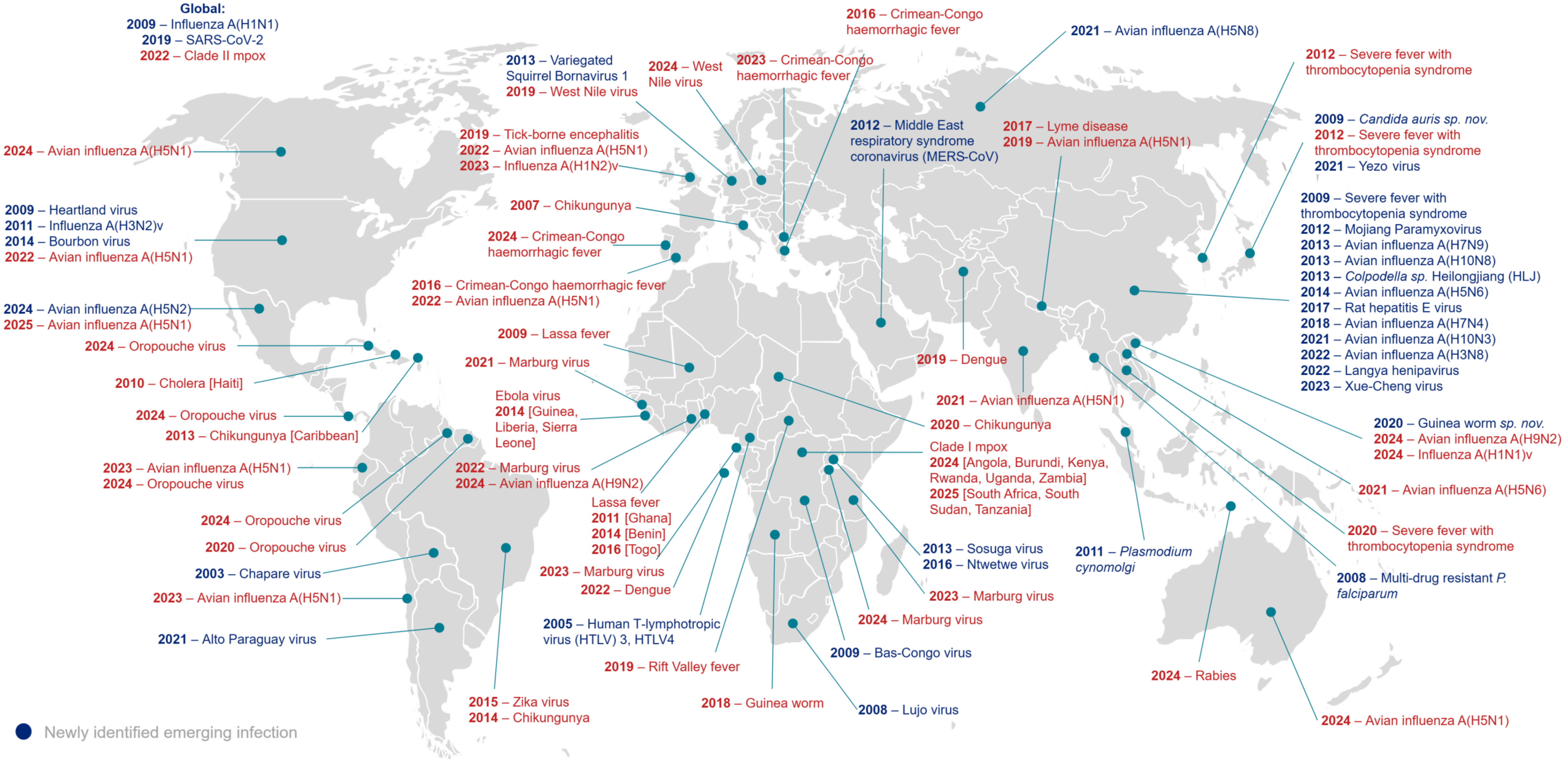
2024
Avian influenza A(H5N1) [Australia, Canada]
Avian influenza A(H9N2) [Ghana]
Crimean-Congo haemorrhagic fever [Portugal]
Influenza A(H1N1)v [Vietnam]
Marburg virus [Rwanda]
Clade I mpox [Angola, Burundi, Kenya, Rwanda, Uganda, Zambia]
Rabies [Timor-Leste]
Oropouche virus [Cuba, Ecuador, Guyana, Panama]
West Nile virus [Poland]
Avian influenza A(H5N2) [Mexico]

2025
Avian influenza A(H5N1) [Mexico]
Clade I mpox [South Africa, South Sudan, Tanzania]

🔵 Newly identified emerging infection
🔴 Disease identified in new area

https://www.gov.uk/government/publications/emerging-infections-characteristics-epidemiology-and-global-distribution/emerging-infections-how-and-why-they-arise

Global map of emerging infections since 2003



Global:
2009 – Influenza A(H1N1)
2019 – SARS-CoV-2
2022 – Clade II mpox

2024 – Avian influenza A(H5N1)

2009 – Heartland virus
2011 – Influenza A(H3N2)v
2014 – Bourbon virus
2022 – Avian influenza A(H5N1)

2024 – Avian influenza A(H5N2)
2025 – Avian influenza A(H5N1)

2024 – Oropouche virus

2010 – Cholera [Haiti]

2024 – Oropouche virus

2013 – Chikungunya [Caribbean]

2023 – Avian influenza A(H5N1)
2024 – Oropouche virus

2024 – Oropouche virus

2020 – Oropouche virus

2003 – Chapare virus

2023 – Avian influenza A(H5N1)

2021 – Alto Paraguay virus

2015 – Zika virus
2014 – Chikungunya

2013 – Variegated Squirrel Bornavirus 1
2019 – West Nile virus

2024 – West Nile virus

2023 – Crimean-Congo haemorrhagic fever

2016 – Crimean-Congo haemorrhagic fever

2019 – Tick-borne encephalitis
2022 – Avian influenza A(H5N1)
2023 – Influenza A(H1N2)v

2007 – Chikungunya

2024 – Crimean-Congo haemorrhagic fever

2016 – Crimean-Congo haemorrhagic fever
2022 – Avian influenza A(H5N1)

2009 – Lassa fever

2021 – Marburg virus

Ebola virus
2014 [Guinea, Liberia, Sierra Leone]

2022 – Marburg virus
2024 – Avian influenza A(H9N2)

Lassa fever
2011 [Ghana]
2014 [Benin]
2016 [Togo]

2023 – Marburg virus

2022 – Dengue

2005 – Human T-lymphotropic virus (HTLV) 3, HTLV4

2019 – Rift Valley fever

2018 – Guinea worm

2008 – Lujo virus

2009 – Bas-Congo virus

2024 – Marburg virus

2023 – Marburg virus

2013 – Sosuga virus
2016 – Ntwetwe virus

Clade I mpox
2024 [Angola, Burundi, Kenya, Rwanda, Uganda, Zambia]
2025 [South Africa, South Sudan, Tanzania]

2020 – Chikungunya

2021 – Avian influenza A(H5N1)

2019 – Dengue

2012 – Middle East respiratory syndrome coronavirus (MERS-CoV)

2017 – Lyme disease
2019 – Avian influenza A(H5N1)

2021 – Avian influenza A(H5N8)

2012 – Severe fever with thrombocytopenia syndrome

2009 – *Candida auris sp. nov.*
2012 – Severe fever with thrombocytopenia syndrome
2021 – Yezo virus

2009 – Severe fever with thrombocytopenia syndrome
2012 – Mojiang Paramyxovirus
2013 – Avian influenza A(H7N9)
2013 – Avian influenza A(H10N8)
2013 – *Colpodella sp.* Heilongjiang (HLJ)
2014 – Avian influenza A(H5N6)
2017 – Rat hepatitis E virus
2018 – Avian influenza A(H7N4)
2021 – Avian influenza A(H10N3)
2022 – Avian influenza A(H3N8)
2022 – Langya henipavirus
2023 – Xue-Cheng virus

2020 – Guinea worm *sp. nov.*
2024 – Avian influenza A(H9N2)
2024 – Influenza A(H1N1)v

2021 – Avian influenza A(H5N6)

2020 – Severe fever with thrombocytopenia syndrome

2008 – Multi-drug resistant *P. falciparum*

2011 – *Plasmodium cynomolgi*

2024 – Rabies

2024 – Avian influenza A(H5N1)

● Newly identified emerging infection

● Disease identified in new area

https://www.gov.uk/government/publications/emerging-infections-characteristics-epidemiology-and-global-distribution/emerging-infections-how-and-why-they-arise

How infections emerge

Between 60% and 80% of emerging infections are derived from animal sources

Infectious disease emergence involves two main steps:

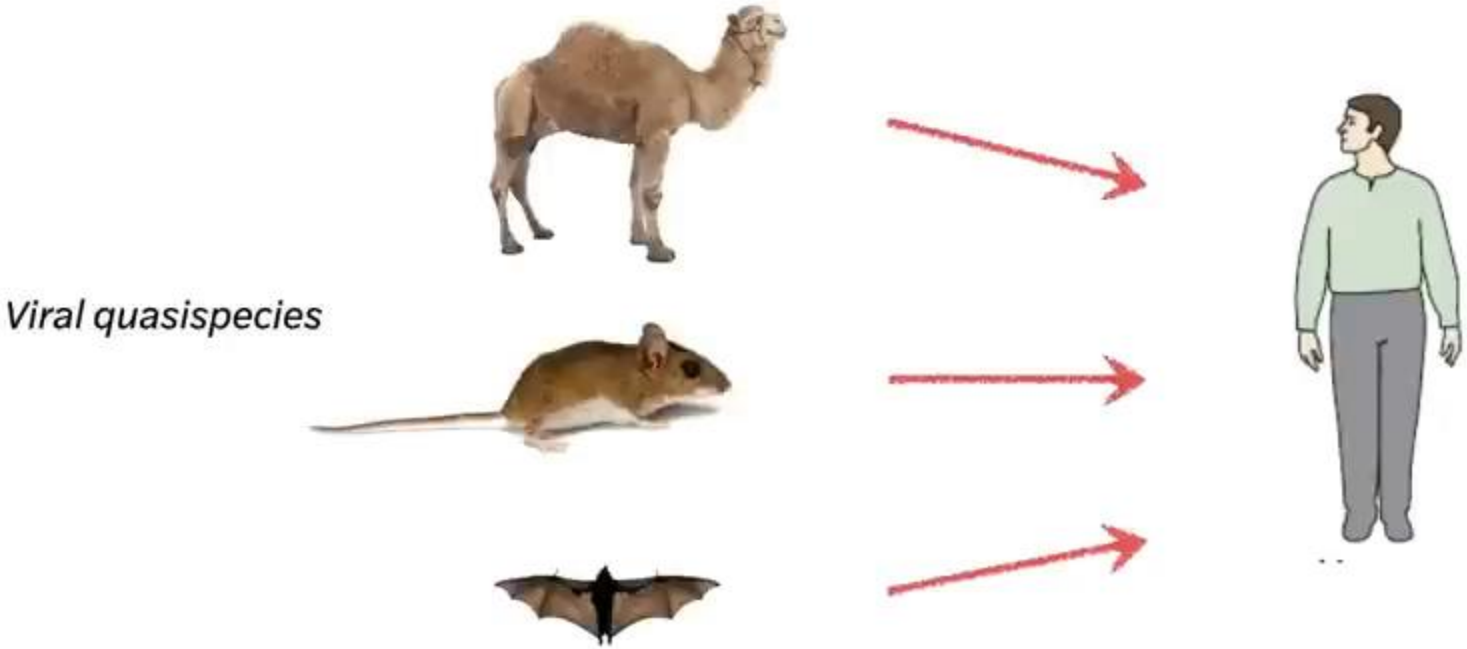
1. An agent is introduced into a new host population.

2.The agent is established and transmitted within the new host population.

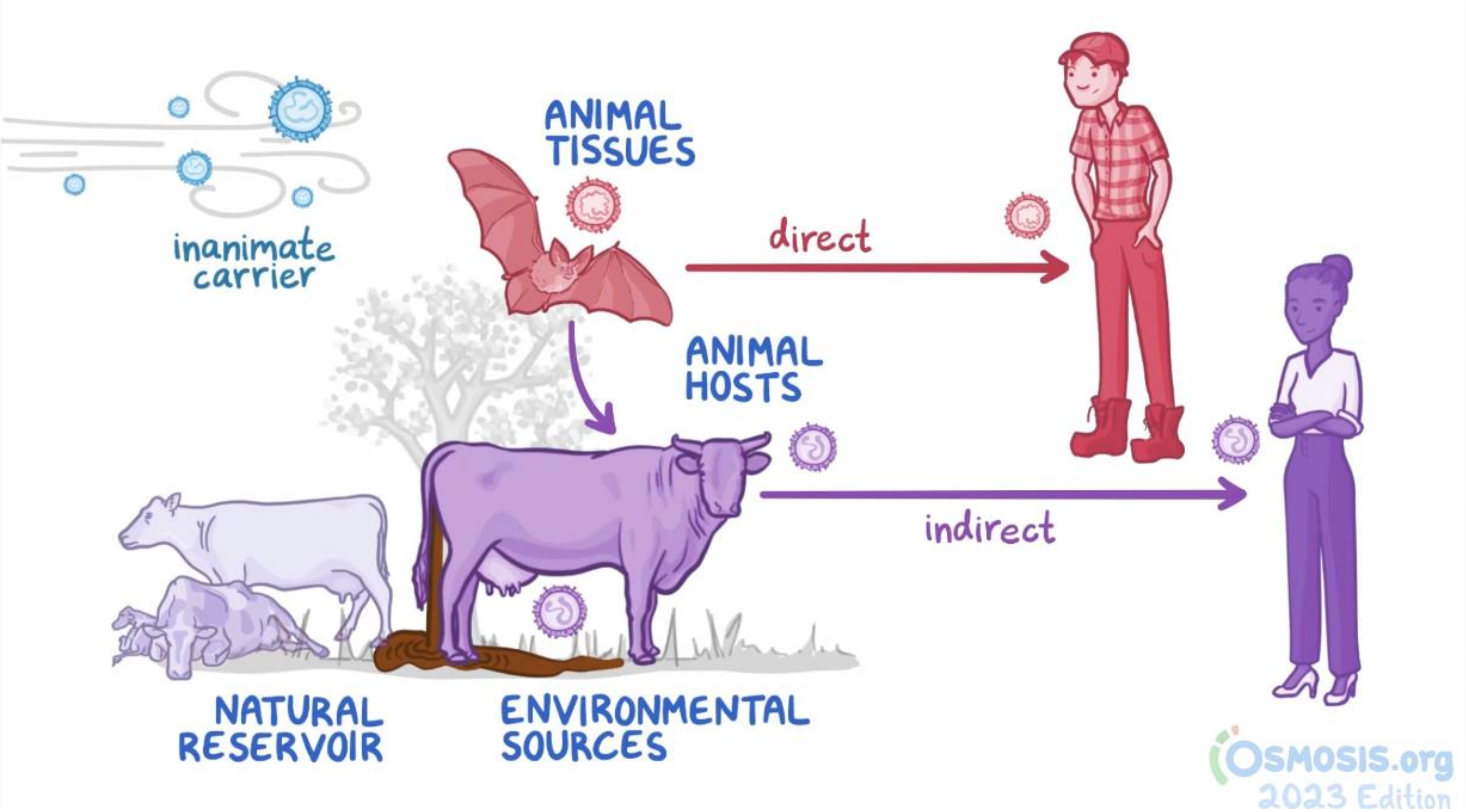
Infections have been emerging for thousands of years as interactions between humans; animals and their environments have increased and changed.

Emerging infections: Two steps

- Encounter
- Establishment and dissemination

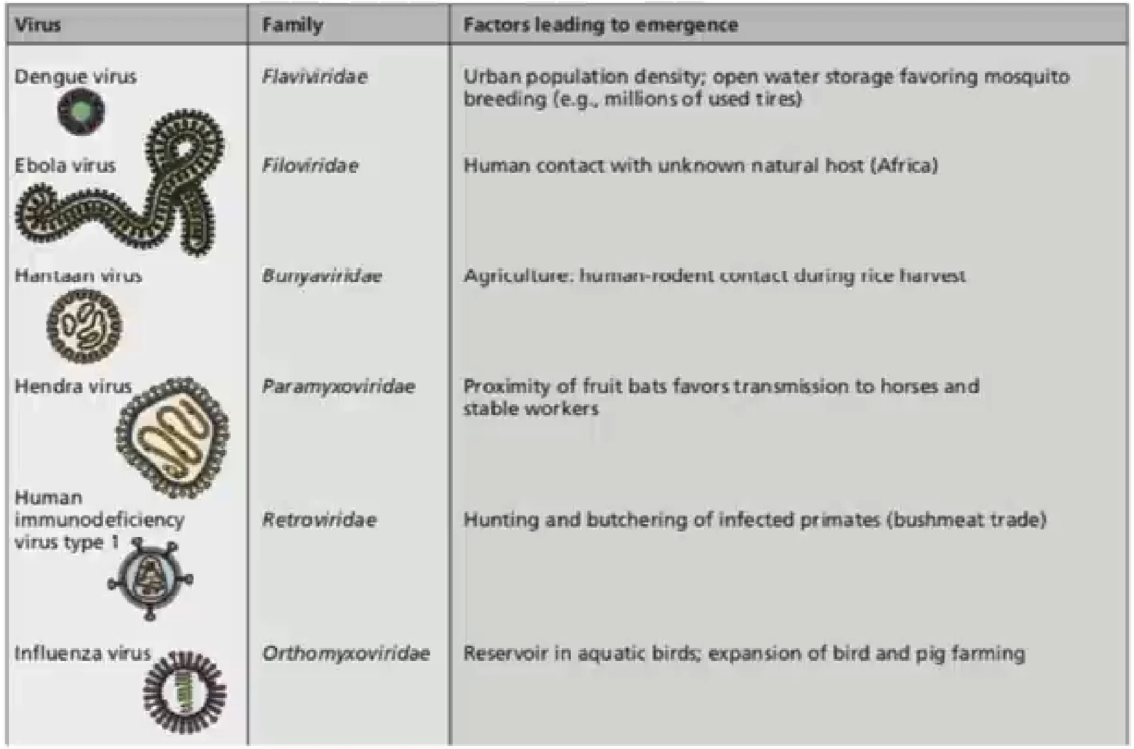


Principles of Virology, ASM Press

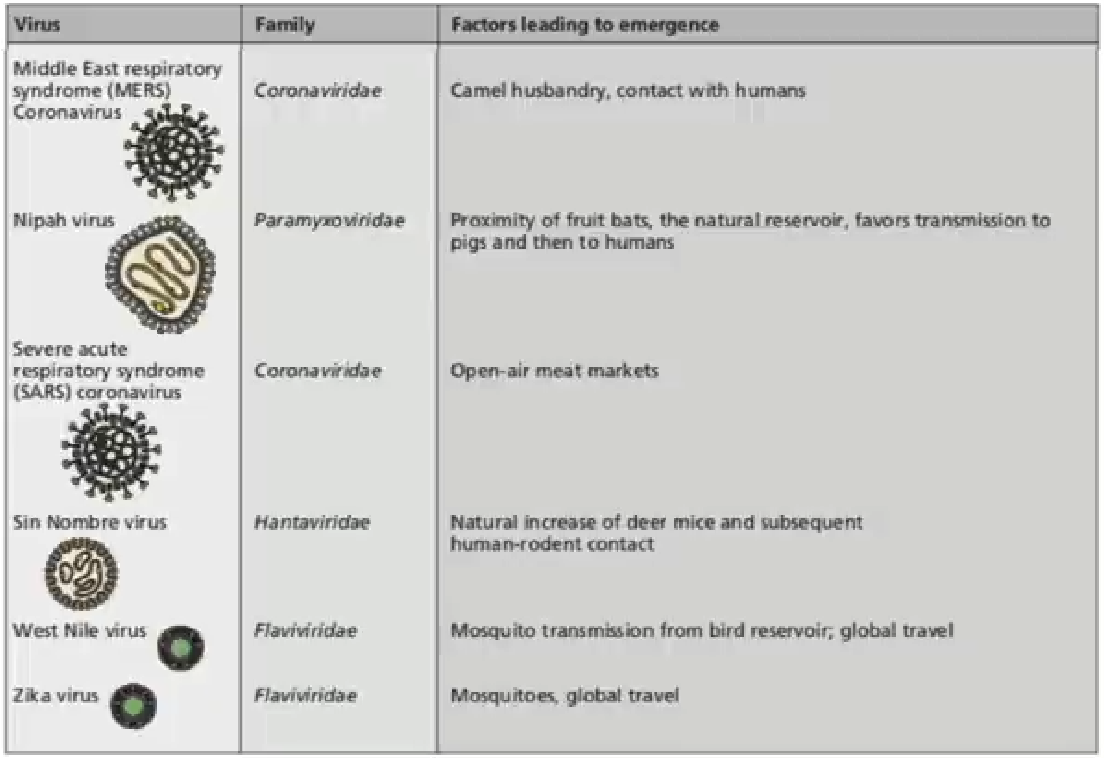


Transmission can occur through direct contact with animal tissues/hosts or environmental sources or through indirect contact, even through inanimate carriers like air. Re-emergence may occure from natural reservoir

Factors that led to emergence of new viruses



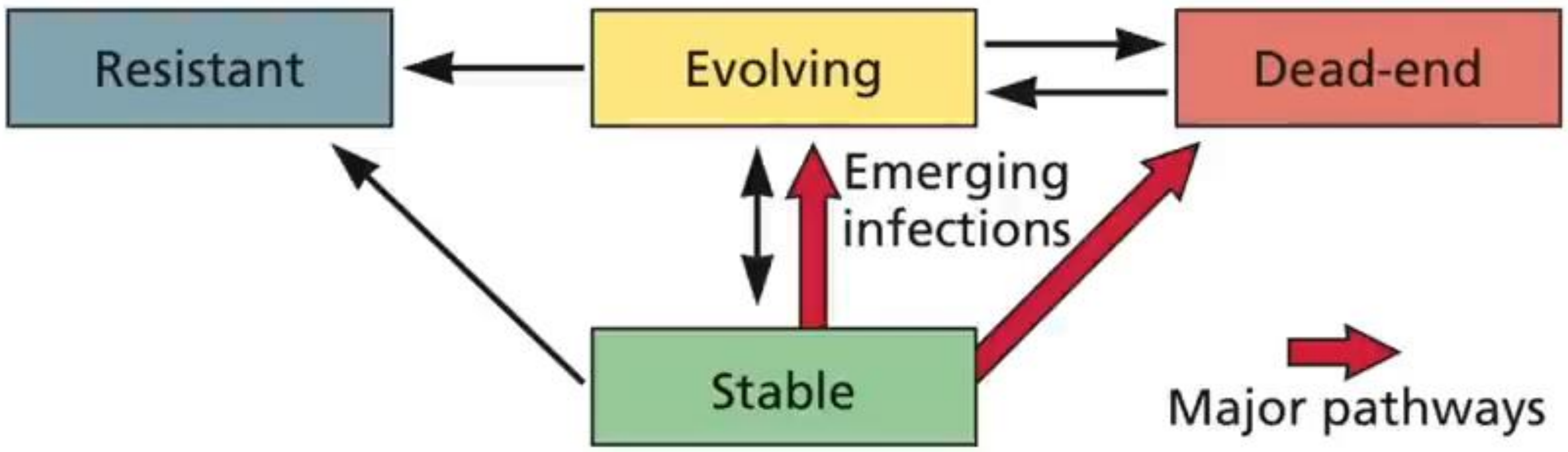
Virus	Family	Factors leading to emergence
Dengue virus	*Flaviviridae*	Urban population density; open water storage favoring mosquito breeding (e.g., millions of used tires)
Ebola virus	*Filoviridae*	Human contact with unknown natural host (Africa)
Hantaan virus	*Bunyaviridae*	Agriculture: human-rodent contact during rice harvest
Hendra virus	*Paramyxoviridae*	Proximity of fruit bats favors transmission to horses and stable workers
Human immunodeficiency virus type 1	*Retroviridae*	Hunting and butchering of infected primates (bushmeat trade)
Influenza virus	*Orthomyxoviridae*	Reservoir in aquatic birds; expansion of bird and pig farming



Virus	Family	Factors leading to emergence
Middle East respiratory syndrome (MERS) Coronavirus	*Coronaviridae*	Camel husbandry, contact with humans
Nipah virus	*Paramyxoviridae*	Proximity of fruit bats, the natural reservoir, favors transmission to pigs and then to humans
Severe acute respiratory syndrome (SARS) coronavirus	*Coronaviridae*	Open-air meat markets
Sin Nombre virus	*Hantaviridae*	Natural increase of deer mice and subsequent human-rodent contact
West Nile virus	*Flaviviridae*	Mosquito transmission from bird reservoir; global travel
Zika virus	*Flaviviridae*	Mosquitoes, global travel
SARS-CoV-2	*Coronaviridae*	**Open-air markets**

Principles of Virology, ASM Press

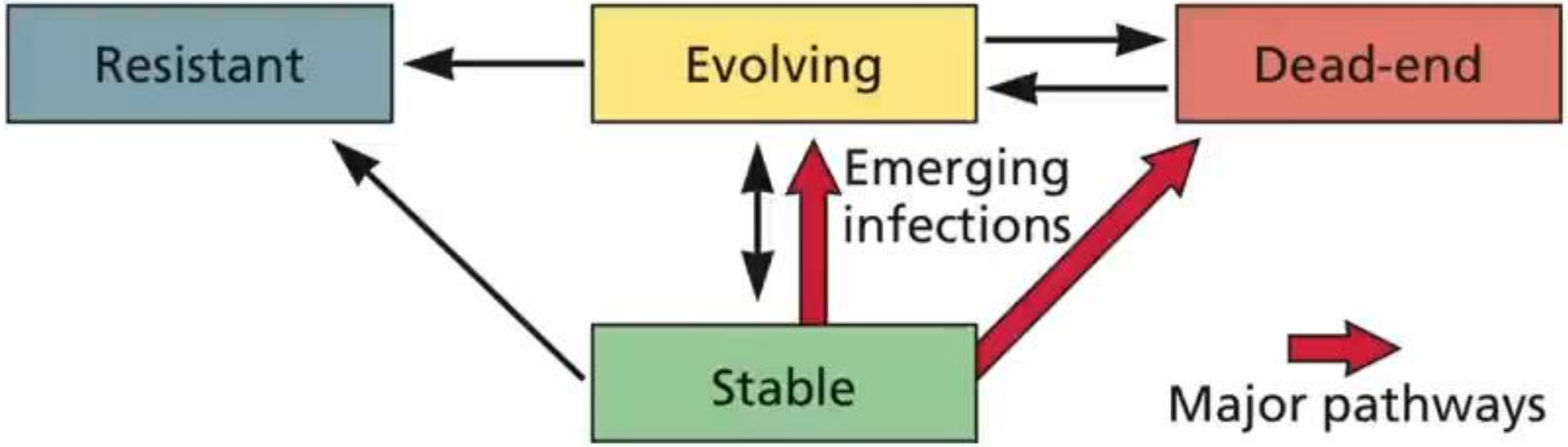
General categories of interactions between hosts and viruses



- Stable: maintains virus in ecosystem
- Evolving: passage of virus to naive population (same or different host)
- Dead-end: one way passage to different species
- Resistant host: infection blocked

Principles of Virology, ASM Press

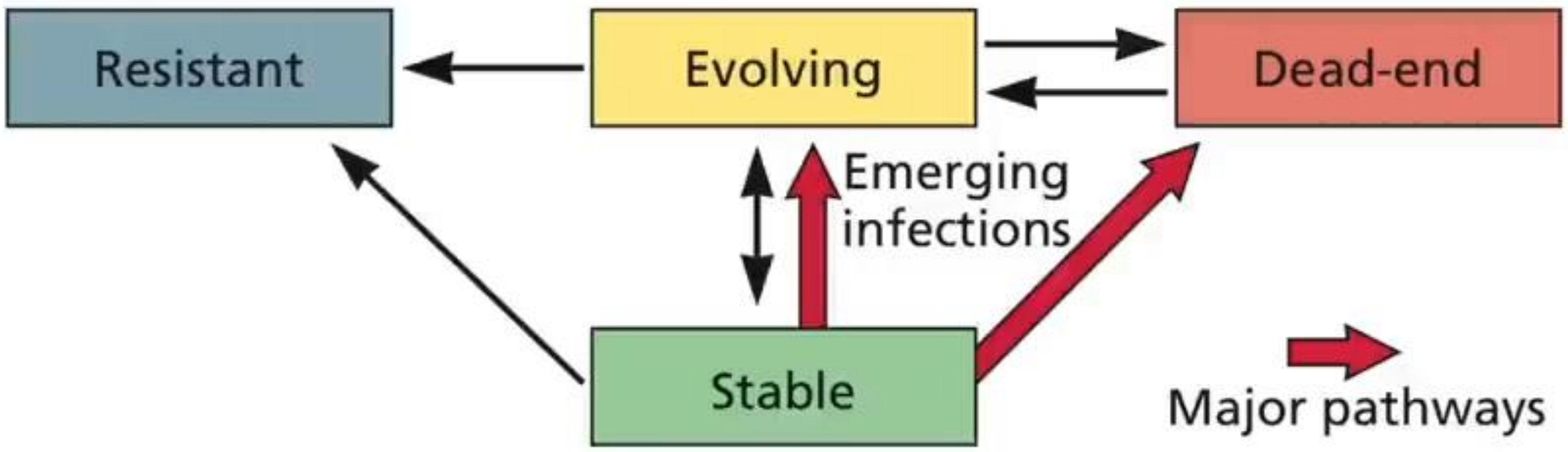
Stable host-virus interactions



- Both participants survive and multiply
- Some are effectively permanent
  - *Humans are sole natural host for measles virus, herpes simplex virus, HCMV, smallpox*
- May include infection of more than one species
  - *Influenza A virus, flaviviruses, togaviruses*

Principles of Virology, ASM Press

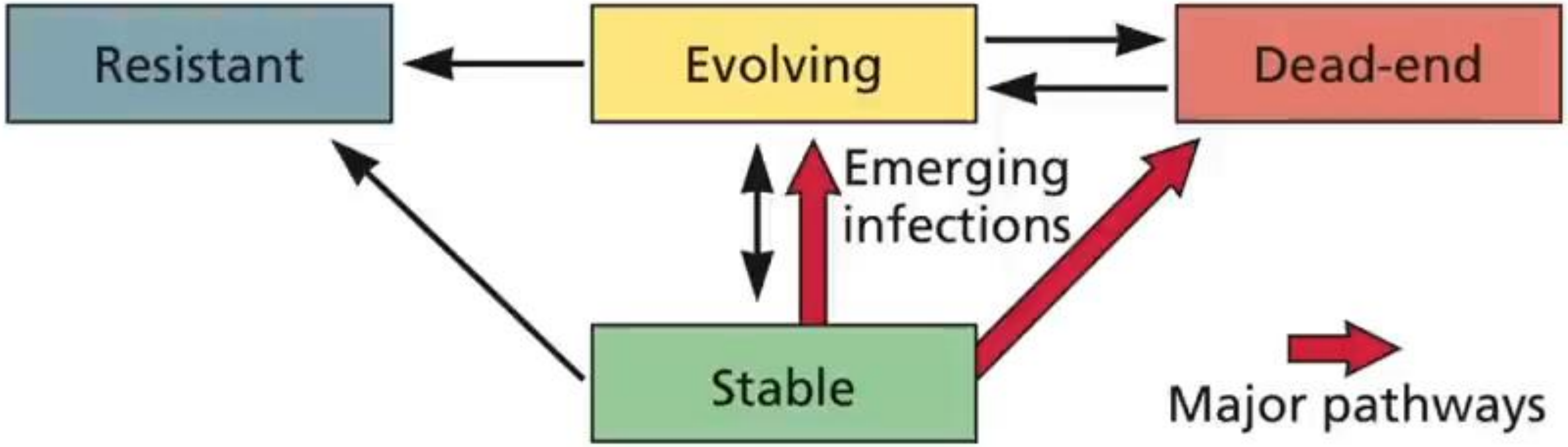
Evolving host-virus relationship



- Hallmarks are instability and unpredictability
- Outcome of infection may range from benign to death
  - Introduction of smallpox and measles to natives of Americas by Old World colonists and slave traders
  - Introduction of West Nile virus into Western Hemisphere, 1999
  - Introduction of myxoma virus to eliminate rabbits into Australia

Principles of Virology, ASM Press

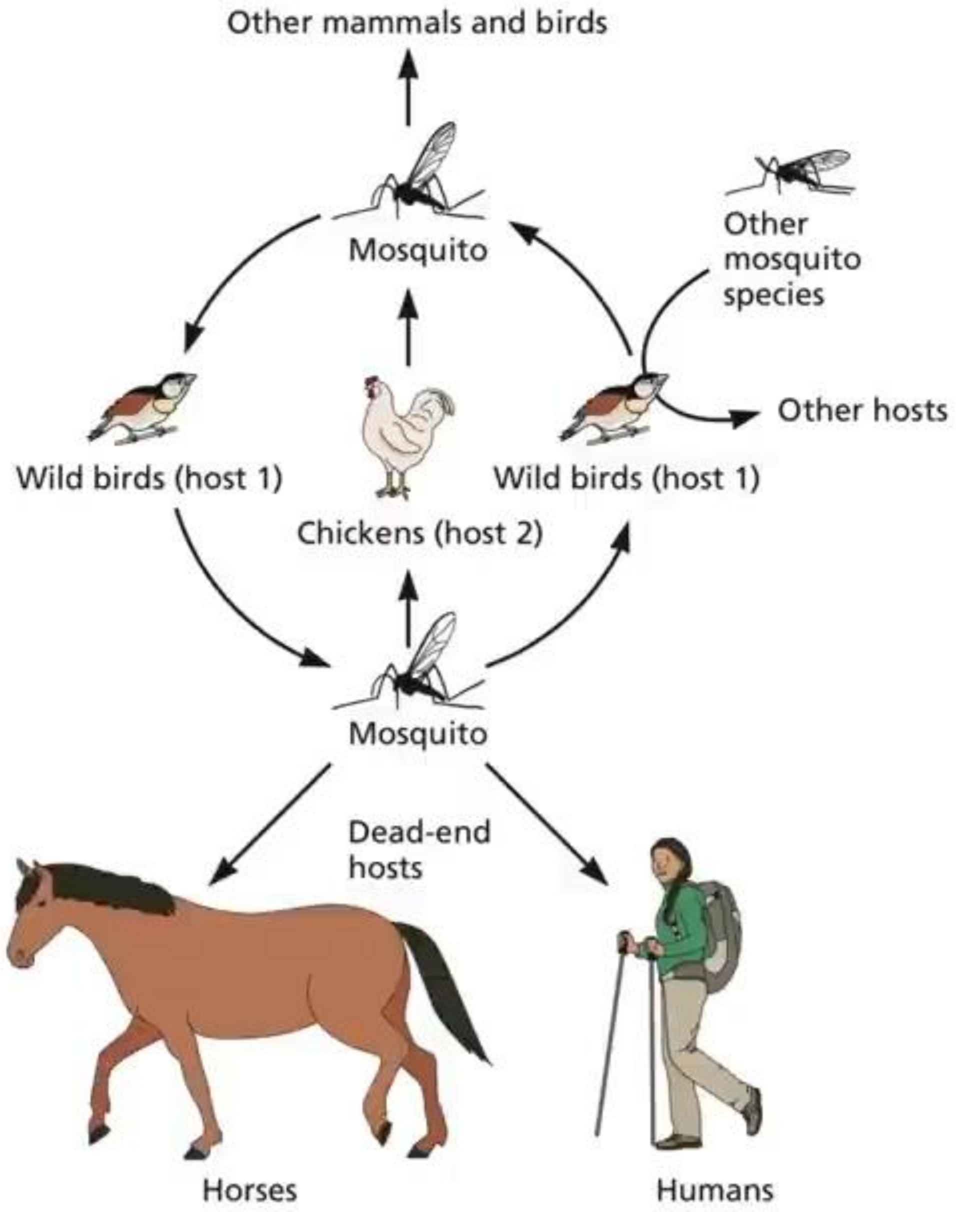
Dead-end interaction



- Frequent outcome of cross-species infection
- No sustained transmission from new infected host to others of the same species

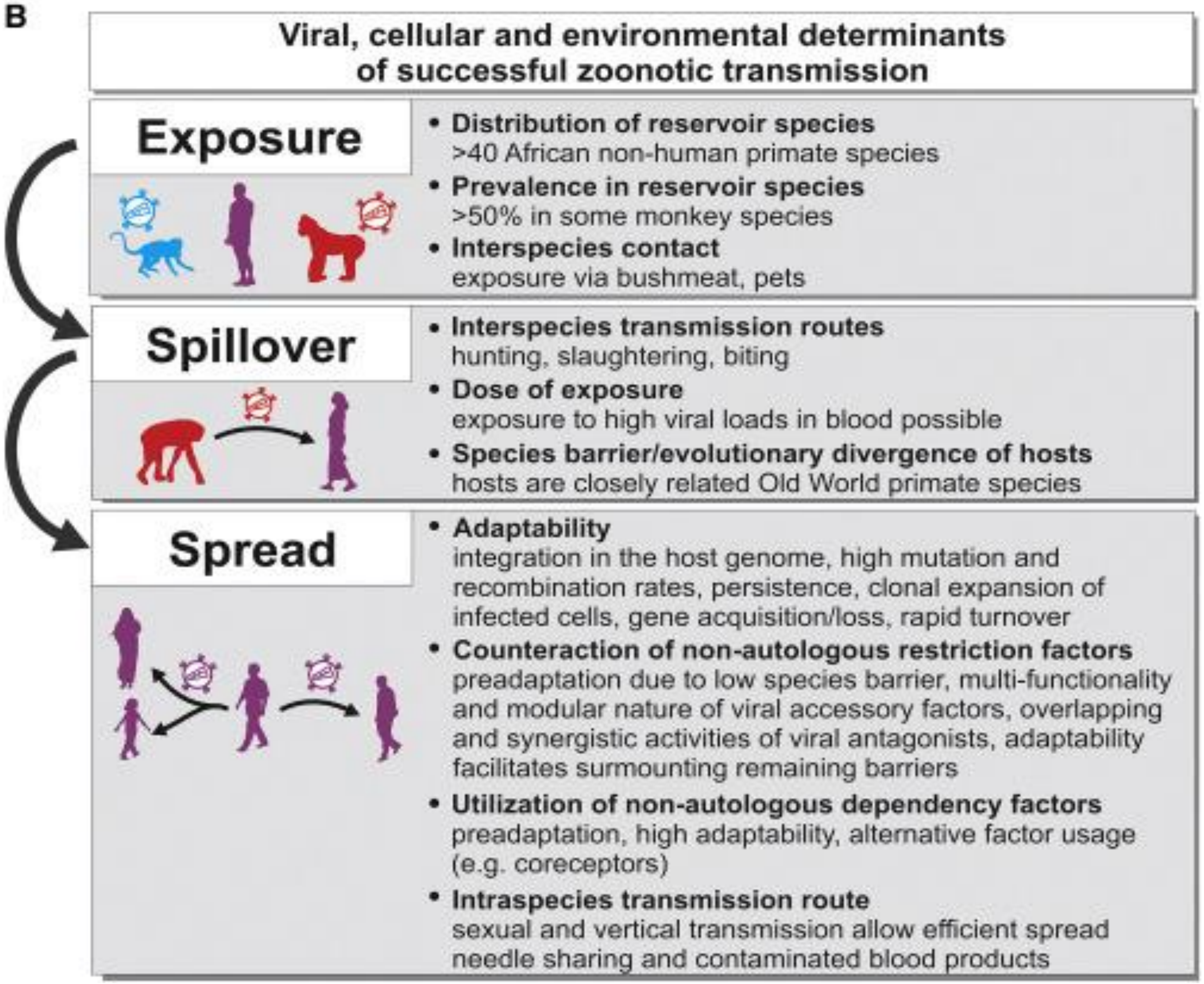
Examples of stable and dead-end host-virus relationships

Stable host-virus interactions



Principles of Virology, ASM Press

Determinants of succesful zoonotic transmission: the example of HIV



B

Viral, cellular and environmental determinants of successful zoonotic transmission

Exposure

- **Distribution of reservoir species**
  >40 African non-human primate species
- **Prevalence in reservoir species**
  >50% in some monkey species
- **Interspecies contact**
  exposure via bushmeat, pets

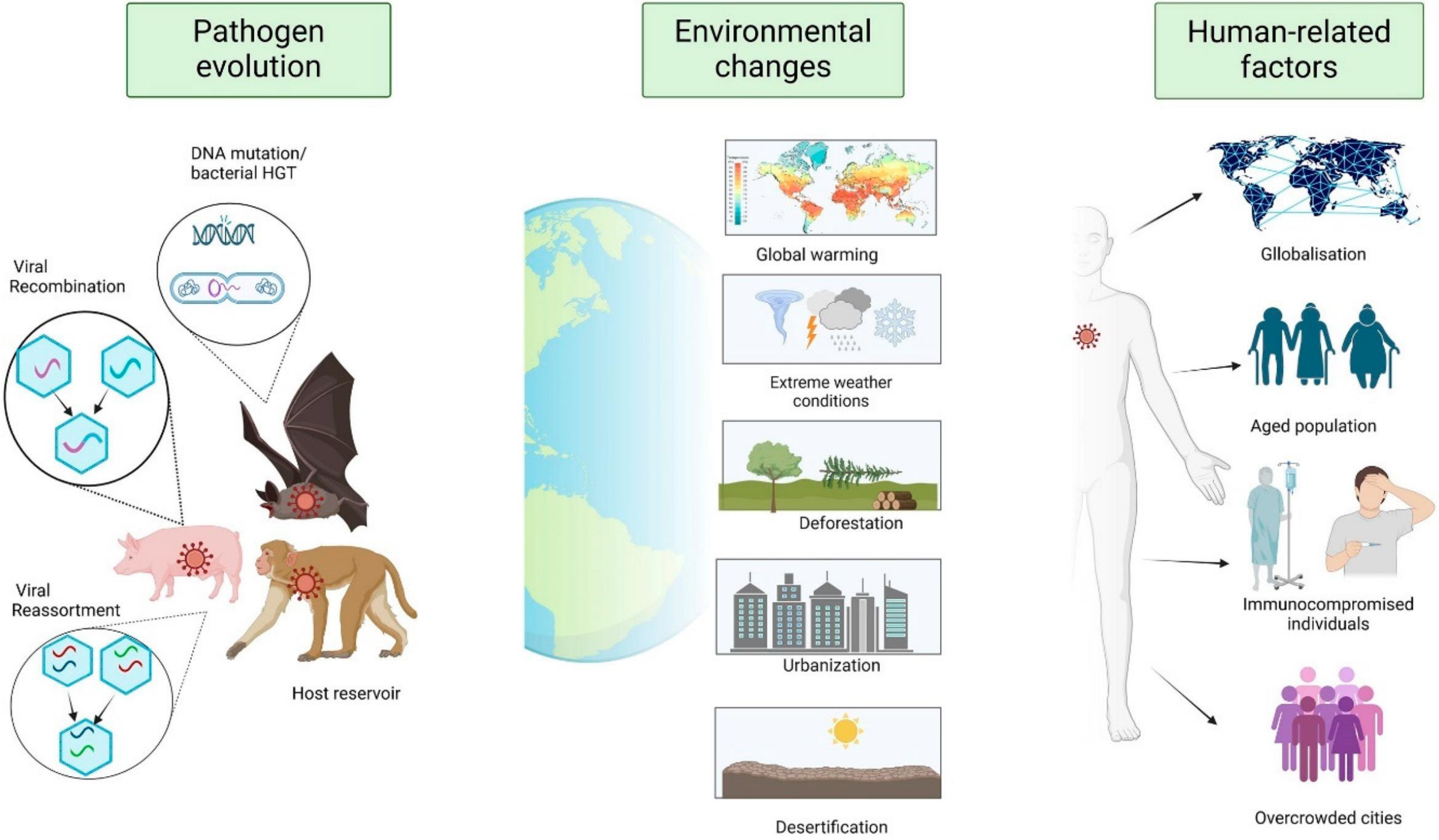
Spillover

- **Interspecies transmission routes**
  hunting, slaughtering, biting
- **Dose of exposure**
  exposure to high viral loads in blood possible
- **Species barrier/evolutionary divergence of hosts**
  hosts are closely related Old World primate species

Spread

- **Adaptability**
  integration in the host genome, high mutation and recombination rates, persistence, clonal expansion of infected cells, gene acquisition/loss, rapid turnover
- **Counteraction of non-autologous restriction factors**
  preadaptation due to low species barrier, multi-functionality and modular nature of viral accessory factors, overlapping and synergistic activities of viral antagonists, adaptability facilitates surmounting remaining barriers
- **Utilization of non-autologous dependency factors**
  preadaptation, high adaptability, alternative factor usage (e.g. coreceptors)
- **Intraspecies transmission route**
  sexual and vertical transmission allow efficient spread
  needle sharing and contaminated blood products

Cell Host & Microbe 25, January 9, 2019



Pathogen evolution

- DNA mutation/ bacterial HGT
- Viral Recombination
- Viral Reassortment
- Host reservoir

Environmental changes

- Global warming
- Extreme weather conditions
- Deforestation
- Urbanization
- Desertification

Human-related factors

- Gllobalisation
- Aged population
- Immunocompromised individuals
- Overcrowded cities

De Gaetano S et al Hygiene 2025

Why **ONE HEALTH** is Important

As Earth's population grows, our connection with animals and the environment changes:

People live closer together

Changes in climate and land use

More global travel and trade

Animals are more than just food

These factors make it easier for diseases to spread between animals and people.

A One Health approach tackles shared health threats by looking at all angles—human, animal, plant, and environmental

www.cdc.gov/onehealth

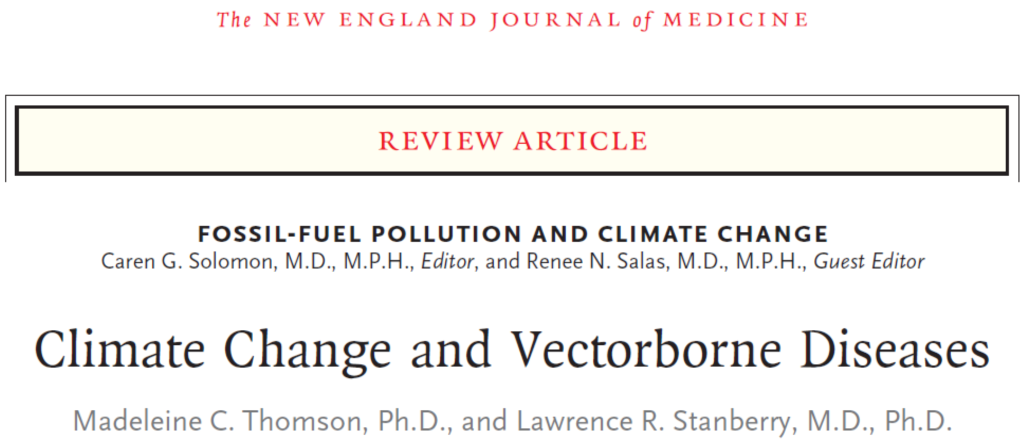
FACTORS that HELP ↑ TRANSMISSION

- CLOSE CONTACT
    - DEFORESTATION
    - CLIMATE CHANGE
    - LARGE-SCALE FARMING
    - FOOD PROCESSING

- CHANGES in SOCIETAL NORMS
    - FOOD PREFERENCES
    - AREAS to LIVE
    - ↓↓↓ VACCINATION RATES & SANITATION

- ↑↑↑ GLOBALIZATION

- ↑↑↑ VULNERABLE POPULATIONS



The NEW ENGLAND JOURNAL *of* MEDICINE

REVIEW ARTICLE

FOSSIL-FUEL POLLUTION AND CLIMATE CHANGE

Caren G. Solomon, M.D., M.P.H., *Editor*, and Renee N. Salas, M.D., M.P.H., *Guest Editor*

Climate Change and Vectorborne Diseases

Madeleine C. Thomson, Ph.D., and Lawrence R. Stanberry, M.D., Ph.D.

The effects of climate change are widespread and rapidly intensifying and are *largely* driven by greenhouse-gas emissions from burning fossil fuels.

The extent of change is most extreme in highland and polar regions, and temperatures in tropical regions are creeping closer to the thermal limits of many organisms. Given the current policies and actions, a warming of 2.5°C to 2.9°C or more by the end of this century is expected

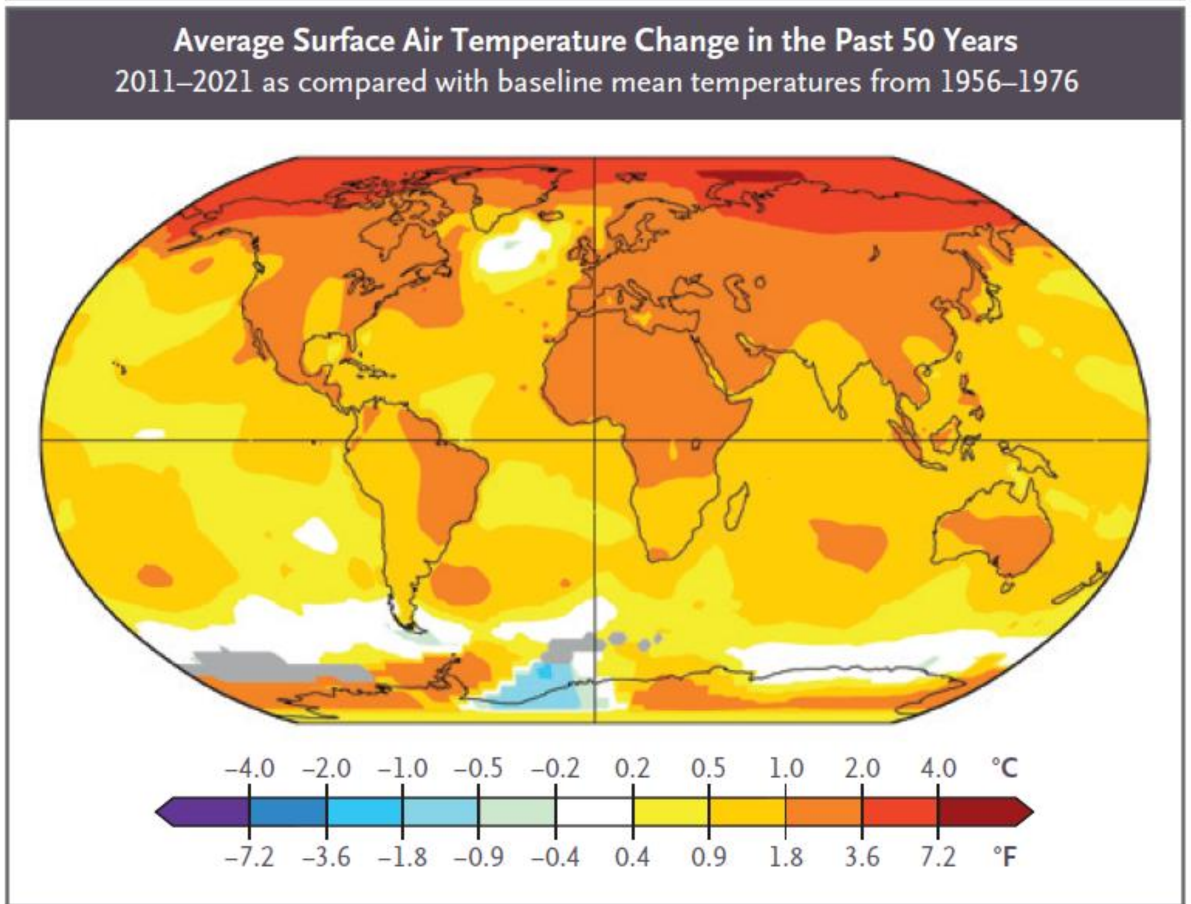
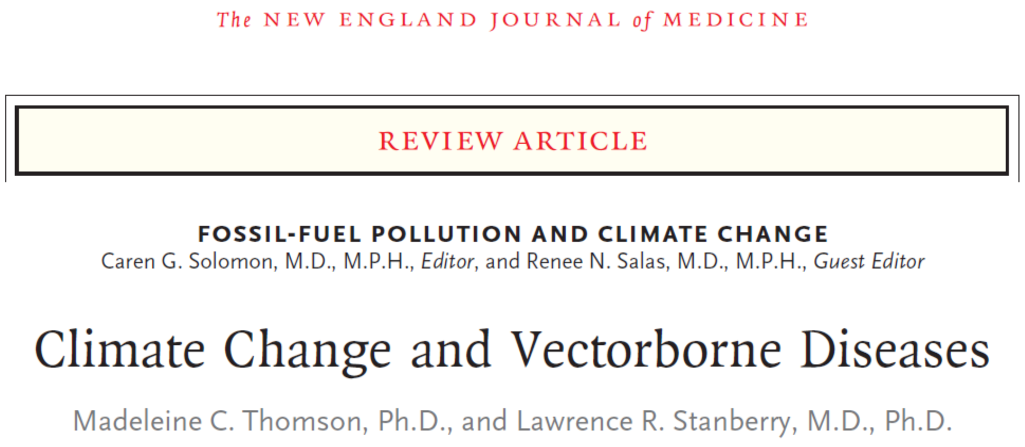


Figure 1. Mean Surface Air Temperatures.

Shown are mean surface air temperatures from 2011 to 2021 as compared with baseline mean temperatures from 1956 to 1976. Adapted from the National Aeronautics and Space Administration Goddard Institute for Space Studies (https://data.giss.nasa.gov/gistemp/maps/index_v4.html).

greenhouse-gas= gas serra



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Caren G. Solomon, M.D., M.P.H., *Editor*, and Renee N. Salas, M.D., M.P.H., *Guest Editor*

Climate Change and Vectorborne Diseases

Madeleine C. Thomson, Ph.D., and Lawrence R. Stanberry, M.D., Ph.D.

Warming temperatures affect the behavior, physiologic characteristics, and life history of both vectors and pathogens as well as the abundance and behavior of reservoir hosts and definitive hosts.

The interactions among temperature, vector, and pathogen can change the risk of human-to-human disease spread and of spillover to humans from reservoir hosts

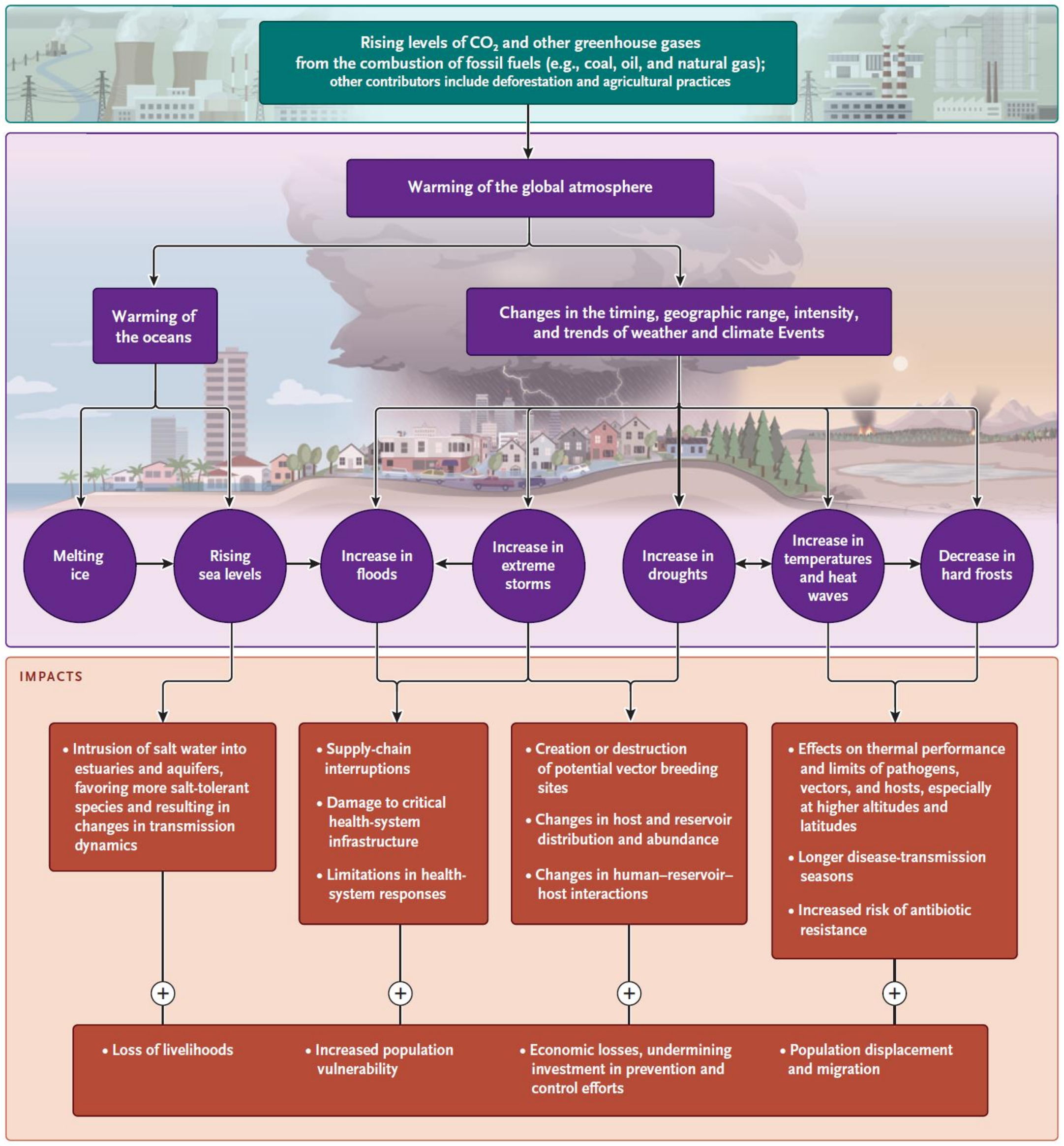


Figure 2. **Pathways between Fossil Fuels and Rising Greenhouse Gases and Vectorborne Diseases.**
The climate experienced at any location and time represents a combination of natural climate variability and, increasingly, climate change. As greenhouse gases accumulate and lead to increased global temperatures, extreme weather events are becoming more frequent, more severe, or both.

greenhouse-gas= gas serra

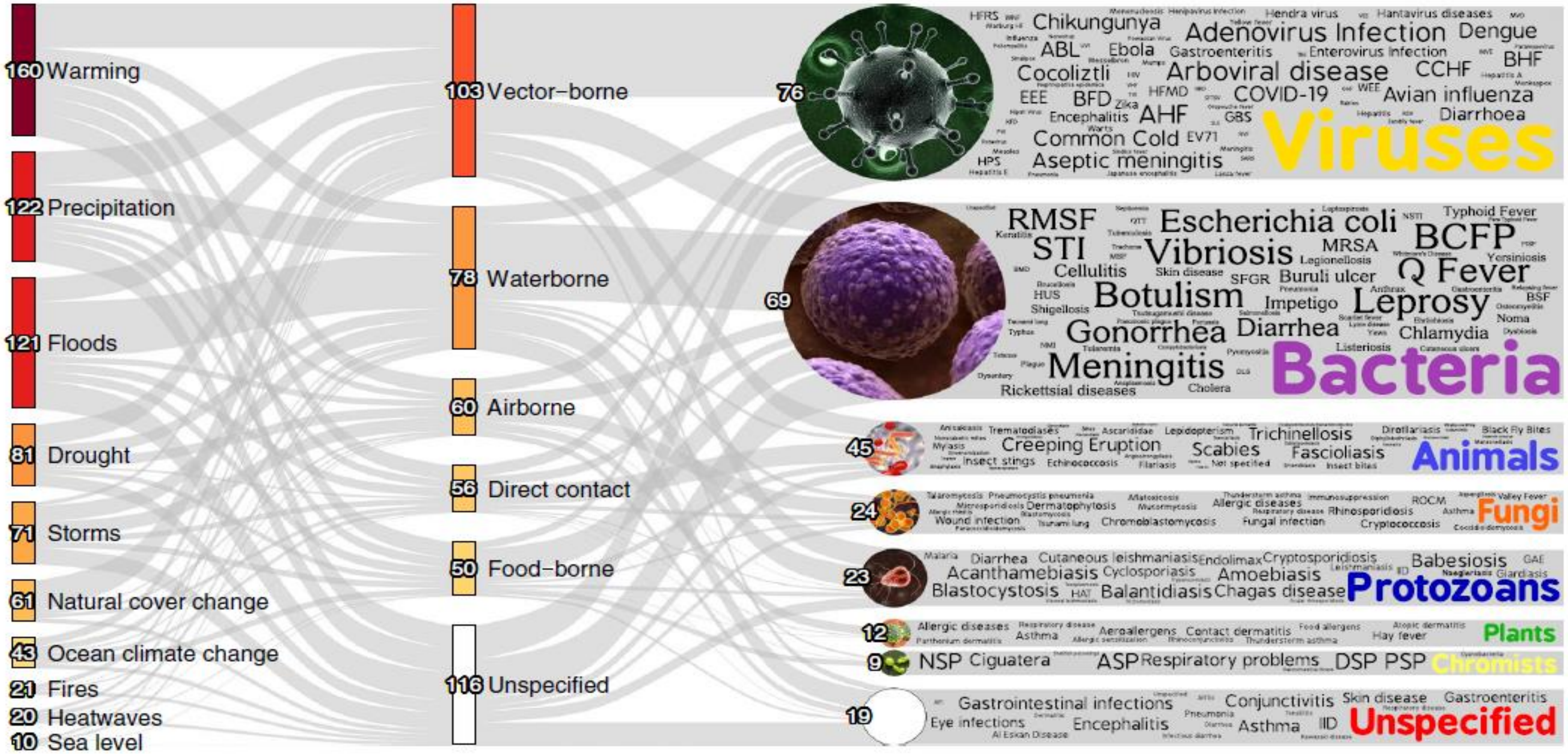
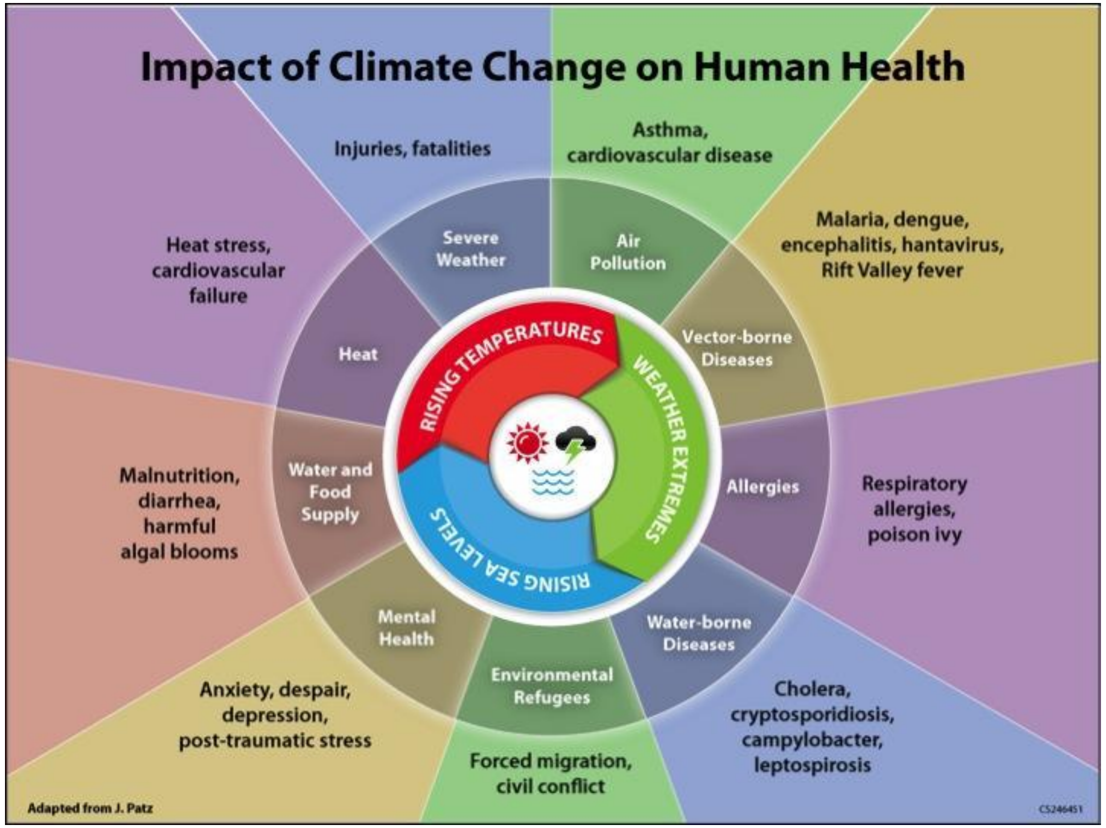


Fig. 3 | Pathogenic diseases aggravated by climatic hazards. Here we display the pathways in which climatic hazards, via specific transmission types, result in the aggravation of specific pathogenic diseases. The thickness of the lines is proportional to the number of unique pathogenic diseases. The colour gradient indicates the proportional quantity of diseases, with darker colours representing larger quantities and lighter colours representing fewer. Numbers at each node are indicative of the number of unique pathogenic diseases (caveats in Supplementary Information 1). An interactive display of the pathways and the underlying data are available at https://camilo-mora.github.io/Diseases/. Several disease names were abbreviated to optimize the use of space in the figure; their extended names are provided in Supplementary Table 1. Credits: word clouds, WordArt.com; bacteria, Wikimedia Commons (www.scientificanimations.com); other images, istockphoto.

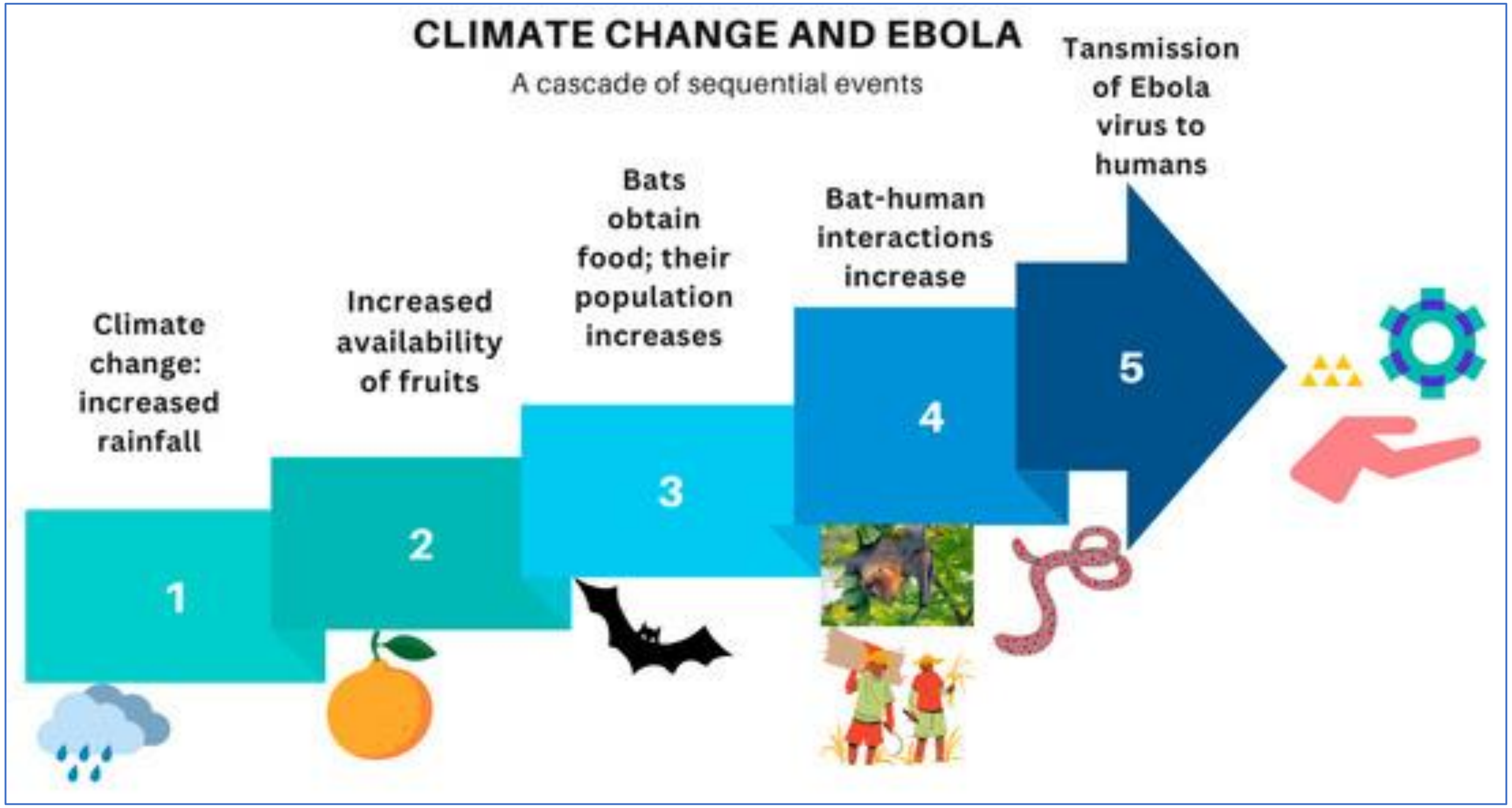


Climate change:

Extreme or persistent changes in temperature, precipitations, humidity, or air pollution can:

- Expand the size of EID reservoir (exposure)
- Increase the area or length of time of favourable conditions for pathogen survival and transmission (spread)
- increase host-pathogen interaction (exposure and spread)
- increase cross species contacts (spillover)
- degrade the overall health of the population (higher susceptibility-spread)

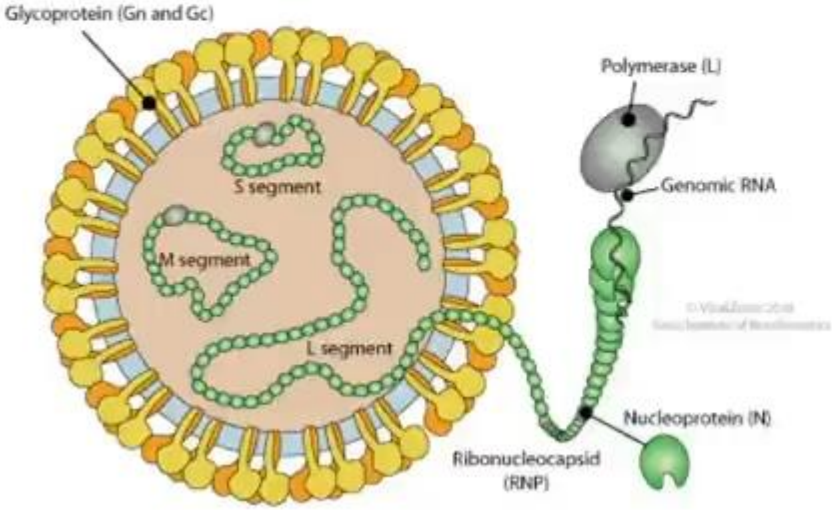
Climate change



Int. J. Environ. Res. Public Health **2025**, *22*(6), 903; https://doi.org/10.3390/ijerph22060903

Changing climate and animal populations

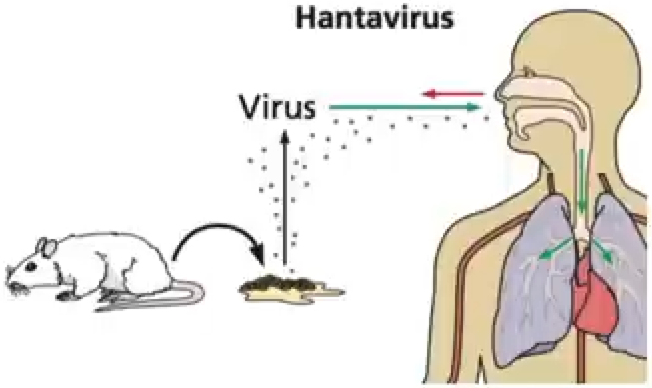
- Hantavirus pulmonary syndrome - first noted in Four Corners area of New Mexico, 1993
- Disease is caused by Sin Nombre virus, endemic in the deer mouse (*Peromyscus maniculatus*, 30% virus positive)
- Originally called Muerto Canyon virus, but residents objected



Bunyaviridae

Changing climate and animal populations

- In 1992-93, abundant rainfall produced a large crop of piñon nuts, food for humans and the deer mouse. Mouse population rose, contact with humans increased.
- Virus is excreted in mouse feces; contaminated blankets or dust from floors provided opportunities for human infection
- Humans not the natural host for Sin Nombre virus, human disease is rare
- Not new - earliest known case 1959



Principles of Virology, ASM Press

Climate change

The reason for the Season

During the winter, people spend more time indoors with the windows sealed, so they are more likely to breathe the same air as someone who is infected and thus contract the virus.
Seasonal viruses may survive better in colder, drier climates, and therefore be able to infect more people

The surge in SARS-CoV-2 cases observed worldwide during the summer of 2022 appears to have been at least partially due to individuals congregating in climate-controlled areas, such as shopping malls, particularly in regions where residential climate control was not widespread

Emerging Microbes & Infections, 13:1, 2356143, DOI: 10.1080/22221751.2024.2356143

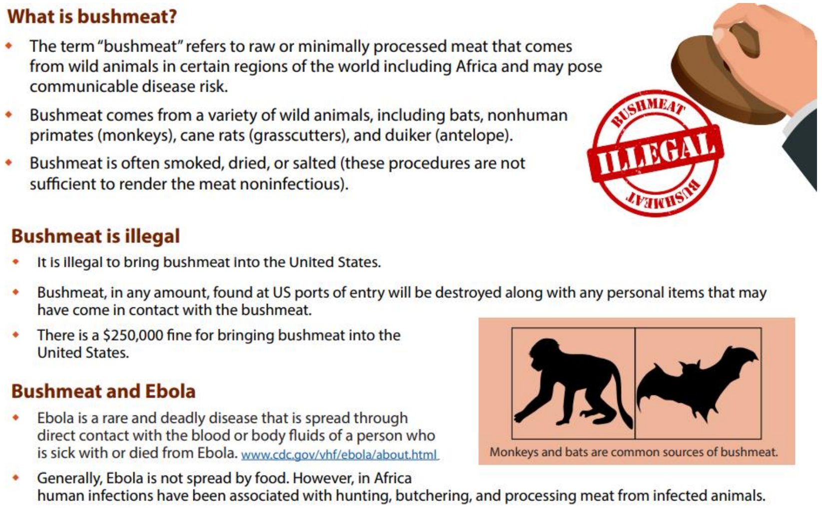
Human demographics and behaviour

Activities such as sexual contact, drug use or outdoor recreational activities can result in increased exposure to an infectious agent.

Infections can then rapidly spread, especially in more heavily populated areas or where there are population movements or upheavals.

‘Bushmeat’ harvested from previously remote forested areas remains a risk for animal-derived emerging infections. Some traditional burial practices have been linked to viral hemorrhagic fevers spread.

Other factors driving emergence include poverty, social inequality and lack of political will.



What is bushmeat?

- The term “bushmeat” refers to raw or minimally processed meat that comes from wild animals in certain regions of the world including Africa and may pose communicable disease risk.
- Bushmeat comes from a variety of wild animals, including bats, nonhuman primates (monkeys), cane rats (grasscutters), and duiker (antelope).
- Bushmeat is often smoked, dried, or salted (these procedures are not sufficient to render the meat noninfectious).

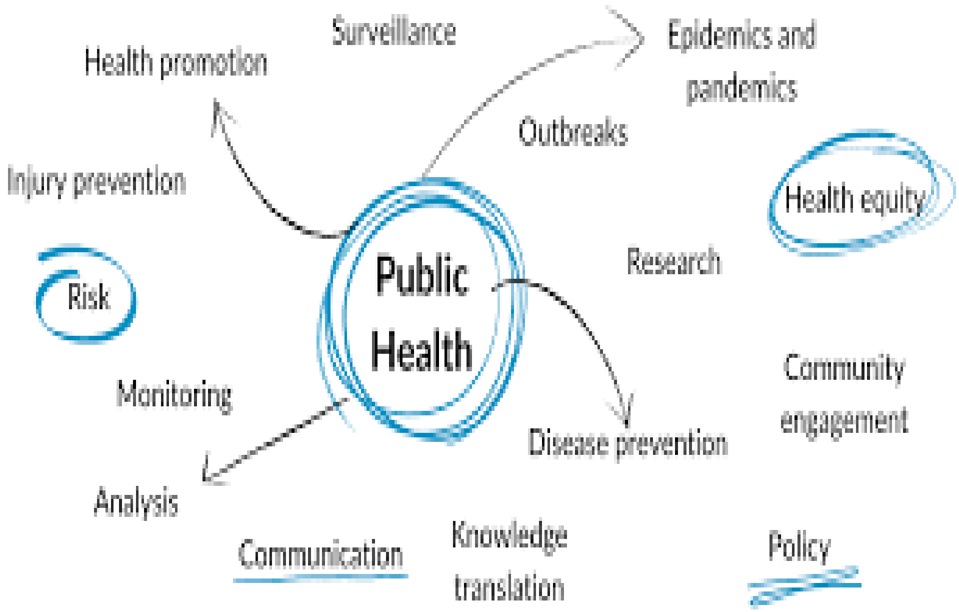
Bushmeat is illegal

- It is illegal to bring bushmeat into the United States.
- Bushmeat, in any amount, found at US ports of entry will be destroyed along with any personal items that may have come in contact with the bushmeat.
- There is a $250,000 fine for bringing bushmeat into the United States.

Bushmeat and Ebola

- Ebola is a rare and deadly disease that is spread through direct contact with the blood or body fluids of a person who is sick with or died from Ebola. www.cdc.gov/vhf/ebola/about.html
- Generally, Ebola is not spread by food. However, in Africa human infections have been associated with hunting, butchering, and processing meat from infected animals.

Monkeys and bats are common sources of bushmeat.

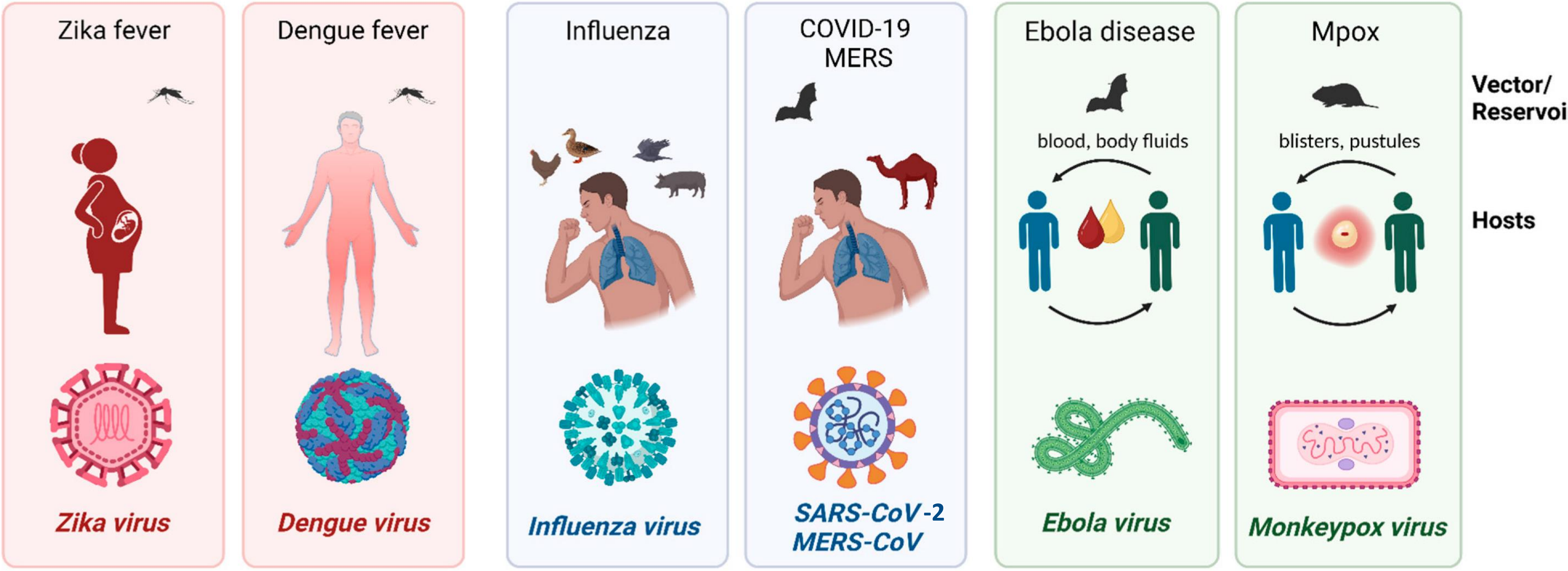


Breakdown in public health measures

The spread of existing infections and the emergence of new ones in many areas of the world can be caused by poor sanitary conditions

Breakdown of public health measures, such as vector control or vaccination programmes, or that due to non optimal preparedness, can result in the re-emergence of previously controlled diseases.

Vector-borne transmission **Droplet transmission** **Direct contact transmission**



Zika fever

Zika virus

Dengue fever

Dengue virus

Influenza

Influenza virus

COVID-19
MERS

SARS-CoV-2
MERS-CoV

Ebola disease

blood, body fluids

Ebola virus

Mpox

blisters, pustules

Monkeypox virus

Vector/ Reservoir

Hosts

A vector is an organism, often an arthropod, that transmits an infectious disease from one individual to another. They can be actively involved in the pathogen's lifecycle or simply carry the pathogen

A reservoir host is a species in which the pathogen endemically circulates and is considered to have coevolved with

Han, J.J.; Song, H.A.; Pierson, S.L.; Shen-Gunther, J.; Xia, Q. Emerging Infectious Diseases Are Virulent Viruses—AreWe Prepared? An Overview. Microorganisms **2023**, 11, 2618. https://doi.org/10.3390/ microorganisms11112618

Why Do Bats Carry So Many Diseases? (like Coronavirus)

https://www.youtube.com/watch?v=Ao0dqJvH4a0

MERS-CoV

- Spread from dromedary camels (endemic in Middle East and Africa)
- Not all infections have camel source
- How is the virus transmitted to humans? Virus does not transmit well among humans
- Camel vaccine in testing (One Health approach)

SARS

- A Chinese doctor who treated first patients traveled to Hong Kong on 21 February 2003, stayed on ninth floor of Metropole Hotel
- He died in hospital 22 February
- Infection spread to 10 people in hotel, who flew to Singapore, Vietnam, Canada, US before symptoms evident
- Infection spread to 8000 people in 29 countries, 10% mortality

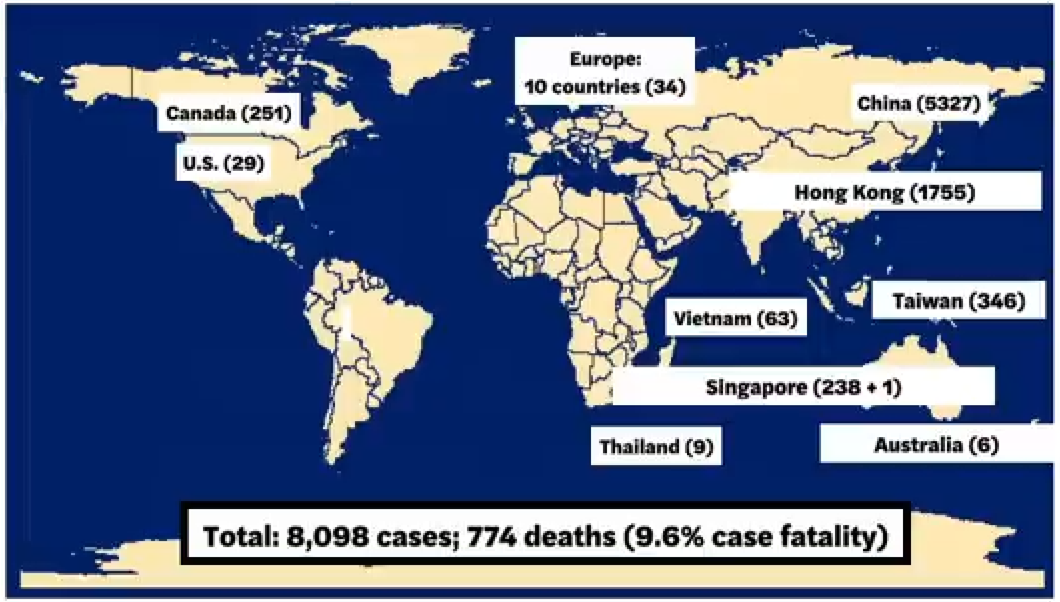
Hong Kong doesn't do things by halves. The first thing that grabs your attention is the forest of skyscrapers towering over the harbour. The second is the sheer energy of the place. Step onto any street and you'll be swept away in a wave of excitement, sound and colour. From the dragon boat races in summer to the Chinese New Year fireworks, from morning tai chi to late night dancing. Whenever you go and whatever you do in Hong Kong, one thing's for certain. You'll never be bored.

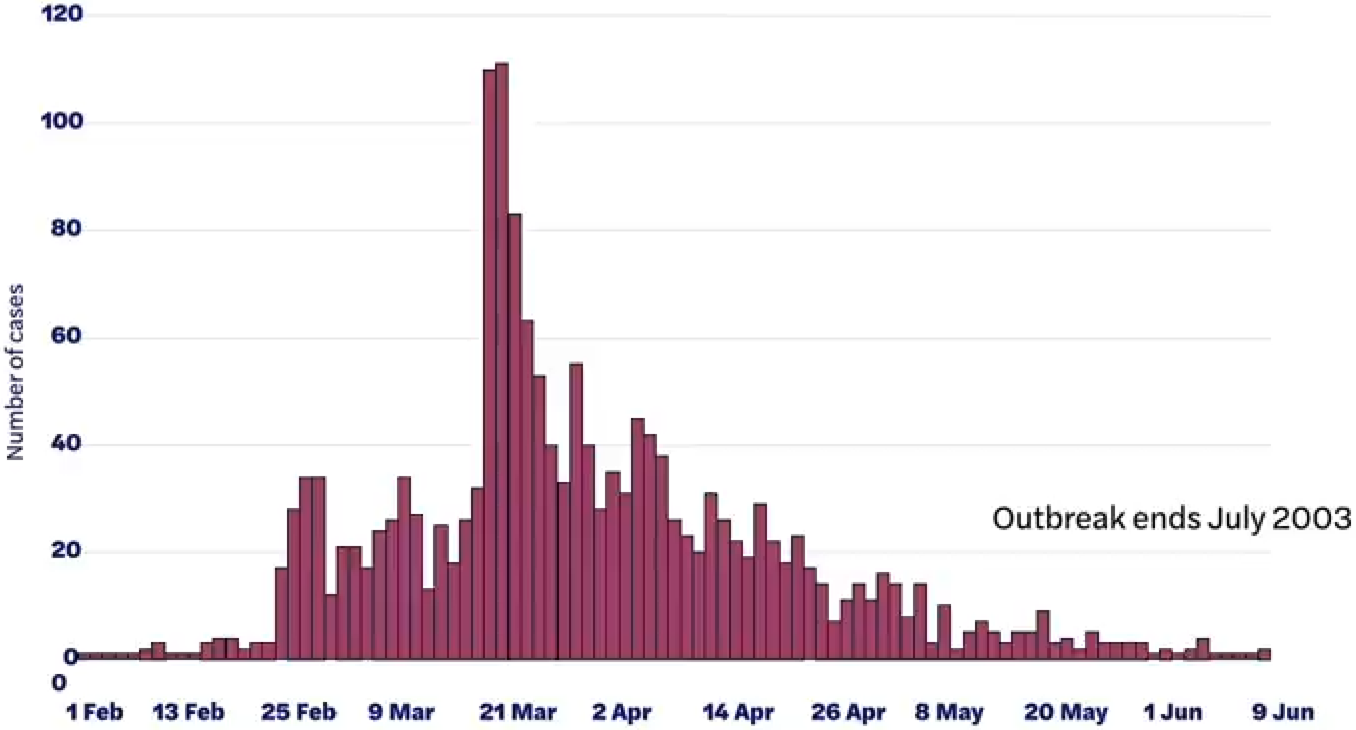
For more information and a free Traveller's Guide to Hong Kong, call 09068 661188 or visit our Web site today.

Calls cost 60p per minute at all times.

DiscoverHongKong.com

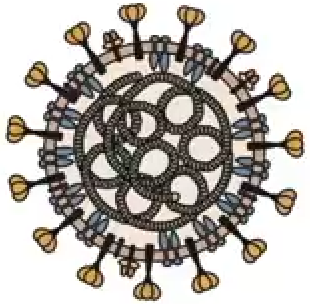
Probable SARS Cases Worldwide Reported to WHO as of Sept. 26, 2003





Outbreak ends July 2003

Not trasnmitted during incubation period
but at peak of symptoms, easier to control

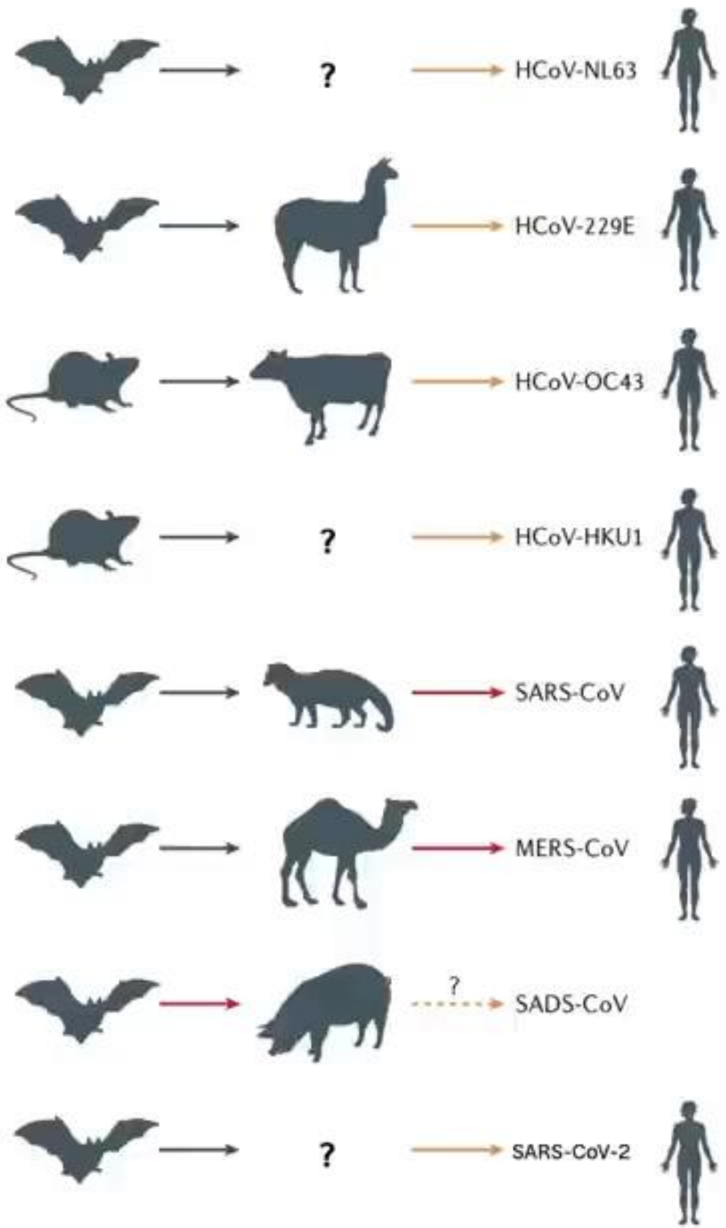


Origin of SARS-CoV

- Highly diverse SARSr-CoV found in horseshoe bats (*Rhinolophus*) in a cave in Yunnan Province
- All genetic elements needed to form SARS-CoV in this cave via recombination (but not direct progenitor)
- No SARS cases in Yunnan Province during outbreak
- Direct progenitor of SARS-CoV thought to have emerged in bats, then infected civet cats which were then transported to Guangdong markets

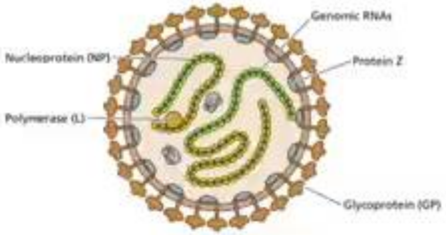
https://doi.org/10.1038/ s41579-018-0118-9

Origins of human coronaviruses - in Nature, not in a lab

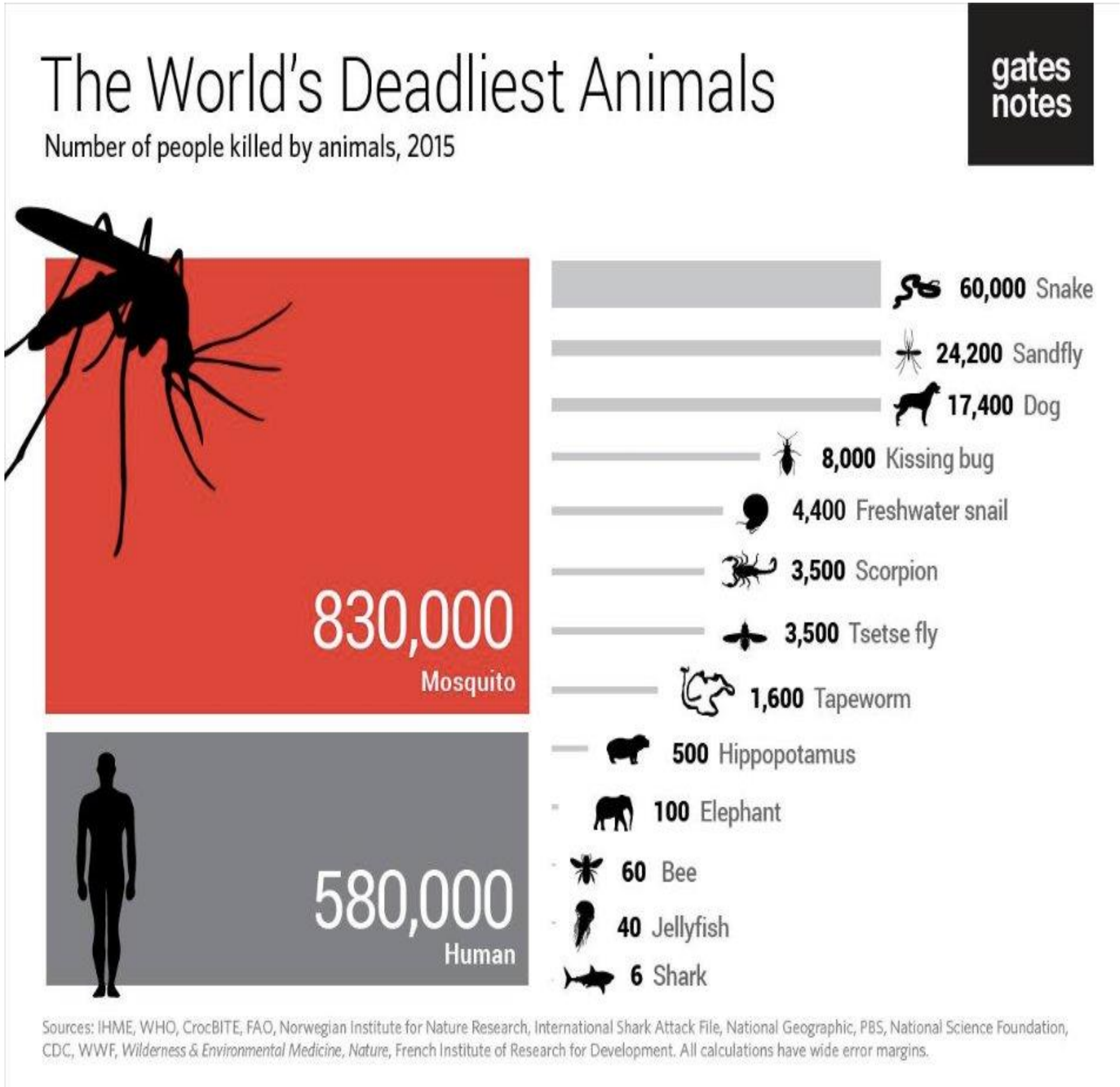


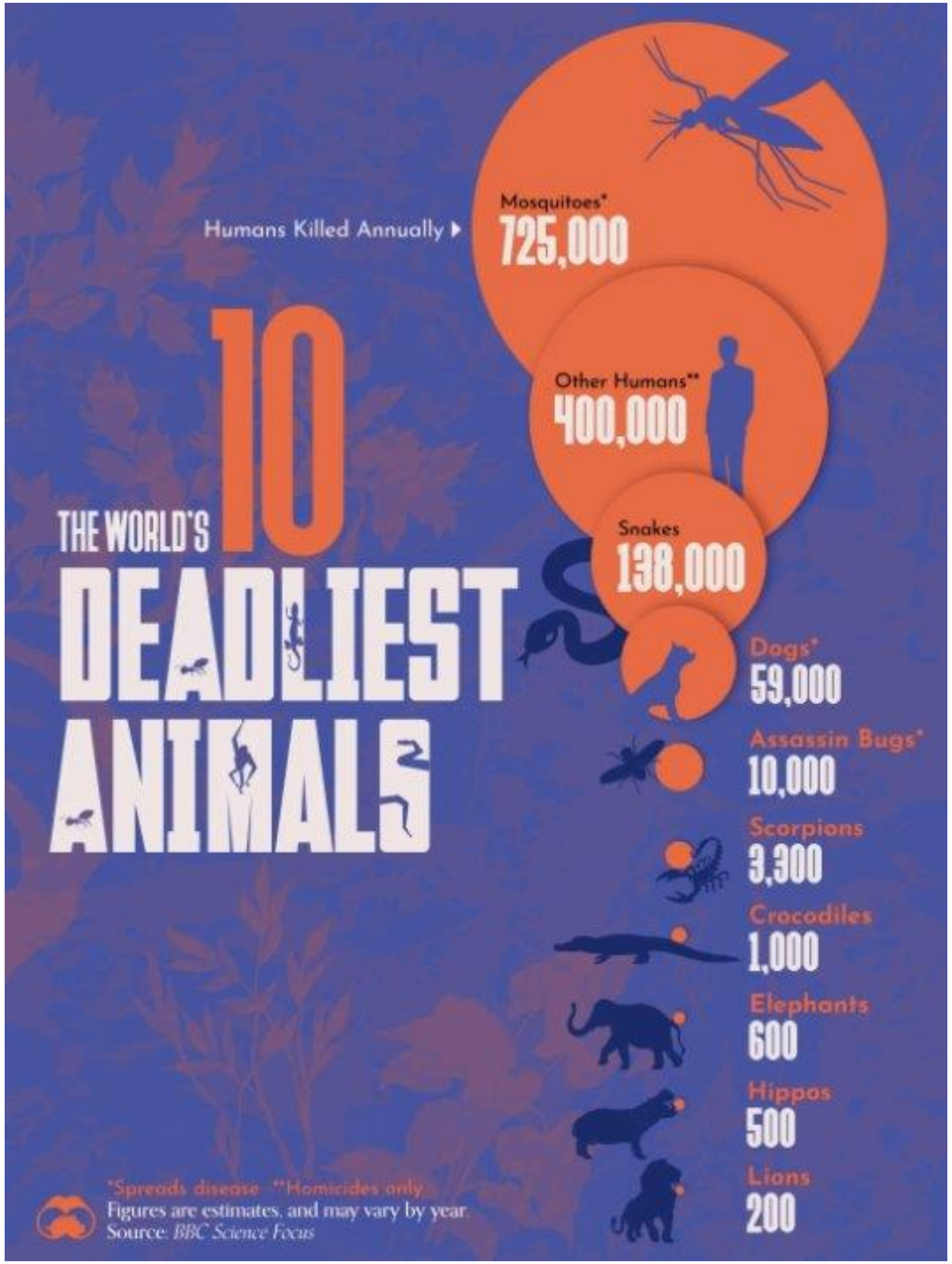
https://doi.org/10.1038/ s41579-018-0118-9

Argentine hemorrhagic fever, Junin virus



- Use of herbicides to control weeds and convert the Argentine pampa to land for growth of maize
- A new shade-tolerant grass grew in shadow of maize
- This grass led to emergence of new dominant mouse, *Calomys musculinus*, reservoir of Junin virus
- Argentine hemorrhagic fever first described in 1953, virus isolated 1958


The World's Deadliest Animals
Number of people killed by animals, 2015
gates notes
830,000
Mosquito
580,000
Human
60,000 Snake
24,200 Sandfly
17,400 Dog
8,000 Kissing bug
4,400 Freshwater snail
3,500 Scorpion
3,500 Tsetse fly
1,600 Tapeworm
500 Hippopotamus
100 Elephant
60 Bee
40 Jellyfish
6 Shark
Sources: IHME, WHO, CrocBITE, FAO, Norwegian Institute for Nature Research, International Shark Attack File, National Geographic, PBS, National Science Foundation, CDC, WWF, Wilderness & Environmental Medicine, Nature, French Institute of Research for Development. All calculations have wide error margins.


THE WORLD'S 10 DEADLIEST ANIMALS
Humans Killed Annually
Mosquitoes*
725,000
Other Humans**
400,000
Snakes
138,000
Dogs*
59,000
Assassin Bugs*
10,000
Scorpions
3,300
Crocodiles
1,000
Elephants
600
Hippos
500
Lions
200
*Spreads disease **Homicides only
Figures are estimates, and may vary by year.
Source: BBC Science Focus

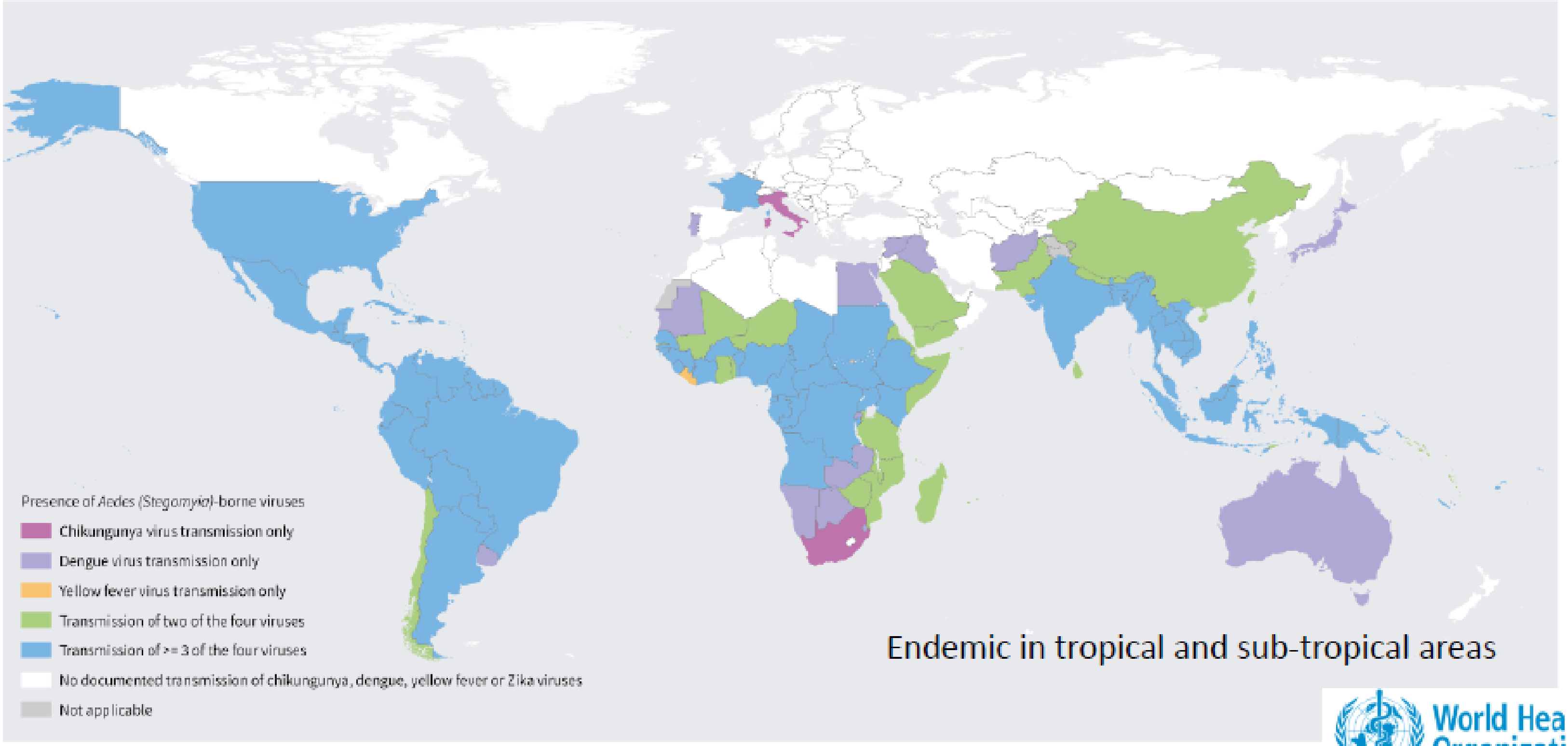
- Arthropod-borne diseases represent an important concern for the global public health
- Annually: about 1,000,000,000 of human cases / over 700,000 deaths

  (17% of the total cases of infectious disease)
- Increase of the global incidence of Arboviruses over the past 50-years

«Climate-sensitive diseases»

- Geographical expansion of invasive and indigenous vector species
- Changes in ecology (i.e., adapted to urban settings)
- Extended seasons of transmission
- Improved climatic and environmental suitability also **in temperate areas**

Countries and territories with current or previous transmission of chikungunya, dengue, yellow fever or Zika viruses



Endemic in tropical and sub-tropical areas

he designations employed and the presentation of the material in this publication do not imply the expression of

Data Source: World Health Organization

World Health Organization

Arboviruses transmission in Southern Europe:


Culex


Ixodes

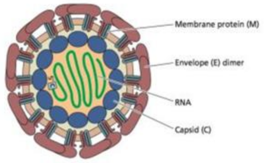

Aedes

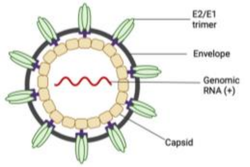

Phlebotomus

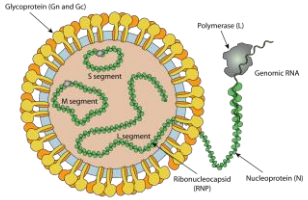

Hyalomma


Culicoides

Family:	Virus:	
Family: Flaviviridae *Genus: Orthoflavivirus*	West Nile	E/I
	Usutu	E/I
	TickBorneEncephalitis	E/I
	Dengue	I/A
	Zika	I
Family: Togaviridae *Genus: Alphavirus*	**Chikungunya**	I/A
Family: Phenuiviridae *Genus: Phlebovirus*	Toscana	E/I
Family: Nairoviridae *Genus: Orthonairovirus*	**CCHFV**	E/I
Family: Peribunyaviridae *Genus: Orthobunyavirus*	Oropouche	I



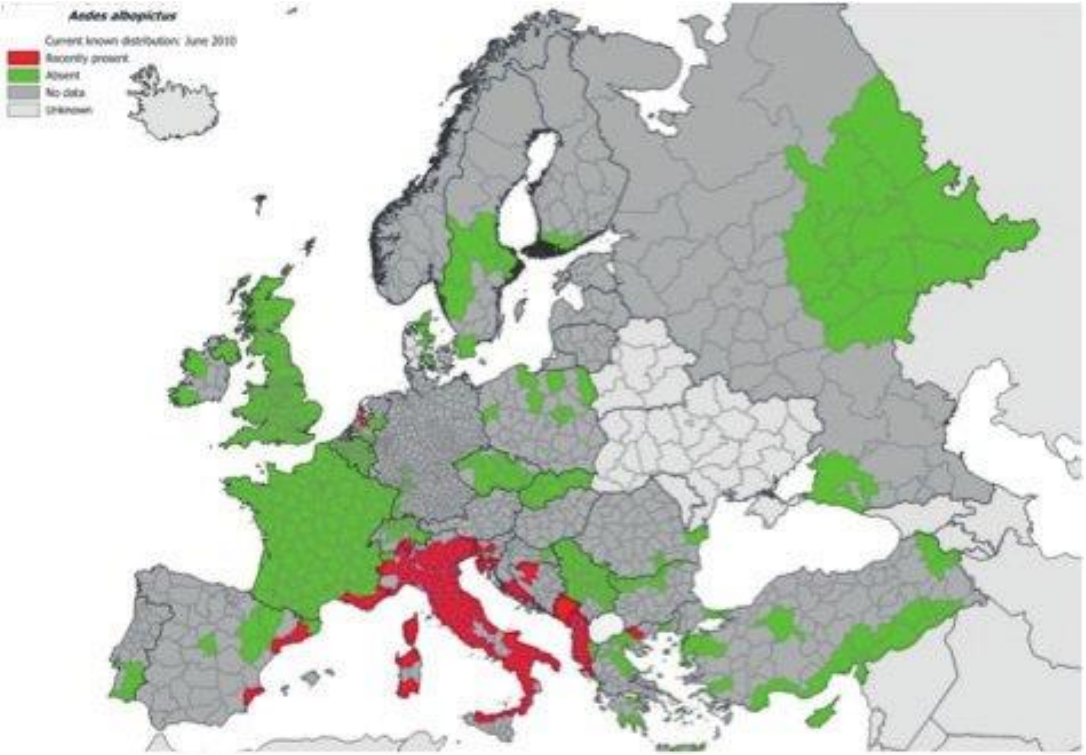


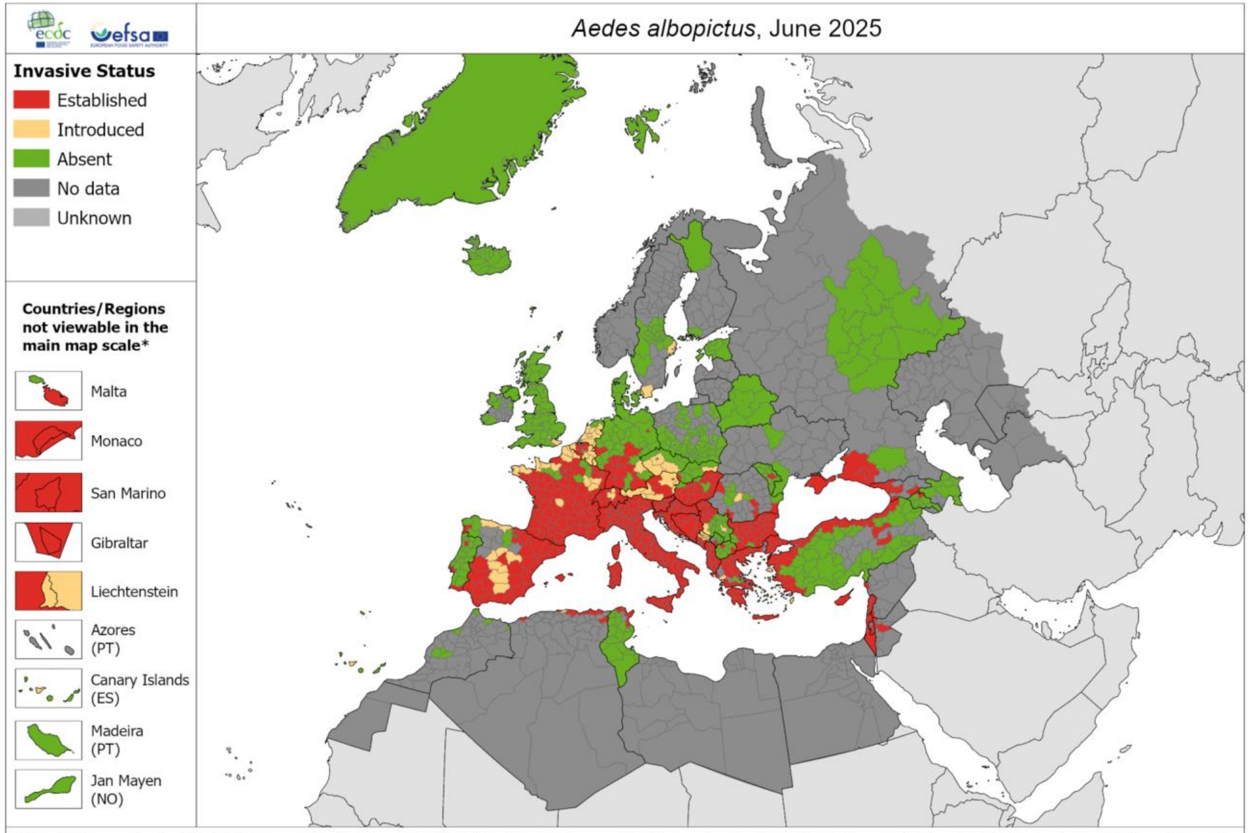


E=endemic; I=imported; A=autochtonous

Aedes albopictus in Europe:

2010

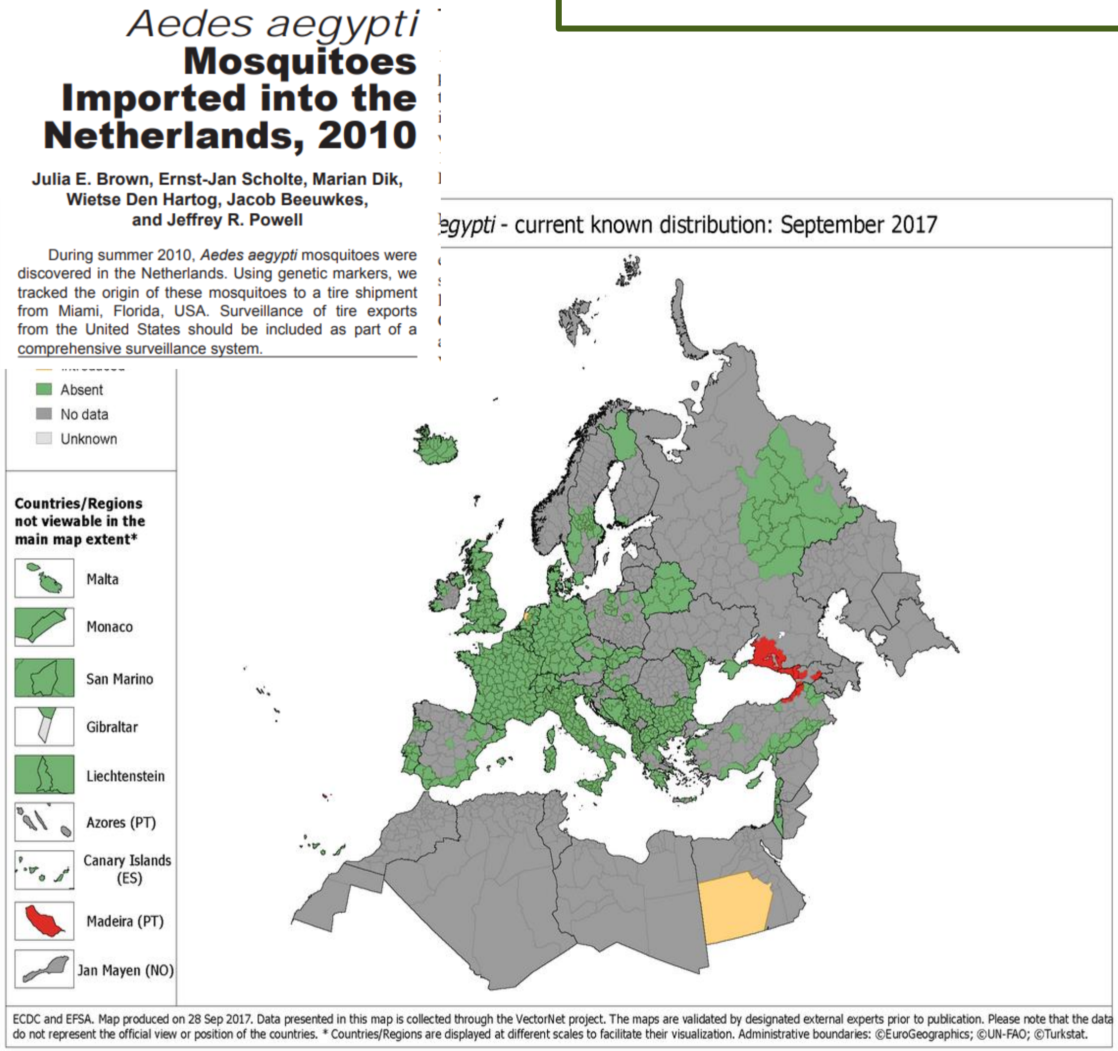




ECDC and EFSA, map produced on 25 Jun 2025. Data presented in this map are collected by the VectorNet project. Maps are validated by external experts prior to publication. Please note that the depicted data do not reflect the official views of the countries.
* Countries/Regions are displayed at different scales to facilitate their visualisation.The boundaries and names shown on this map do not imply official endorsement or acceptance by the European Union.Administrative boundaries © EuroGeographics, UNFAO.

Since 2024 there were changes in 16 regions.

Aedes aegypti in Europe:

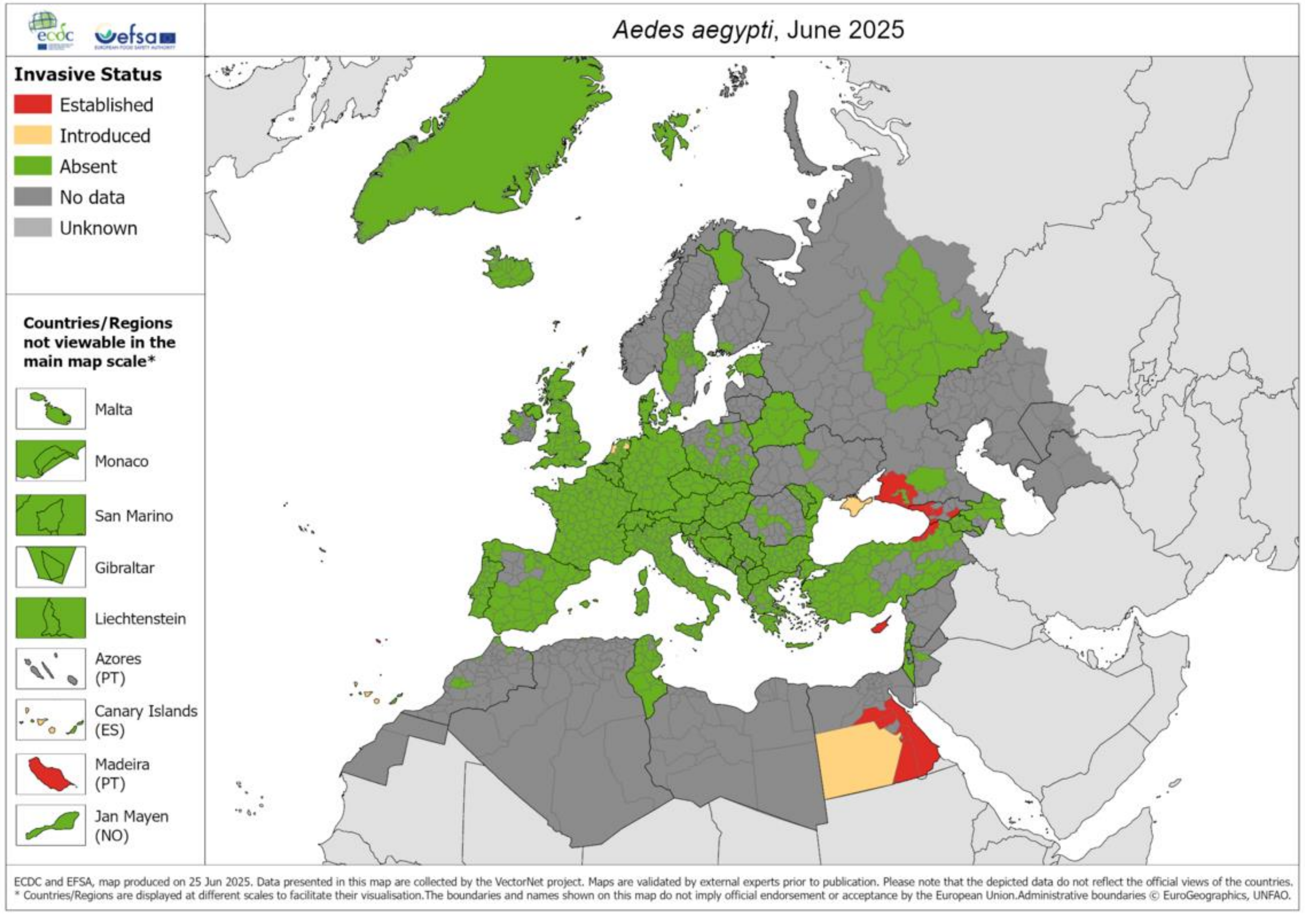


Aedes aegypti **Mosquitoes Imported into the Netherlands, 2010**

Julia E. Brown, Ernst-Jan Scholte, Marian Dik, Wietse Den Hartog, Jacob Beeuwkes, and Jeffrey R. Powell

During summer 2010, *Aedes aegypti* mosquitoes were discovered in the Netherlands. Using genetic markers, we tracked the origin of these mosquitoes to a tire shipment from Miami, Florida, USA. Surveillance of tire exports from the United States should be included as part of a comprehensive surveillance system.

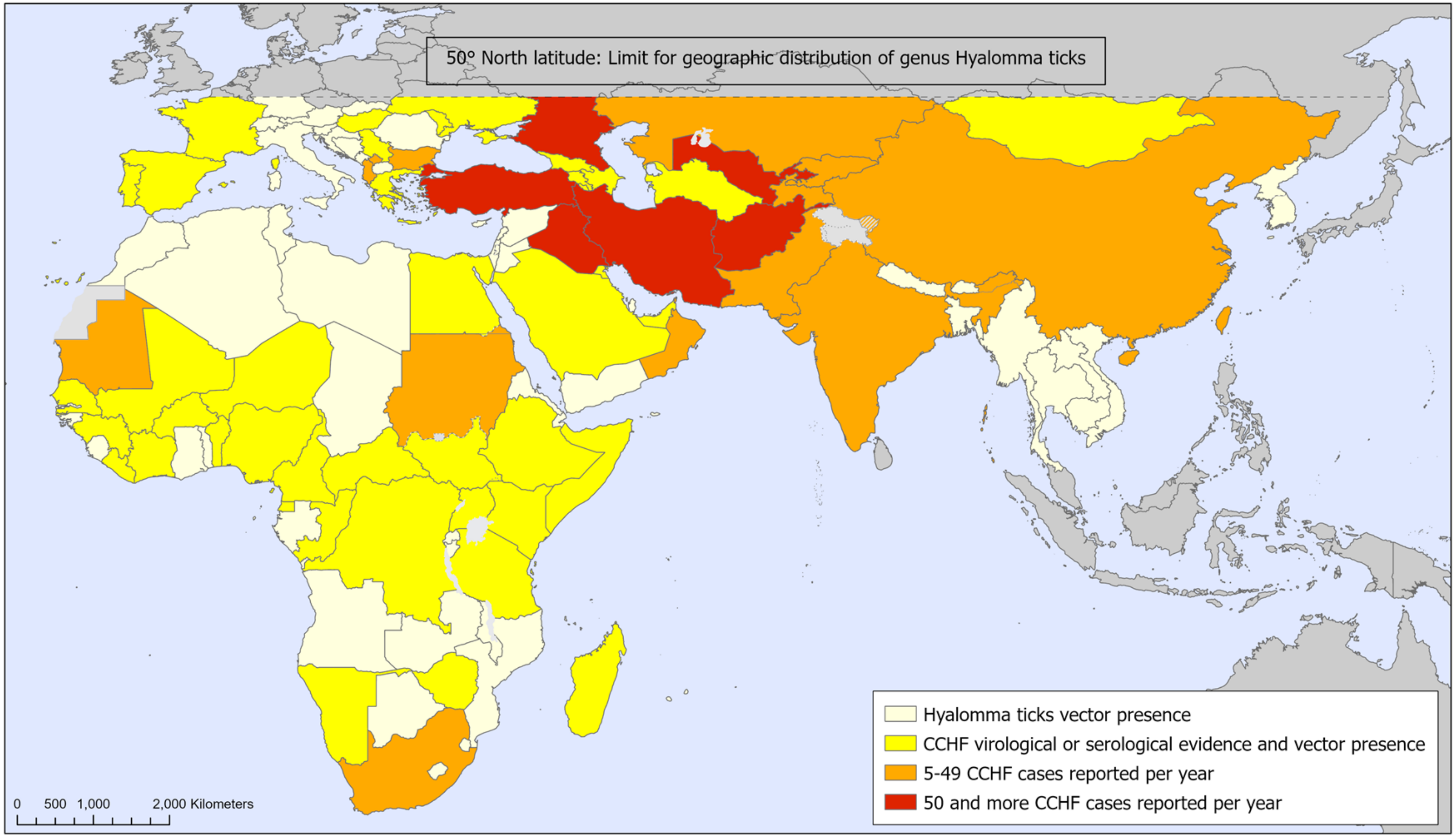
ECDC and EFSA. Map produced on 28 Sep 2017. Data presented in this map is collected through the VectorNet project. The maps are validated by designated external experts prior to publication. Please note that the data do not represent the official view or position of the countries. * Countries/Regions are displayed at different scales to facilitate their visualization. Administrative boundaries: ©EuroGeographics; ©UN-FAO; ©Turkstat.



ECDC and EFSA, map produced on 25 Jun 2025. Data presented in this map are collected by the VectorNet project. Maps are validated by external experts prior to publication. Please note that the depicted data do not reflect the official views of the countries.
* Countries/Regions are displayed at different scales to facilitate their visualisation.The boundaries and names shown on this map do not imply official endorsement or acceptance by the European Union.Administrative boundaries © EuroGeographics, UNFAO.

Since 2024 there were changes in 2 regions in Egypt.

Geographic distribution of Crimean-Congo Haemorrhagic Fever (2022)



Data Source: WHO - Viral Haemorrhagic Fevers (VHF)
Map Production: Jewgeni Bader, EYE Secretariat

Map Creation Date: **01 September 2022**

World Health Organization

DENGUE-DENV

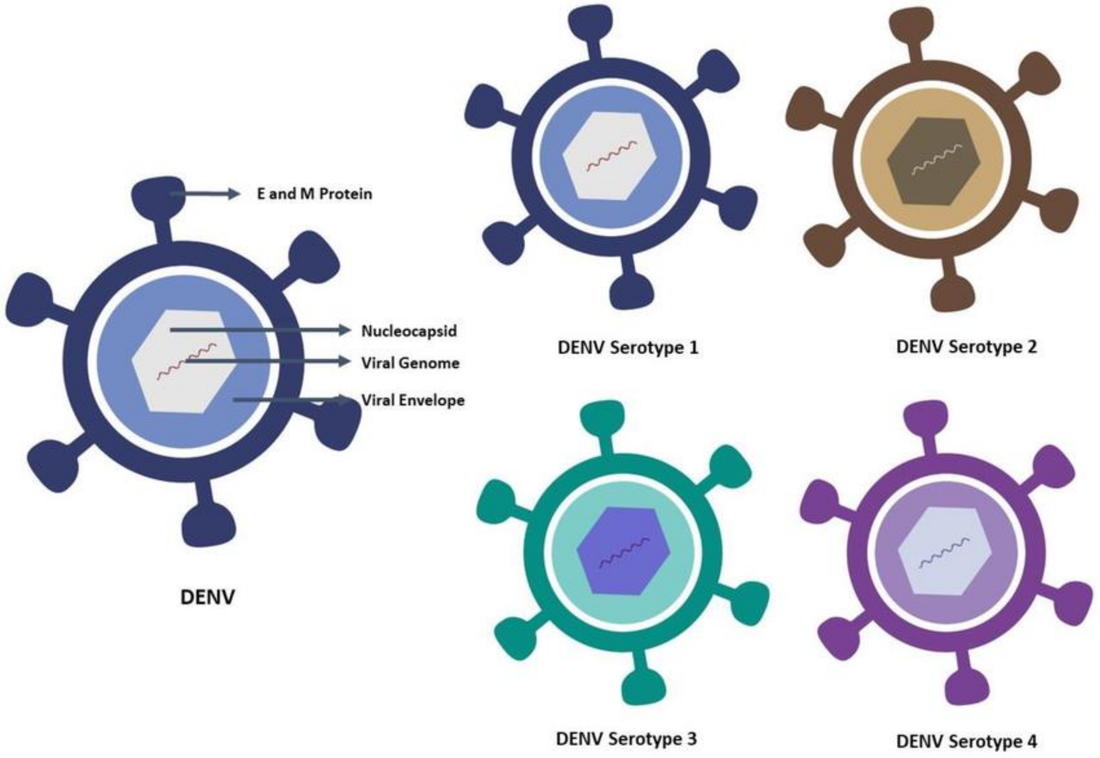
4 serotypes (DENV-1, DENV-2, DENV-3, DENV-4), a single-stranded RNA virus of the Flaviviridae family

The 4 dengue viruses are similar —share 65% of their genomes — but even within a single serotype, there is some genetic variation.

Despite these variations, infection with each of the dengue serotypes results in the same disease and range of clinical symptoms (Guzman, Nat Mic 2010)

Dengue is the most prevalent mosquito-borne viral disease globally

Endemic in over 100 tropical and subtropical countries



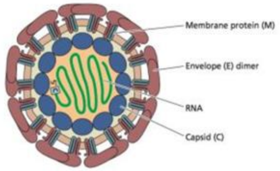
Zeyaullah, Vaccine 2022

DENGUE-DENV

Dengue virus (DENV): 1943 isolato da pazienti in Giappone. From 1970's dramatic increase in severe dengue cases Before 1970, only 9 countries had experienced severe dengue epidemics. The disease is now endemic in more than 100 countries.

Vettore principale:

Aedes aegypti
(Aedes albopictus)



Family: Flaviviridae
Genus: Orthoflavivirus

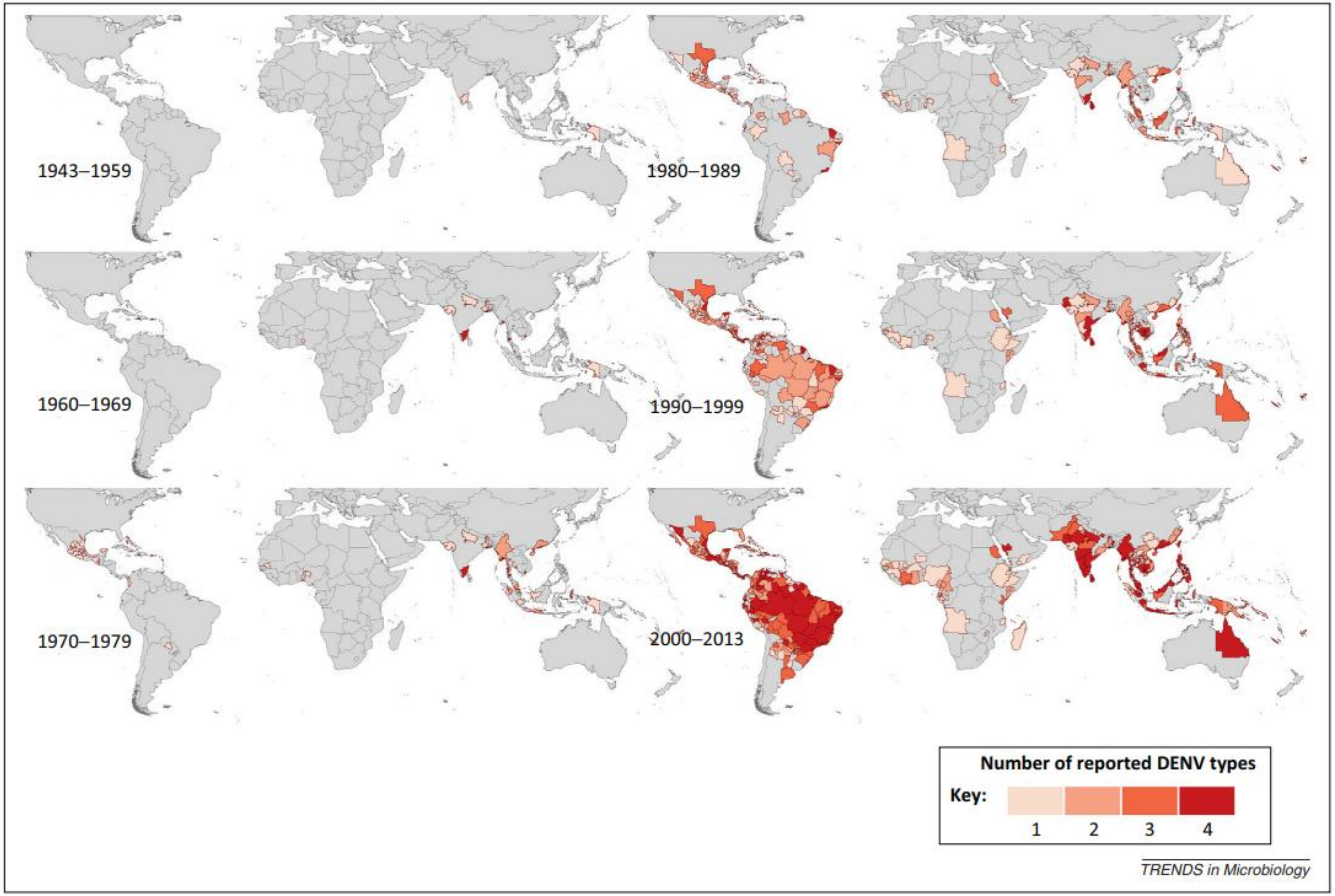
4 sierotipi:
DENV-1,
DENV-2,
DENV-3,
DENV-4

Animali:

NHPs, pipistrelli, roditori, altri animali

Sylvatic cycles of DENVs involving NHPs have been shown to exist in Asia and Africa, where DENV has been isolated from forest mosquitoes that feed on NHPs and from NHPs themselves. There is no good evidence yet for sylvatic DENV circulation in NHPs in the Americas.

SXW Gwee et al. One Health 2021
MJ Valentine et al. Parasit Vec 2019



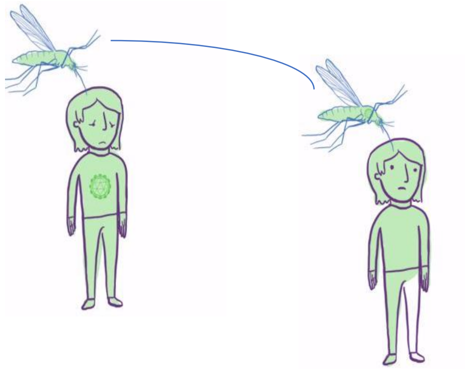
TRENDS in Microbiology

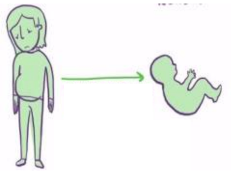
Figure 5. DENV Co-circulation. Cumulative number of DENV types reported by decade since 1943.

Dengue is the most rapidly spreading vector-borne disease worldwide, with over half the global population at risk for infection

DENGUE-DENV

Trasmissione:

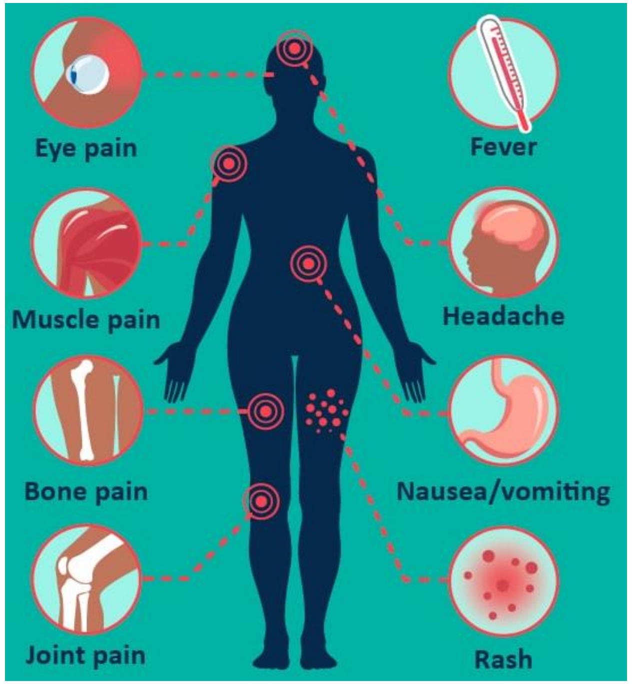




⚣

Clinica:

80% asintomatico



About 1 in 20 people who get sick with dengue will develop severe dengue. Severe dengue car result in shock, internal bleeding, and death (DHF)

Trattamento:

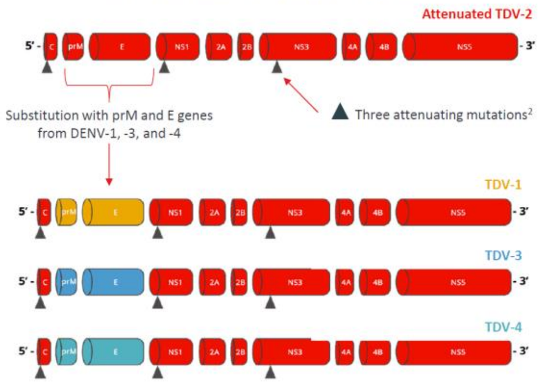
Di supporto non specifico

Vaccino:

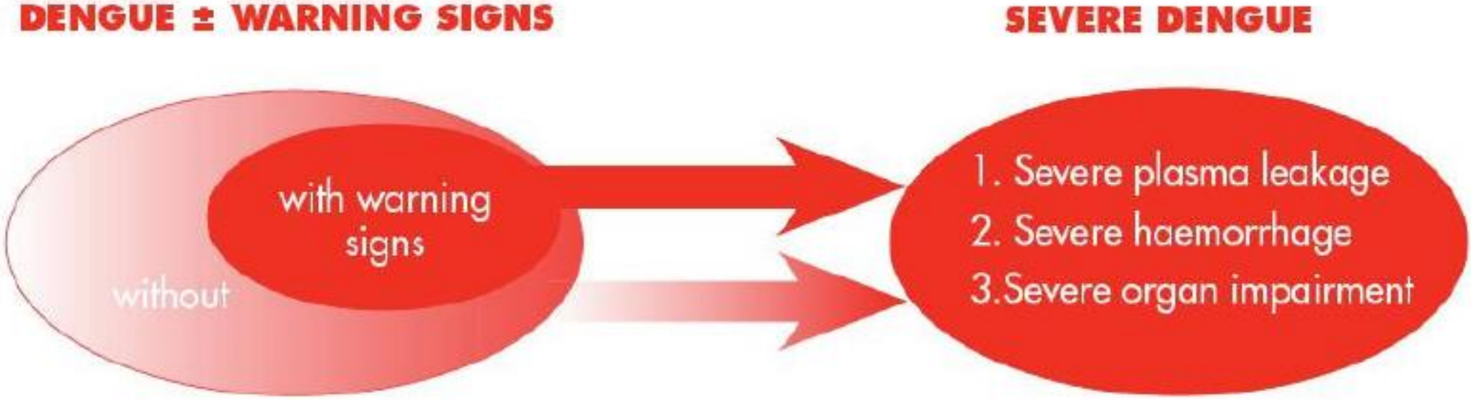
QDENGA è l'unico vaccino contro la dengue la cui commercializzazione è stata autorizzata da AIFA a febbraio 2023, (EMA 12/2022), 2 dosi a distanza di 3 mesi

TAK-003 is based on a live, attenuated DENV-2 virus backbone expressing E and prM proteins of all four DENV serotypes

Genetic structure and design of TAK-003$^{1-3}$



Dengue Case Classification and Levels of Severity



CRITERIA FOR DENGUE ± WARNING SIGNS

Probable dengue

live in /travel to dengue endemic area.

Fever and 2 of the following criteria:

- Nausea, vomiting
- Rash
- Aches and pains
- Tourniquet test positive
- Leukopenia
- Any warning sign

Laboratory-confirmed dengue

(important when no sign of plasma leakage)

Warning signs*

- Abdominal pain or tenderness
- Persistent vomiting
- Clinical fluid accumulation
- Mucosal bleed
- Lethargy, restlessness
- Liver enlargment >2 cm
- Laboratory: increase in HCT concurrent with rapid decrease in platelet count

*(requiring strict observation and medical intervention)

CRITERIA FOR SEVERE DENGUE

Severe plasma leakage

leading to:

- Shock (DSS)
- Fluid accumulation with respiratory distress

Severe bleeding

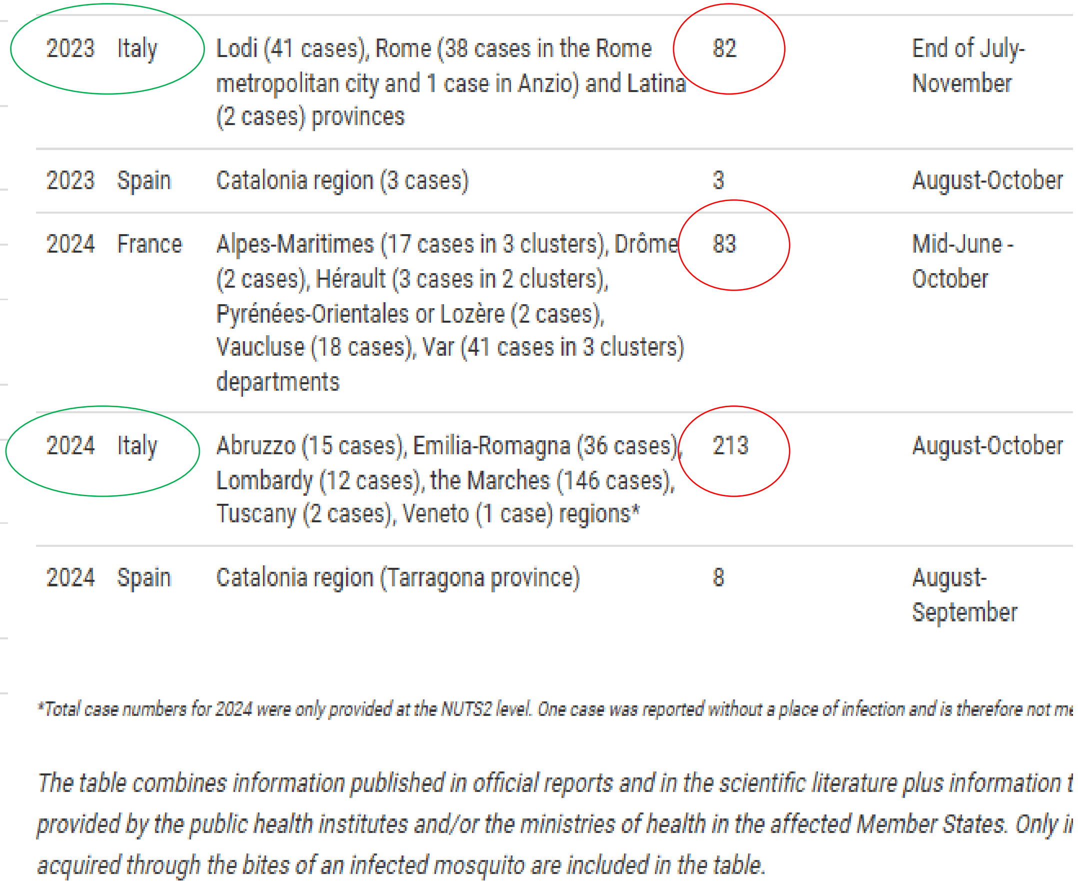
as evaluated by clinician

Severe organ involvement

- Liver: AST or ALT >=1000
- CNS: Impaired consciousness
- Heart and other organs

Dengue:

EUROPEAN CENTRE FOR DISEASE PREVENTION AND CONTROL

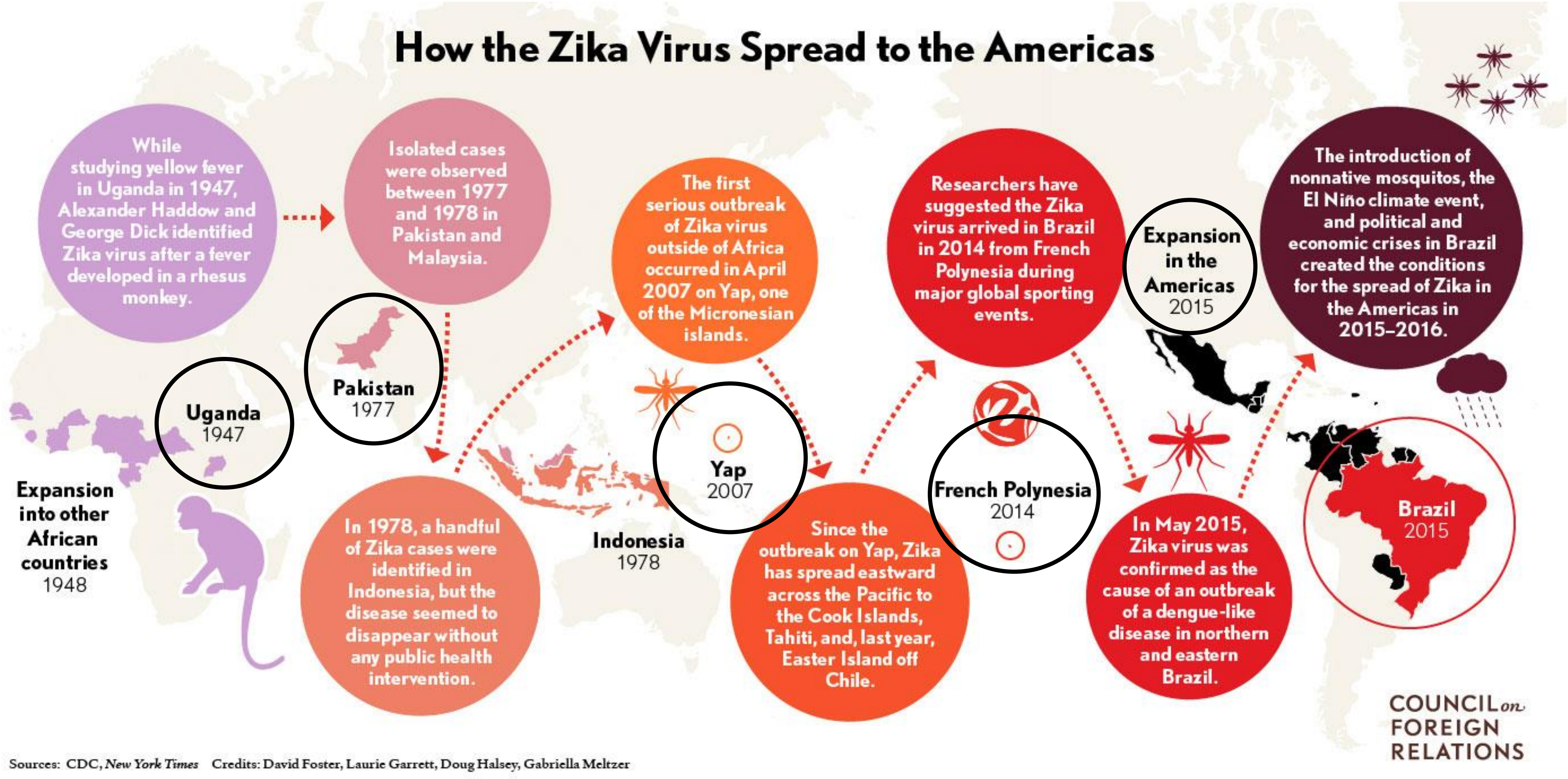


Year	Country	Department or regions affected	Number of autochthonous cases	Probable period of virus circulation
2010	Croatia	Korčula Island and the Pelješac peninsula	10	August–October
2010	France	Alpes-Maritimes department	2	August–September
2013	France	Bouches–du-Rhône department	1	September-October
2014	France	Var and Bouches-du-Rhône departments	4	July-September
2015	France	Gard department	8	July–September
2018	France	Alpes Maritimes, Hérault, and Gard departments	8	September–October
2018	Spain	Catalonia region, Murcia region or province of Cádiz	6	August-October
2019	Spain	Catalonia region	1	September
2019	France	Alpes-Maritimes and Rhône departments	9	July-September
2020	France	Hérault, Var, Alpes-Maritime, and Gard departments	13	July-October
2020	Italy	Veneto region	10	August
2021	France	Var and Hérault departments	2	July and September
2022	France	Pyrénées-Orientales, Hautes-Pyrénées, Haute-Garonne, Tarn et Garonne, Var, Alpes-Maritimes and Corse-du-Sud departments	65	June-September
2022	Spain	Ibiza	6	August-October
2023	France	Val-de-Marne (3 cases), Bouches–du-Rhône (14 cases in 2 clusters), Pyrénées-Orientales (11 cases), Hérault (3 cases), Gard (9 cases), Alpes-Maritimes (3 cases) and Drôme (2 cases) departments	45	July-October
2023	Italy	Lodi (41 cases), Rome (38 cases in the Rome metropolitan city and 1 case in Anzio) and Latina (2 cases) provinces	82	End of July-November
2023	Spain	Catalonia region (3 cases)	3	August-October
2024	France	Alpes-Maritimes (17 cases in 3 clusters), Drôme (2 cases), Hérault (3 cases in 2 clusters), Pyrénées-Orientales or Lozère (2 cases), Vaucluse (18 cases), Var (41 cases in 3 clusters) departments	83	Mid-June - October
2024	Italy	Abruzzo (15 cases), Emilia-Romagna (36 cases), Lombardy (12 cases), the Marches (146 cases), Tuscany (2 cases), Veneto (1 case) regions*	213	August-October
2024	Spain	Catalonia region (Tarragona province)	8	August-September

**Total case numbers for 2024 were only provided at the NUTS2 level. One case was reported without a place of infection and is therefore not me*

The table combines information published in official reports and in the scientific literature plus information t provided by the public health institutes and/or the ministries of health in the affected Member States. Only i acquired through the bites of an infected mosquito are included in the table.

Where and when we met Zika...



How the Zika Virus Spread to the Americas

While studying yellow fever in Uganda in 1947, Alexander Haddow and George Dick identified Zika virus after a fever developed in a rhesus monkey.

Uganda
1947

Expansion into other African countries
1948

Isolated cases were observed between 1977 and 1978 in Pakistan and Malaysia.

Pakistan
1977

In 1978, a handful of Zika cases were identified in Indonesia, but the disease seemed to disappear without any public health intervention.

Indonesia
1978

The first serious outbreak of Zika virus outside of Africa occurred in April 2007 on Yap, one of the Micronesian islands.

Yap
2007

Since the outbreak on Yap, Zika has spread eastward across the Pacific to the Cook Islands, Tahiti, and, last year, Easter Island off Chile.

Researchers have suggested the Zika virus arrived in Brazil in 2014 from French Polynesia during major global sporting events.

French Polynesia
2014

In May 2015, Zika virus was confirmed as the cause of an outbreak of a dengue-like disease in northern and eastern Brazil.

Expansion in the Americas
2015

Brazil
2015

The introduction of nonnative mosquitos, the El Niño climate event, and political and economic crises in Brazil created the conditions for the spread of Zika in the Americas in 2015–2016.

Sources: CDC, *New York Times* Credits: David Foster, Laurie Garrett, Doug Halsey, Gabriella Meltzer

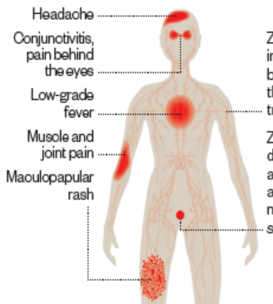
COUNCIL *on* FOREIGN RELATIONS

ORIGINS OF THE ZIKA OUTBREAK AND ITS POTENTIAL THREAT

Researchers are working to understand more about the Zika virus – how it is transmitted, its link to microcephaly and Guillain-Barré syndrome, and whether a vaccine can be developed. By Dawn Connelly.

TRANSMISSION, SYMPTOMS AND DIAGNOSIS

The main route of transmission for Zika virus is through the bite of an infected mosquito, although other routes have been reported. Symptoms develop 2–10 days after infection and are usually mild, lasting up to a week. There is no specific treatment.



Zika virus is present in blood and may be transmitted through blood transfusions.

Zika virus has been detected in semen at least two months after infection and may be transmitted sexually.

SEXUAL TRANSMISSION

Public health England advises men returning from Zika transmission zones who have experienced symptoms to use a condom for six months, or one month if no symptoms.

DIAGNOSIS

Acute infection is identified through polymerase chain reaction in specialist labs. Serological tests may indicate anti-Zika antibodies but can cross react with other flaviviruses. Treat with rest, fluids and paracetamol. Do not give aspirin in case dengue is present.

Public Health England has advised women returning from Zika transmission areas to avoid becoming pregnant for 28 days.

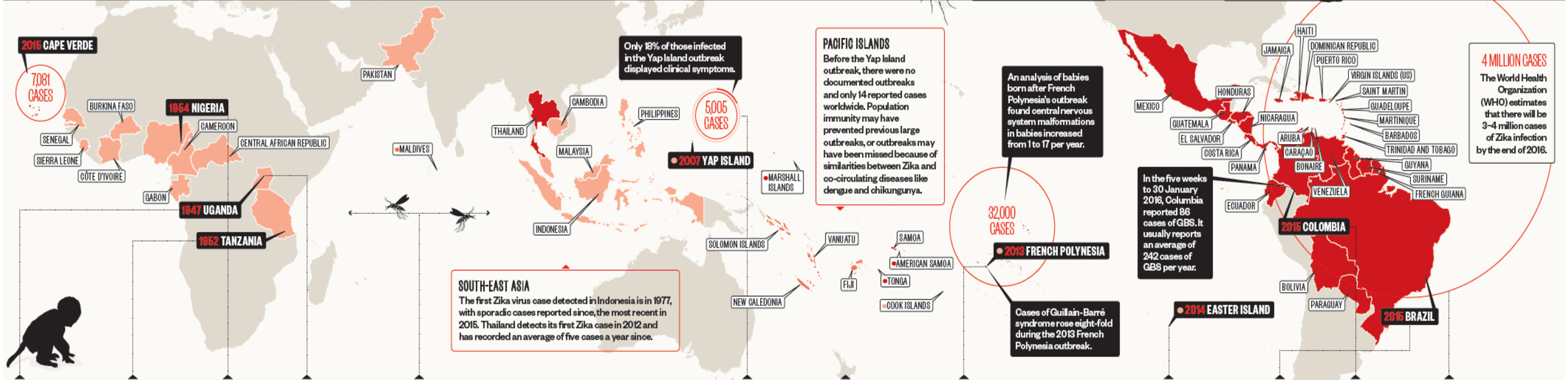
Zika virus can be transmitted from mother to child during pregnancy.

EXPLOSION OF CASES

Zika virus is a flavivirus related to yellow fever, dengue, West Nile and Japanese encephalitis. It is mainly transmitted by mosquitoes and was first identified in Africa over 60 years ago.

Zika transmission as of 22 February 2016
- ● Reported in the past two months
- ● Reported in the past nine months
- ● Cases or transmission before 2015

The *A. aegypti* mosquito can only fly 400 metres in its lifetime, so people, rather than mosquitoes, spread the disease.



Only 18% of those infected in the Yap Island outbreak displayed clinical symptoms.

PACIFIC ISLANDS

Before the Yap Island outbreak, there were no documented outbreaks and only 14 reported cases worldwide. Population immunity may have prevented previous large outbreaks, or outbreaks may have been missed because of similarities between Zika and co-circulating diseases like dengue and chikungunya.

An analysis of babies born after French Polynesia's outbreak found central nervous system malformations in babies increased from 1 to 17 per year.

Cases of Guillain-Barré syndrome rose eight-fold during the 2013 French Polynesia outbreak.

SOUTH-EAST ASIA

The first Zika virus case detected in Indonesia is in 1977, with sporadic cases reported since, the most recent in 2015. Thailand detects its first Zika case in 2012 and has recorded an average of five cases a year since.

In the five weeks to 30 January 2016, Columbia reported 86 cases of GBS. It usually reports an average of 242 cases of GBS per year.

4 MILLION CASES

The World Health Organization (WHO) estimates that there will be 3–4 million cases of Zika infection by the end of 2016.

1947
The Zika virus is first identified in Zika Forest in Uganda in 1947 in a captive, sentinel rhesus monkey.

1952
Zika virus antibodies are subsequently detected in humans in Uganda and Tanzania.

1954
Zika virus is isolated from a young girl in Nigeria in 1954.

1964
A researcher infected with Zika provides the first proof that Zika causes human infection.

1960s–1980s
Zika virus is detected in mosquitoes and rhesus monkeys across equatorial Africa and Asia. Sporadic cases are reported in humans but these are rare and mild.

2007
The first large outbreak of Zika virus disease is in Yap Island, Micronesia, where it is estimated to have affected 5,005 people, which represents 73% of residents age three years and older.

2012
Two distinct lineages of Zika virus are identified — African and Asian.

2013–2014
The next major outbreak happens in French Polynesia in 2013–2014, affecting an estimated 32,000 people. Outbreaks are also reported in the Cook Islands and New Caledonia.

2014
The virus then spreads to Oceania, arriving in The Americas at Easter Island by 2014.

2015
May: Brazil reports local transmission of Zika virus.

2015
October: Columbia and Cape Verde report local transmission of Zika.

2016
February: As evidence of a link between Zika and birth defects mounts, the WHO declares a public health emergency.

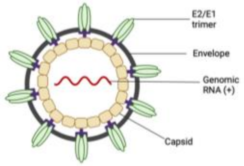
Arbovirosi di importazione con eventi di trasmissione «autoctona»: virus Chikungunya

Chikungunya virus (CHIKV) has caused over 70 epidemics between 1952 and 2018. It was first identified in 1952 in Tanzania, and isolated from infected patients' sera, and Aedes and Culex spp. Mosquitoes in 1953

Vettore principale:

Aedes aegypti
Aedes albopictus

Famiglia:



Family: Togaviridae
Genus: Alphavirus

ECSA (East-Central, South Africa)
WA (West Africa)
Asian
IOL (Indian Ocean lineage)

Reservoir animale:

Virus isolated from: NHPs, palm squirrel (*Xerus erythropus*), and bats of the *Scotophillus* species

In Africa, during inter-epidemic periods, CHIKV is believed to be preserved via a sylvatic transmission cycle involving arboreal mosquitoes and wild primates.
This is in contrast to Asia, where the virus principally cycles between the two main vectors (i.e., *Ae aegypti* and *Ae albopictus*) and humans. The role of vertebrate animals of new endemic regions has been poorly investigated to date

Arbovirosi di importazione con eventi di trasmissione «autoctona»: virus Chikungunya

Vettore principale:

Aedes aegypti
Aedes albopictus

The vector competence of Ae albopictus, experimentally assessed in 1976, was demonstrated during of Reunion Island (2005). Where Ae aegypti was absent and CHIKV-positive and competent mosquito pools of Ae albopictus were detected
A single mutation in the envelope viral gene E1 of an ECSA strain (alanine to valine at position 226, A226V E1) was considered responsible for the increased fitness of CHIKV in Ae albopictus and the acquisition of a more effective competence. This mutation allowed for the geographic expansion of CHIKV throughout sub-Saharan Africa and Southeast Asia, and into Europe.

Nevertheless, CHIKV isolated from some of the European autochthonous cases lacked the A226V substitution in E1, indicating that other factors or mutations can determine the virus adaptation to Ae albopictus. Indeed, substitutions in the E2 and E3 genes have also been involved in the process. These mutations are suggested to enhance the infection in the mosquito midgut, probably altering the entry process at the fusion step in the endosome

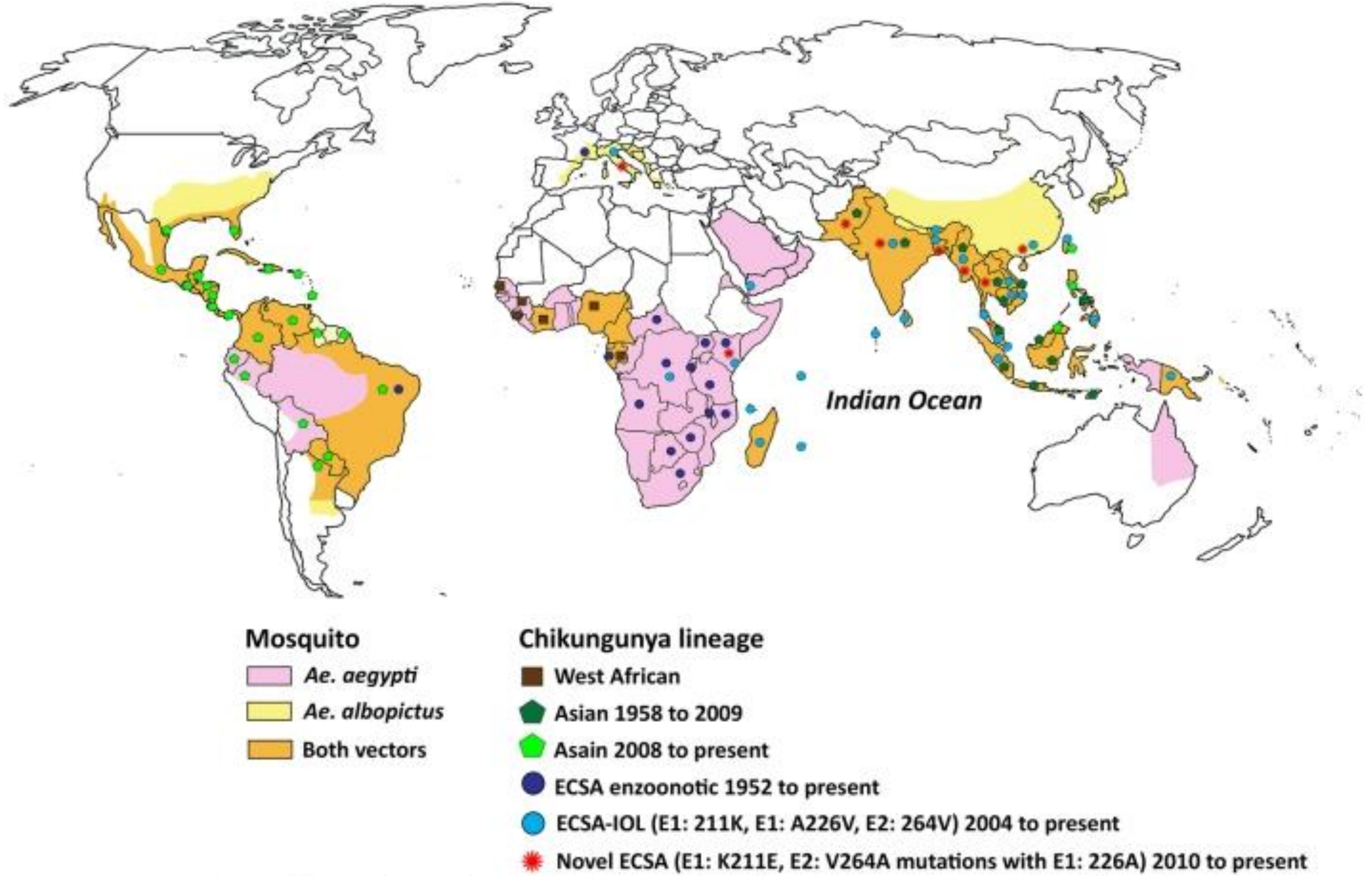
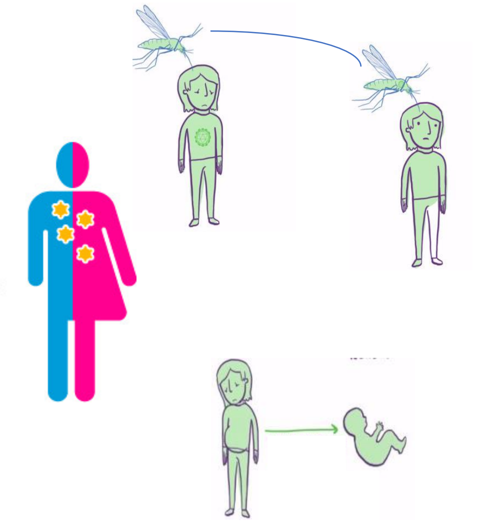


Fig. 1 Geographical distribution of CHIKV lineages during 1952–2020 and that of its primary mosquito vectors. Different CHIKV lineages are represented by distinct colored symbols. The map also shows the distribution of the primary CHIKV mosquito vectors. Areas shown in pink indicate the range of *Ae. aegypti*, those shown in yellow indicate the range of *Ae. albopictus*, and the range of both primary vectors is indicated in orange. The range of both primary vectors was obtained from [16]. Distribution of chikungunya virus data were obtained from a number of studies [9, 17–51]

Arbovirosi di importazione con eventi di trasmissione «autoctona»: virus Chikungunya

Trasmissione:



Clinica:

Sintomi nel 72-95% degli infetti.

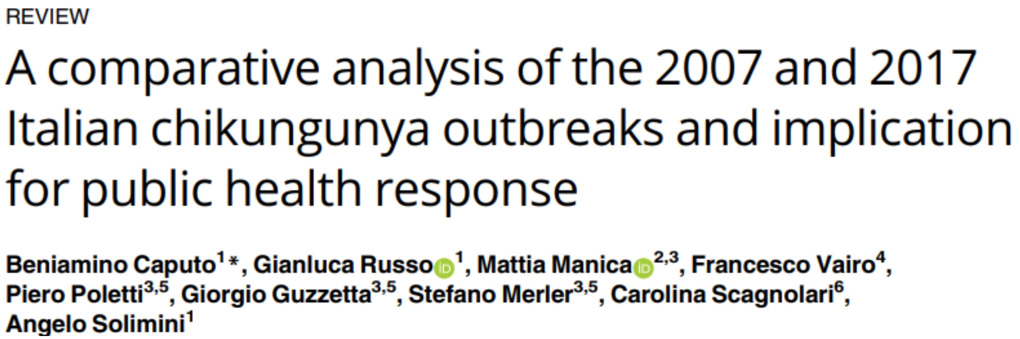
in fase acuta febbre anche >39° C nel 92% dei casi, accompagnata frequentemente da dolori articolari (87% dei casi)

Sintomi comuni sono mal di testa mialgia, affaticamento, rash, nausea, vomito. Meno frequenti le manifestazioni oculari

I dolori articolari possono perdurare anche per mesi (Reunion 42% casi sequelae per oltre 18 mesi)

Trattamento:

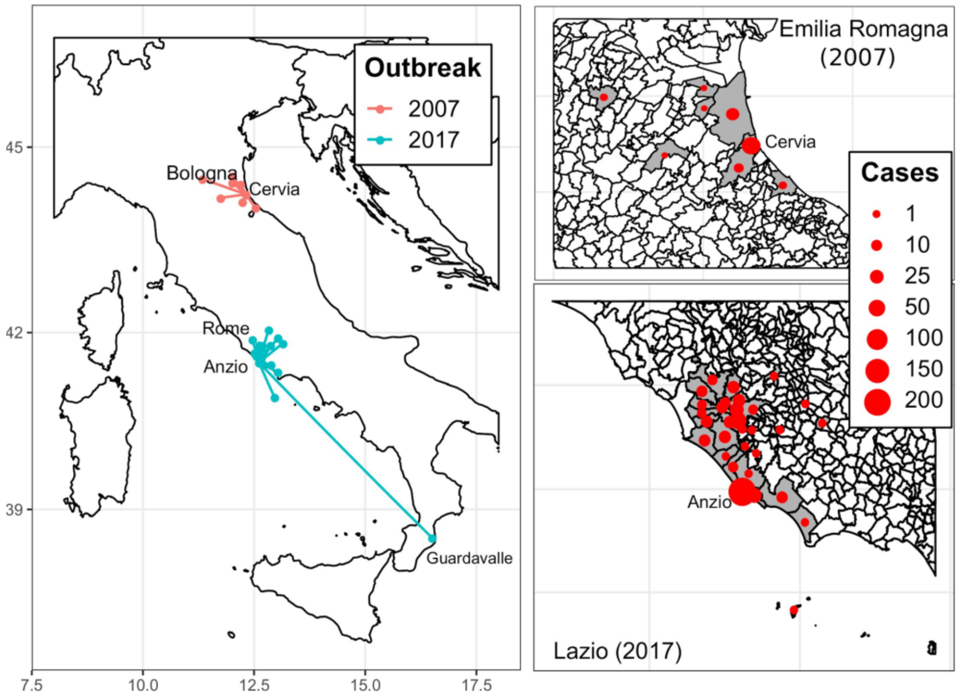
Di supporto non specifico



REVIEW

A comparative analysis of the 2007 and 2017 Italian chikungunya outbreaks and implication for public health response

Beniamino Caputo[1]*, Gianluca Russo[1], Mattia Manica[2,3], Francesco Vairo[4], Piero Poletti[3,5], Giorgio Guzzetta[3,5], Stefano Merler[3,5], Carolina Scagnolari[6], Angelo Solimini[1]

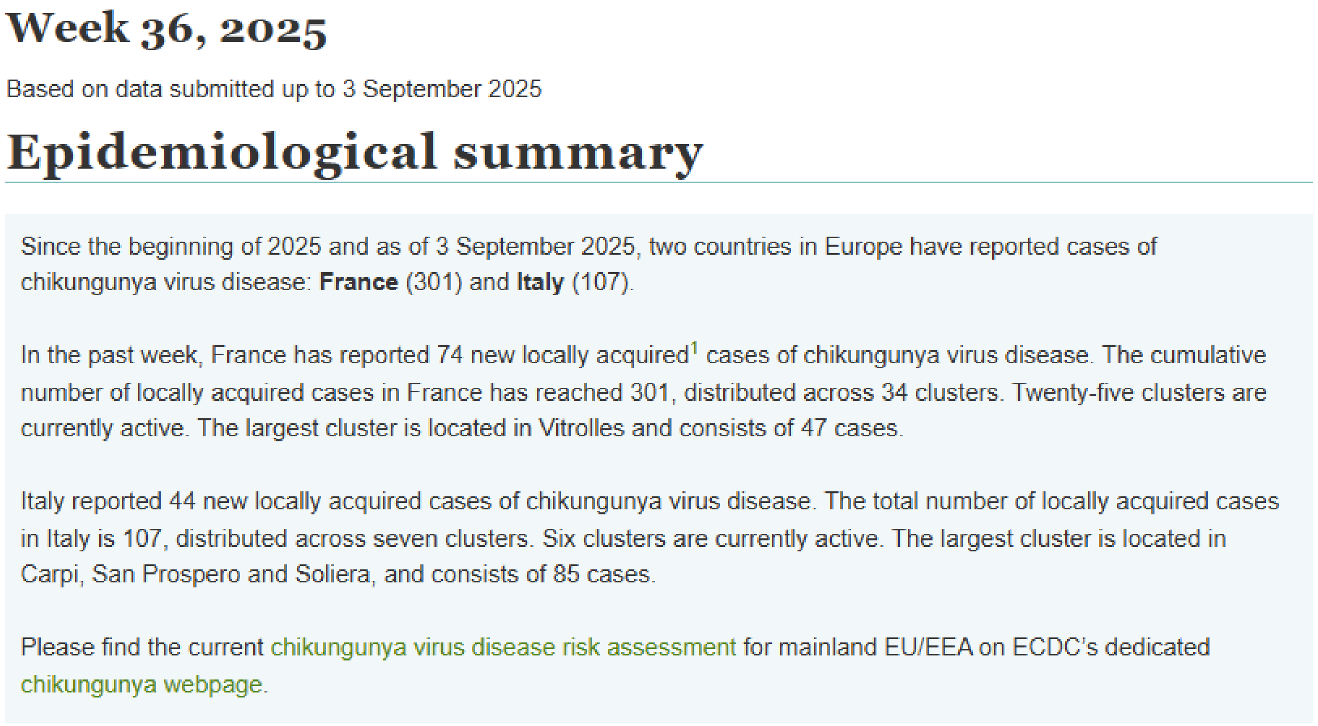


The first outbreak took place **in 2007** in Northeast Italy near the Adriatic coast, and it represented the first documented autochthonous CHIKV transmission on continental Europe.

In total, **337 cases were notified during 2007, 217 of which were laboratory-confirmed**. The outbreak started from Castiglione di Cervia and Castiglione di Ravenna and generated smaller transmission chains mainly in 5 other towns in the same region (Emilia-Romagna).

The second CHIKV outbreak occurred in **2017** and was characterized by 3 main foci (Anzio, Rome, and Guardavalle Marina) in 2 different regions, **Lazio and Calabria**. In total, the most updated data report **499 probable cases, 270 were laboratory-confirmed.**

Chikungunya:



Week 36, 2025

Based on data submitted up to 3 September 2025

Epidemiological summary

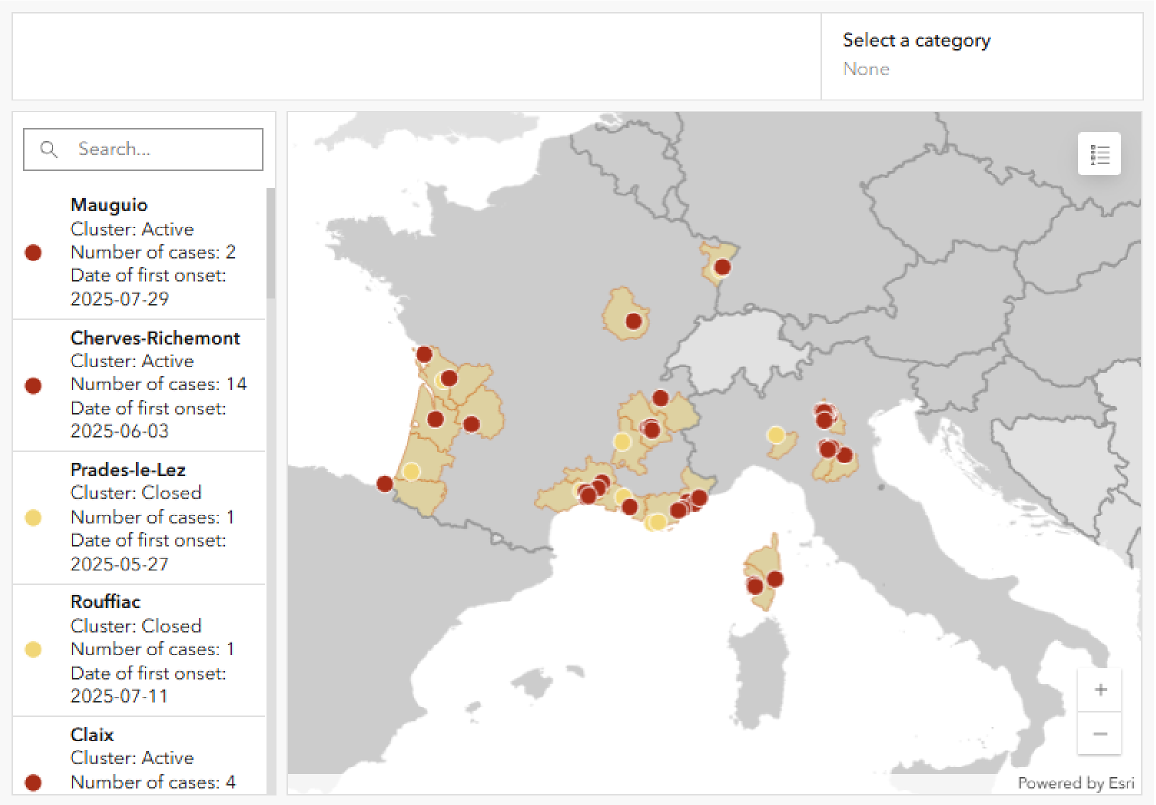
Since the beginning of 2025 and as of 3 September 2025, two countries in Europe have reported cases of chikungunya virus disease: **France** (301) and **Italy** (107).

In the past week, France has reported 74 new locally acquired[1] cases of chikungunya virus disease. The cumulative number of locally acquired cases in France has reached 301, distributed across 34 clusters. Twenty-five clusters are currently active. The largest cluster is located in Vitrolles and consists of 47 cases.

Italy reported 44 new locally acquired cases of chikungunya virus disease. The total number of locally acquired cases in Italy is 107, distributed across seven clusters. Six clusters are currently active. The largest cluster is located in Carpi, San Prospero and Soliera, and consists of 85 cases.

Please find the current chikungunya virus disease risk assessment for mainland EU/EEA on ECDC's dedicated chikungunya webpage.

Spatial distribution of locally acquired chikungunya virus disease cases in 2025 till 3 September 2025



● **Mauguio**
Cluster: Active
Number of cases: 2
Date of first onset: 2025-07-29

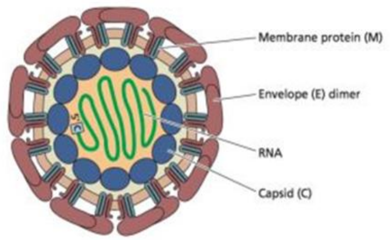
● **Cherves-Richemont**
Cluster: Active
Number of cases: 14
Date of first onset: 2025-06-03

● **Prades-le-Lez**
Cluster: Closed
Number of cases: 1
Date of first onset: 2025-05-27

● **Rouffiac**
Cluster: Closed
Number of cases: 1
Date of first onset: 2025-07-11

● **Claix**
Cluster: Active
Number of cases: 4

Arbovirosi endemiche in Italia: West-Nile



West Nile virus: isolato per la prima volta nel 1937 in Uganda (distretto West Nile). Il virus è diffuso in Africa, Asia occidentale, Europa, Australia e America.

Vector:

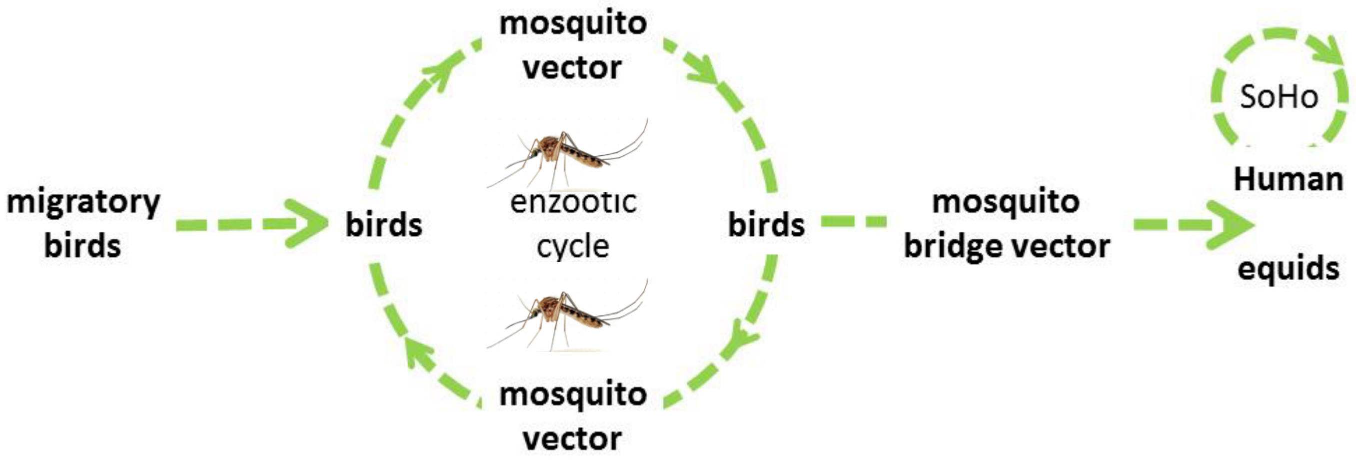
In Europa:
Culex pipiens (Cx. pipiens pipiens, Cx. pipiens molestus) e *Culex modestus* i principali

Amplifying host:

Uccelli selvatici
(rapaci e corvidi sviluppano frequentemente sintomi e si rileva outcome fatale)

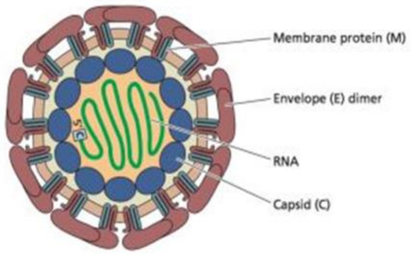
Dead-end host:

Mammiferi (e.g. Uomini/Equidi)



SoHo= substance of Human origin

Arbovirosi endemiche in Italia: Encefalite da zecche (TBE)



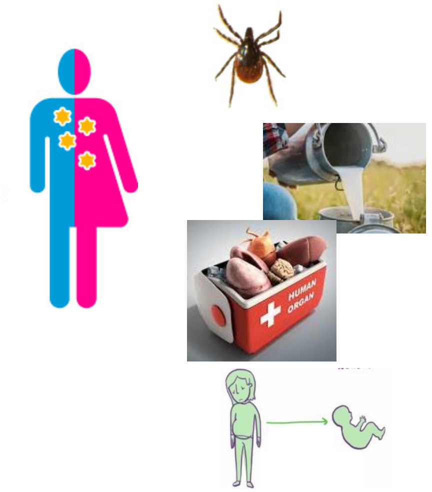
Vettore:

Ixodes ricinus e *Ixodes persulcatus*, operano sia come vettori che come serbatoi (*I. persulcatus* è diffusa in Europa orientale e Russia). Anche *Dermacentor* ed *Haemaphysalis* possono trasmettere l'infezione.

Reservoir animale:

Il virus infetta roditori, caprioli, ovini, caprini che contribuiscono al mantenimento del ciclo di trasmissione dell'infezione. Gli uccelli contribuiscono a trasportare passivamente zecche infette durante le loro migrazioni.

Trasmissione:



Clinica:

Sintomi possono comparire in due fasi
- 1st sintomi generic simil influenzali
- 2nd SNC meningite e/o encefalite

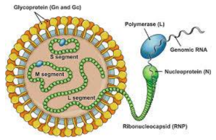
- European subtype: mortality rate 0.5% - 2%, up to 10% of people suffer long-term or permanent neurological problems.
- Far Eastern subtype: mortality rate up to 35%, higher rate of severe long-term/permanent neurological problems.
- Siberian subtype: mortality rate 1% to 3% and patients tend to develop chronic or long-term disease.

Arbovirosi endemiche in Italia: Virus Toscana (TOSV)

Toscana virus: isolato per la prima volta nel 1971 da *P. perncios*us (Monte Argentario)

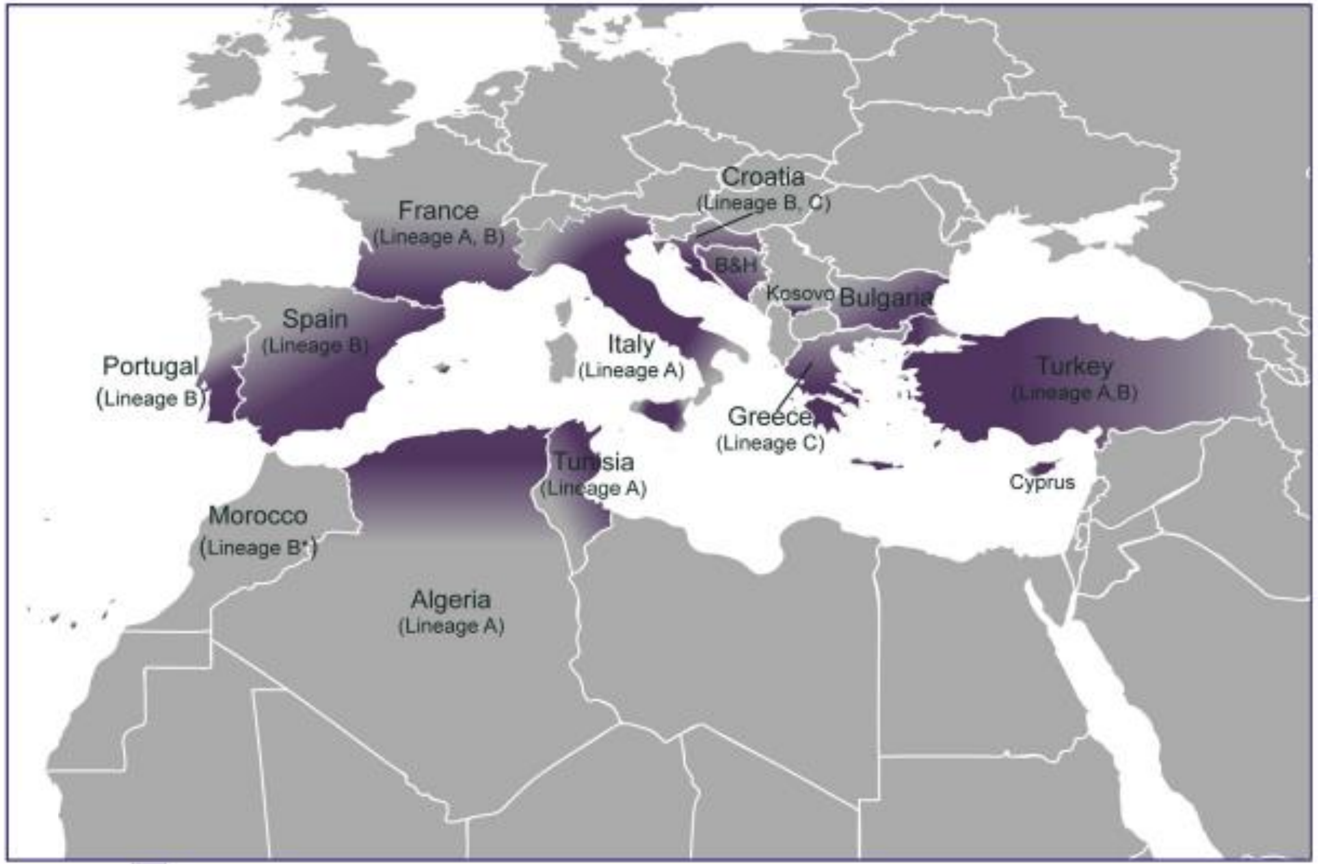
Family: Phenuiviridae
Genus: Phlebovirus

3 genotypes of TOSV
(lineages A, B, and C)

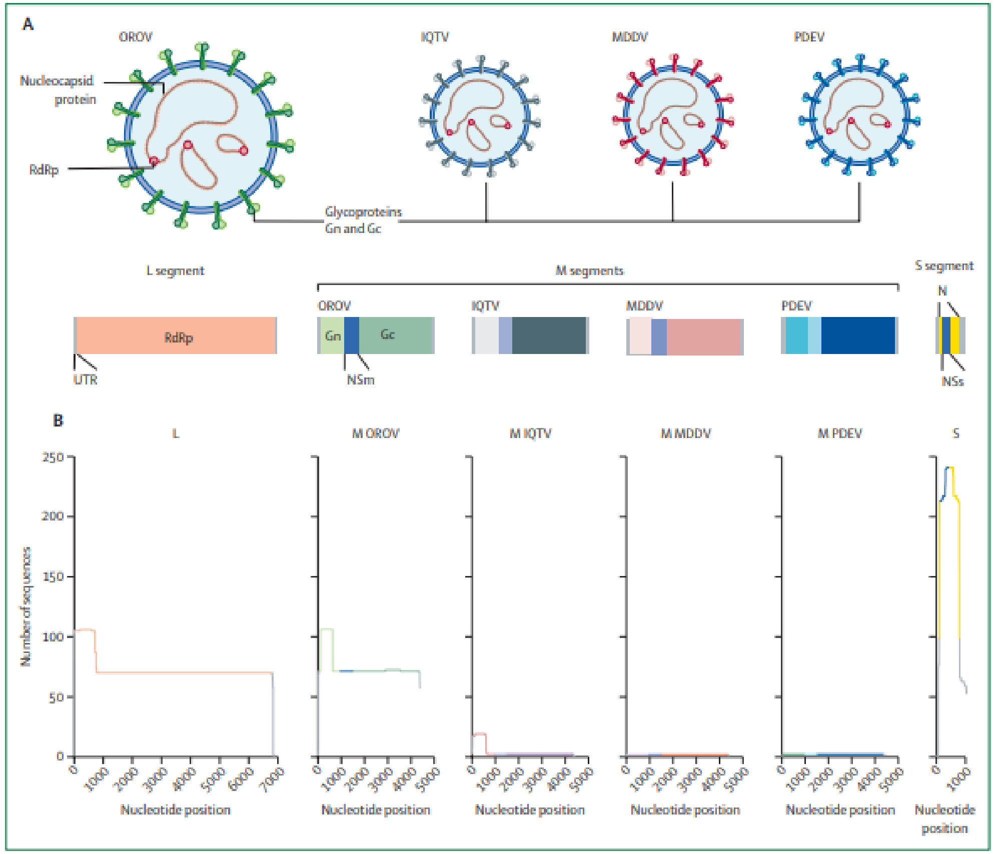


Phlebotomus perniciosus
Phlebotomus perfiliewi
Sergentomyia

Animali: studi sierologici hanno rilevato anticorpi anti-TOSV in cavalli, maiali, bovini, pecore, cani, gatti e pipistrelli

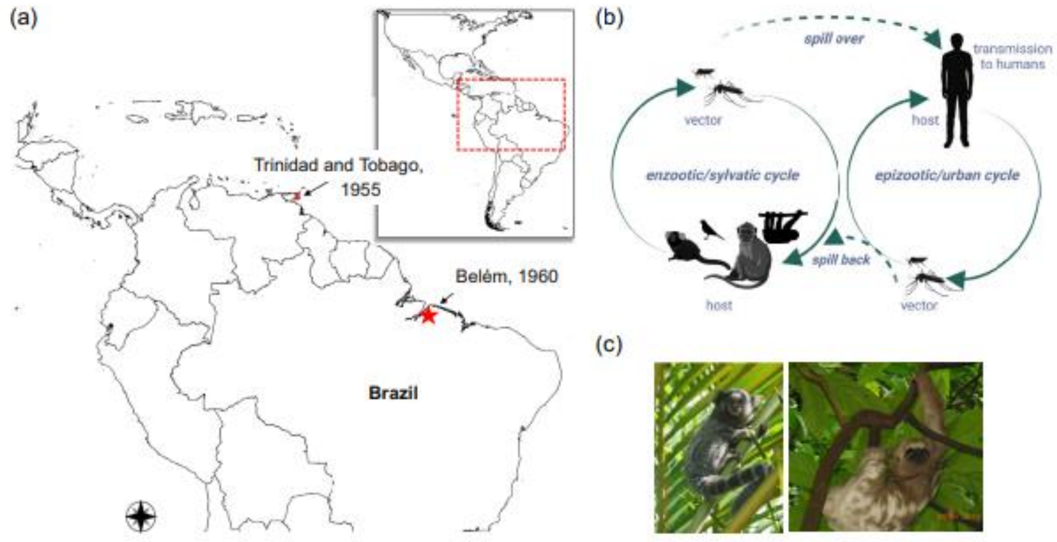


What about the silent invader?



Oropouche virus belongs to the Simbu serogroup of the viral genus *Orthobunyavirus* in the *Peribunyaviridae* family

The virus was first detected in 1955 in a febrile forest worker in a village in Trinidad and Tobago, near the Oropouche River



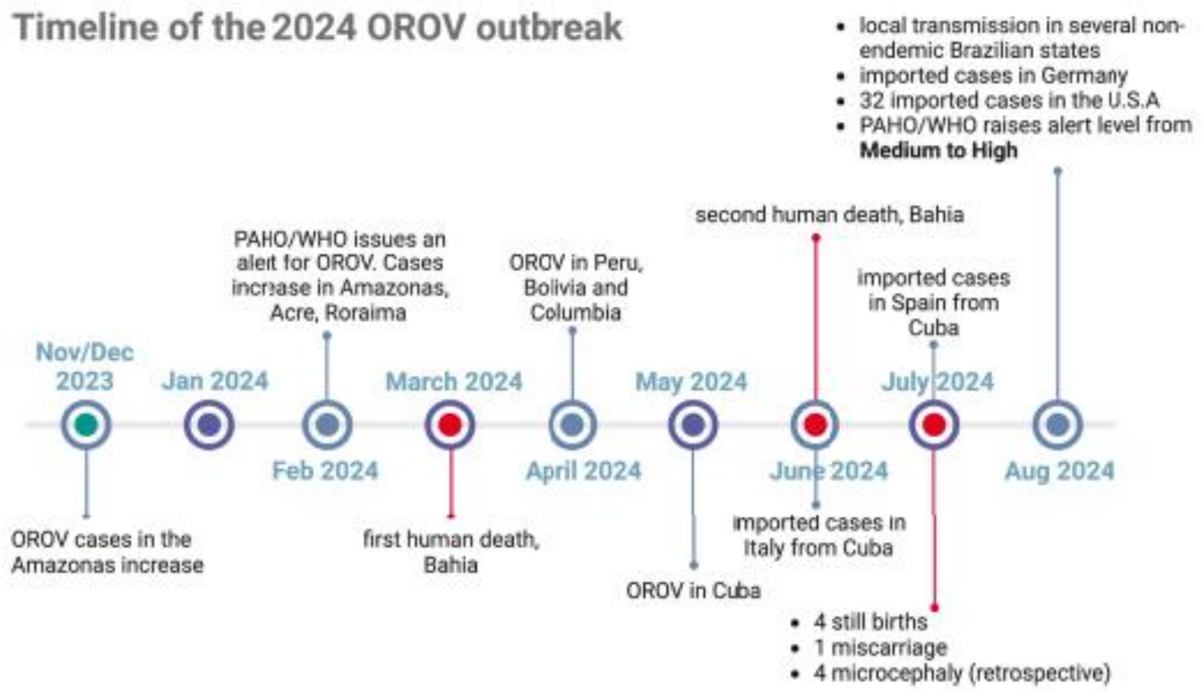
OROV was isolated from the mosquito species Mansonia venezuelensis and Aedes serratus

OROV RNA has also been found in Aedes scapularis, A. serratus, Culex fatigans and Psorophora fero

When OROV spills over into humans, it can initiate an urban cycle where the likely vector is the biting midge Culicoides paraensis

What about the silent invader?

Where has Oropouche virus disease been found?


Timeline of the 2024 OROV outbreak

OROV cases in the Amazonas increase

PAHO/WHO issues an alert for OROV. Cases increase in Amazonas, Acre, Roraima

first human death, Bahia

OROV in Peru, Bolivia and Columbia

OROV in Cuba

second human death, Bahia

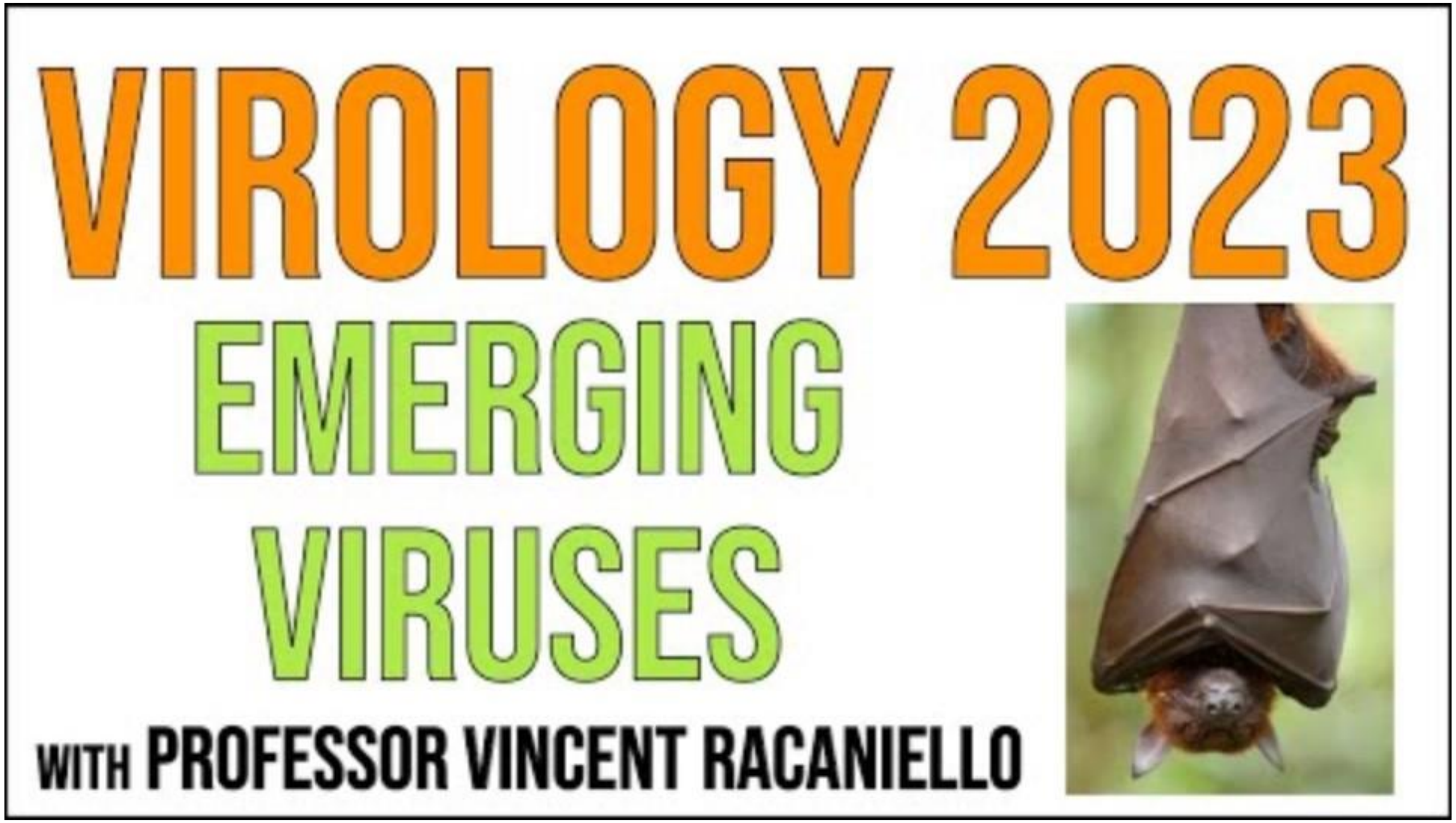
imported cases in Italy from Cuba

imported cases in Spain from Cuba

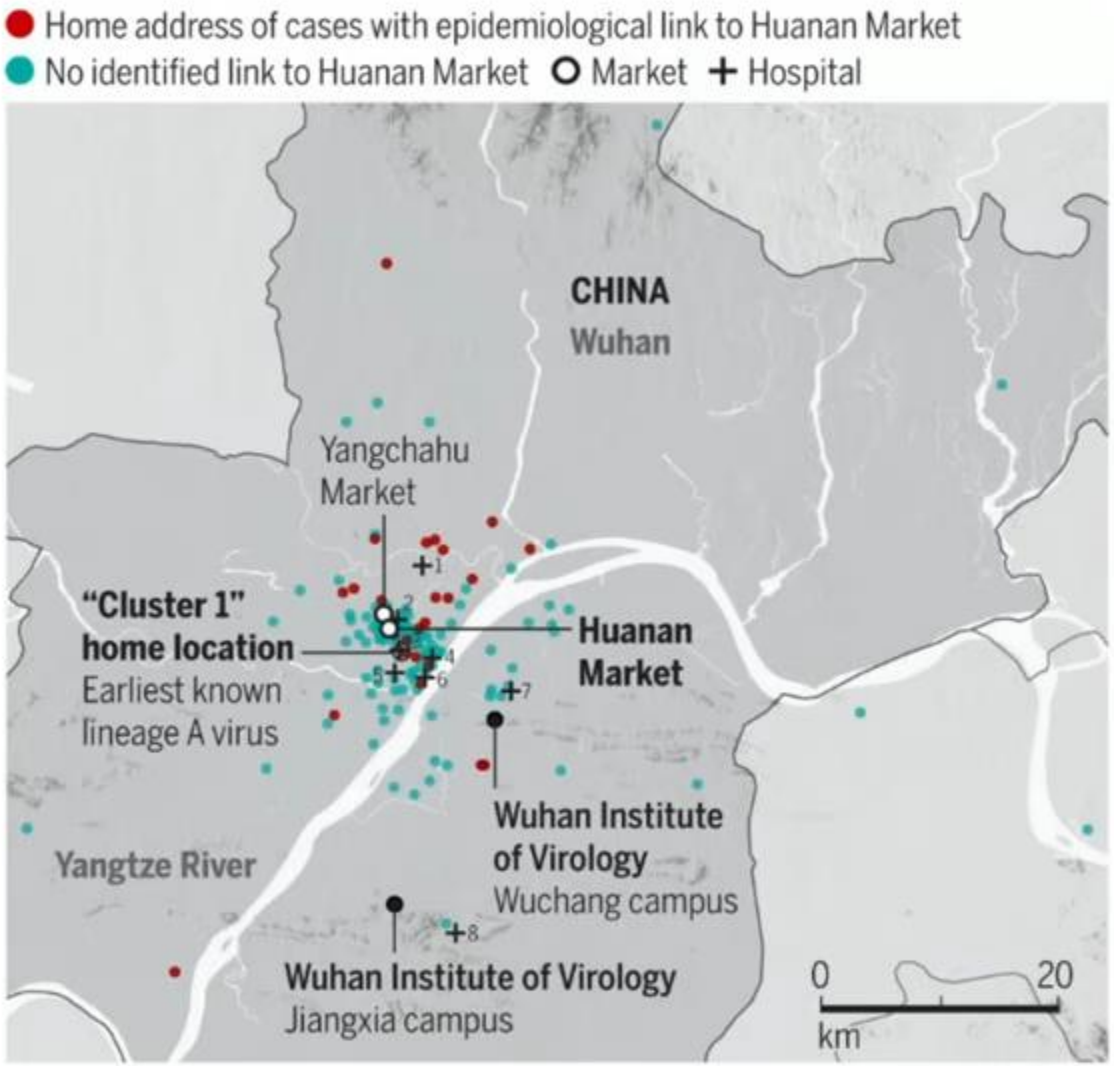
- 4 still births
- 1 miscarriage
- 4 microcephaly (retrospective)

- local transmission in several non-endemic Brazilian states
- imported cases in Germany
- 32 imported cases in the U.S.A
- PAHO/WHO raises alert level from **Medium to High**

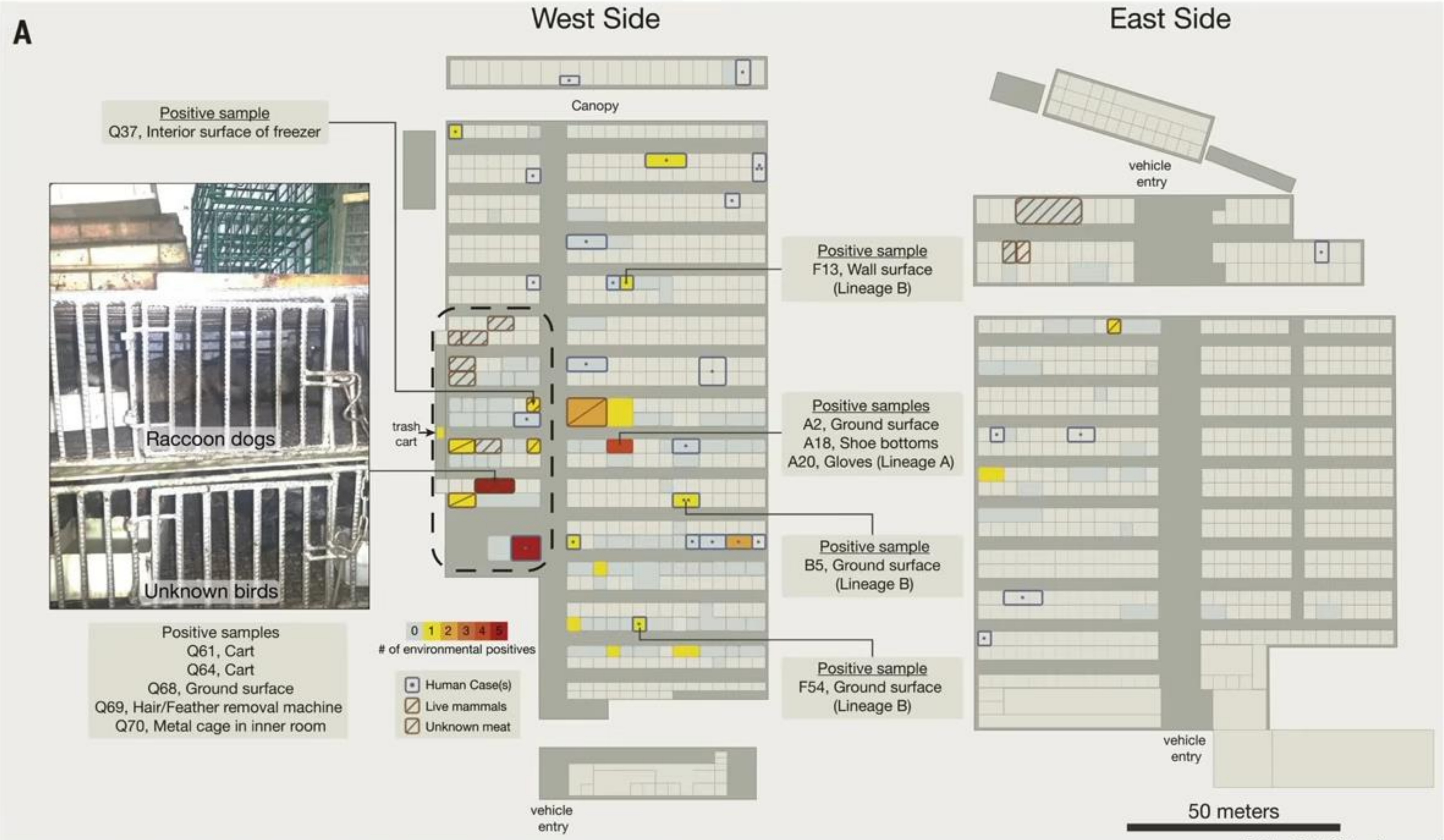
If curious…


VIROLOGY 2023
EMERGING VIRUSES
WITH PROFESSOR VINCENT RACANIELLO

We have evidence that SARS-CoV-2 was a zoonosis; no evidence of other origins



DOI: 10.1126/science.abp871



Positive sample
Q37, Interior surface of freezer

Positive sample
F13, Wall surface
(Lineage B)

Positive samples
A2, Ground surface
A18, Shoe bottoms
A20, Gloves (Lineage A)

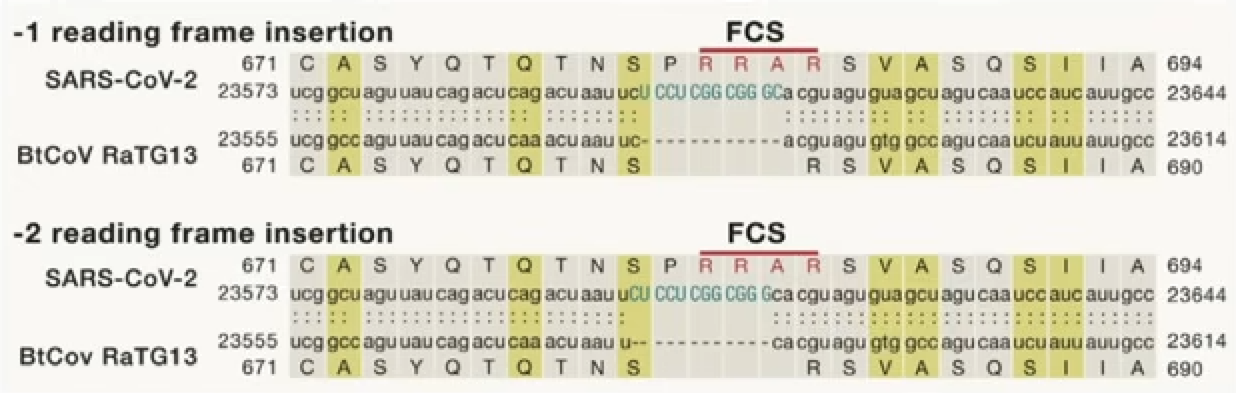
Positive sample
B5, Ground surface
(Lineage B)

Positive sample
F54, Ground surface
(Lineage B)

Positive samples
Q61, Cart
Q64, Cart
Q68, Ground surface
Q69, Hair/Feather removal machine
Q70, Metal cage in inner room

DOI: 10.1126/science.abp871

Furin cleavage site



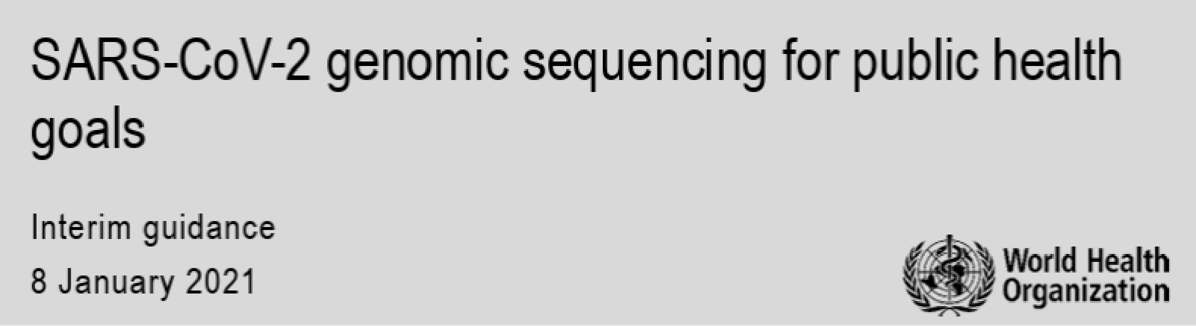
```
-1 reading frame insertion                                        FCS
                 671   C   A   S   Y   Q   T   Q   T   N   S   P   R   R   A   R   S   V   A   S   Q   S   I   I   A      694
SARS-CoV-2     23573 ucg gcu agu uau cag acu cag acu aau ucU CCU CGG CGG GCa cgu agu gua gcu agu caa ucc auc auugcc  23644

BtCoV RaTG13   23555 ucg gcc agu uau cag acu caa acu aau uc- --- --- --- --a cgu agu gtg gcc agu caa ucu auu auugcc  23614
                 671   C   A   S   Y   Q   T   Q   T   N   S                   R   S   V   A   S   Q   S   I   I   A      690

-2 reading frame insertion                                        FCS
                 671   C   A   S   Y   Q   T   Q   T   N   S   P   R   R   A   R   S   V   A   S   Q   S   I   I   A      694
SARS-CoV-2     23573 ucg gcu agu uau cag acu cag acu aau uCU CCU CGG CGG Gca cgu agu gua gcu agu caa ucc auc auugcc  23644

BtCov RaTG13   23555 ucg gcc agu uau cag acu caa acu aau u-- --- --- --- -ca cgu agu gtg gcc agu caa ucu auu auugcc  23614
                 671   C   A   S   Y   Q   T   Q   T   N   S                   R   S   V   A   S   Q   S   I   I   A      690
```

- Absent from closest relatives of SARS-CoV-2 but these have been poorly sampled
- Common in other CoVs including human common cold CoVs
- Is suboptimal and caused by out-of-frame insertion
- Two adjacent CGG codons not indicative of genetic engineering, 99.8% conserved in >2,300,000 complete genomes, e.g strong functional constraints

SARS-CoV-2: importance of sequencing in near-real time

Global Initiative on Sharing All Influenza Data, is a global science initiative established in 2008 to provide access to genomic data of influenza viruses. The database was expanded to include the coronavirus responsible for the COVID-19 pandemic as well as other pathogens

- ✓ Great efforts from scientific community for technological innovation in the field of viral Whole Genome Sequencing
- ✓ Institution of sequencing network for integrated surveillance for epidemiological from local to global level
- ✓ Importance of Sharing data in public database



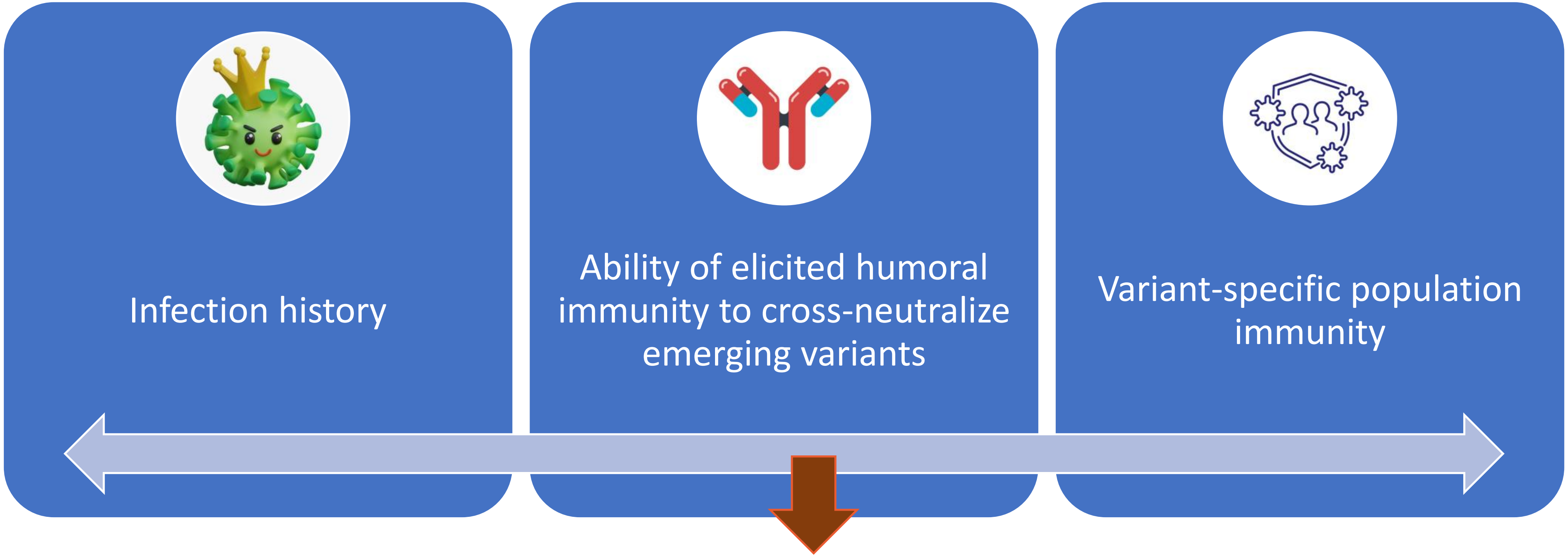
SARS-CoV-2 genomic sequencing for public health goals

Interim guidance

8 January 2021

World Health Organization

SARS-CoV-2 evolution major driving factors



Infection history

Ability of elicited humoral immunity to cross-neutralize emerging variants

Variant-specific population immunity

large number of mutations

to adapt better to its hosts

Need for vaccine and therapeutics (e.g. mAbs) update

nature

Article

SARS-CoV-2 evolution on a dynamic immune landscape

https://doi.org/10.1038/s41586-024-08477-8

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N. Alexia Raharinirina[1,6], Nils Gubela[1,2,6], Daniela Börnigen[3,6], Maureen Rebecca Smith[3,6], Djin-Ye Oh[4], Matthias Budt[4], Christin Mache[4], Claudia Schillings[1], Stephan Fuchs[5], Ralf Dürrwald[4], Thorsten Wolff[4], Martin Hölzer[5], Sofia Paraskevopoulou[5] & Max von Kleist[1,3] ✉