UNIVERSITÀ DEGLI STUDI DI MILANO
FACOLTÀ DI MEDICINA E CHIRURGIA

L'infettivologia fra nuove minacce e possibili soluzioni

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Milano 14 ottobre 2022

COI Disclosures

Gilead, InfectoPharm, Janssen,

MSD, VIIV, GSK, Pfizer

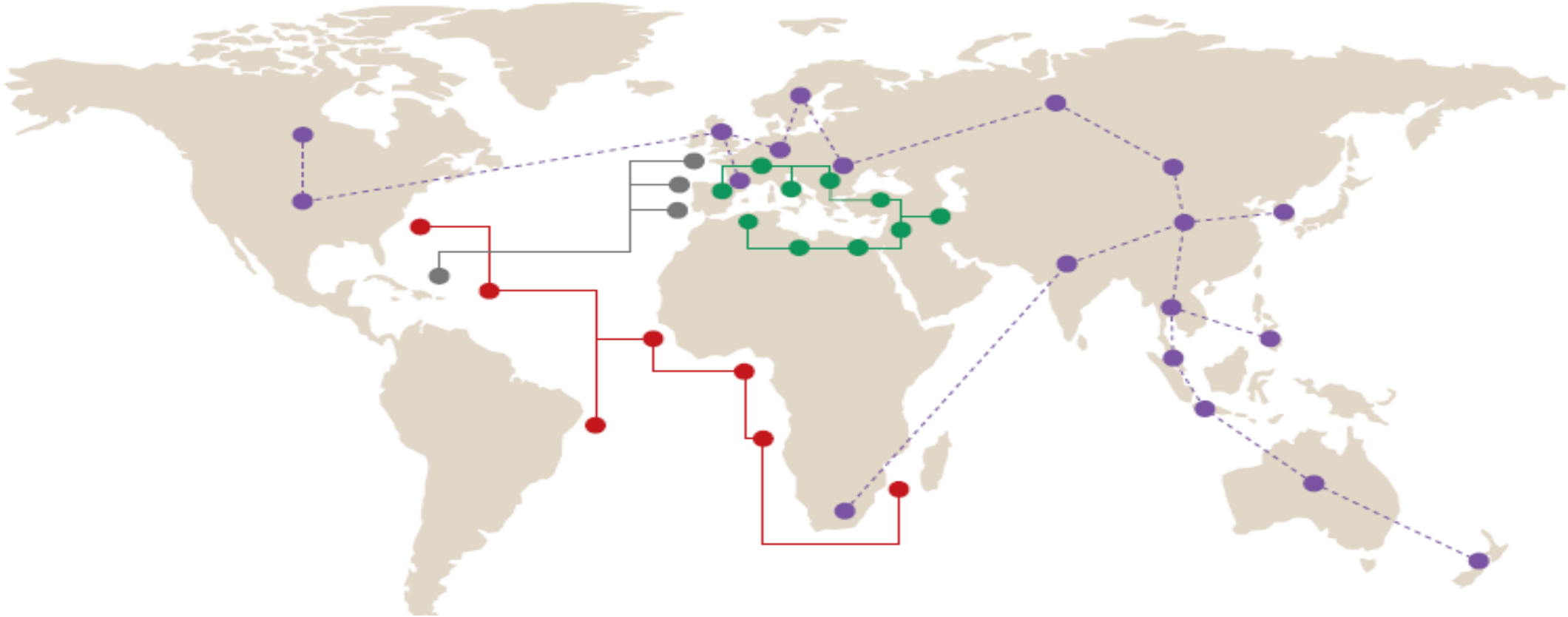
Infectious disease in an era of global change

Post-Columbus contact and European colonization: smallpox, measles and other diseases (fifteenth to eighteenth century)

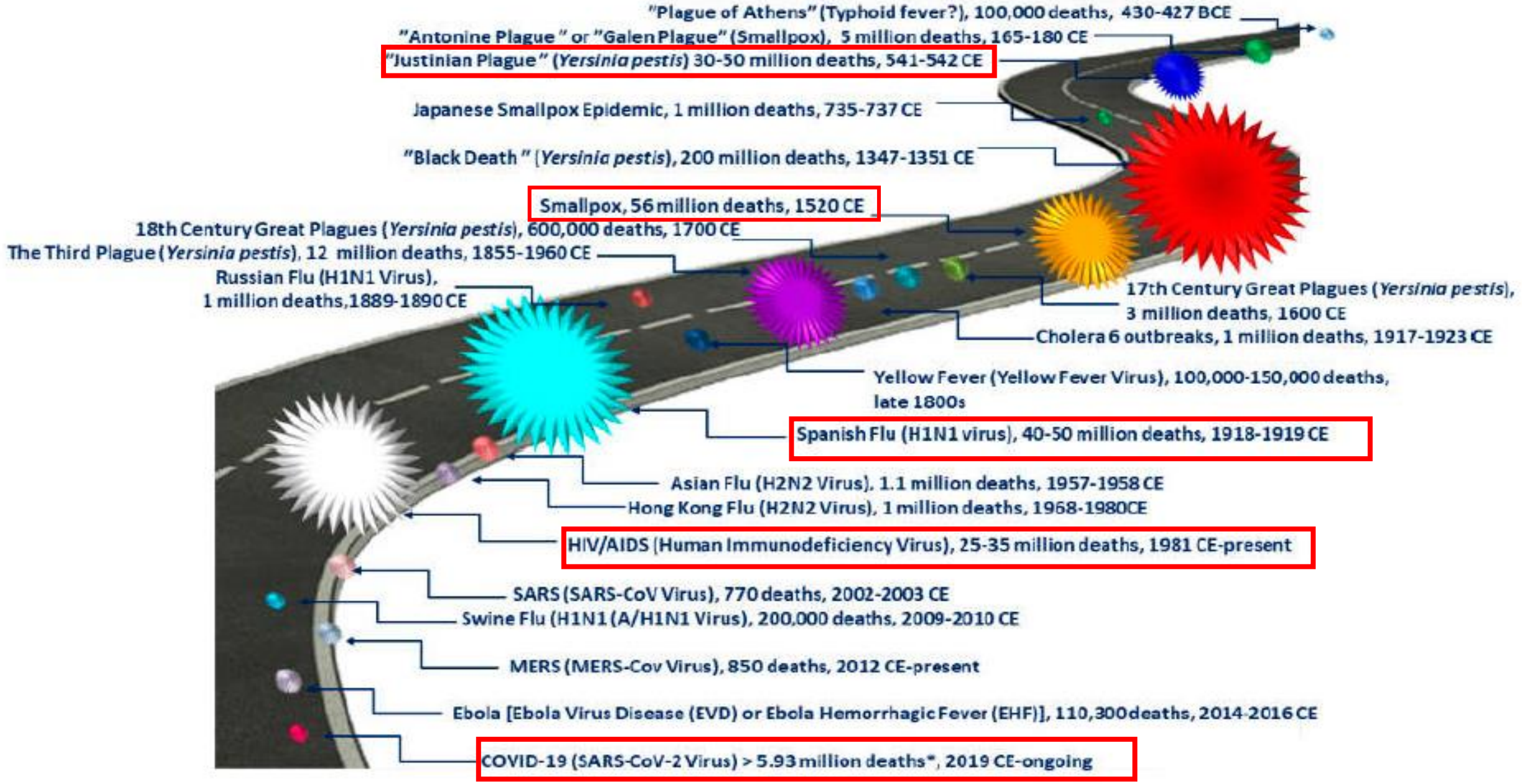
Classical antiquity trade and war: Antonine plague (second century) Plague of Cyprian (third century) Justinian plague (sixth century)

Transatlantic slave trade and European colonization: *P. falciparum* malaria (sixteenth to nineteenth century)

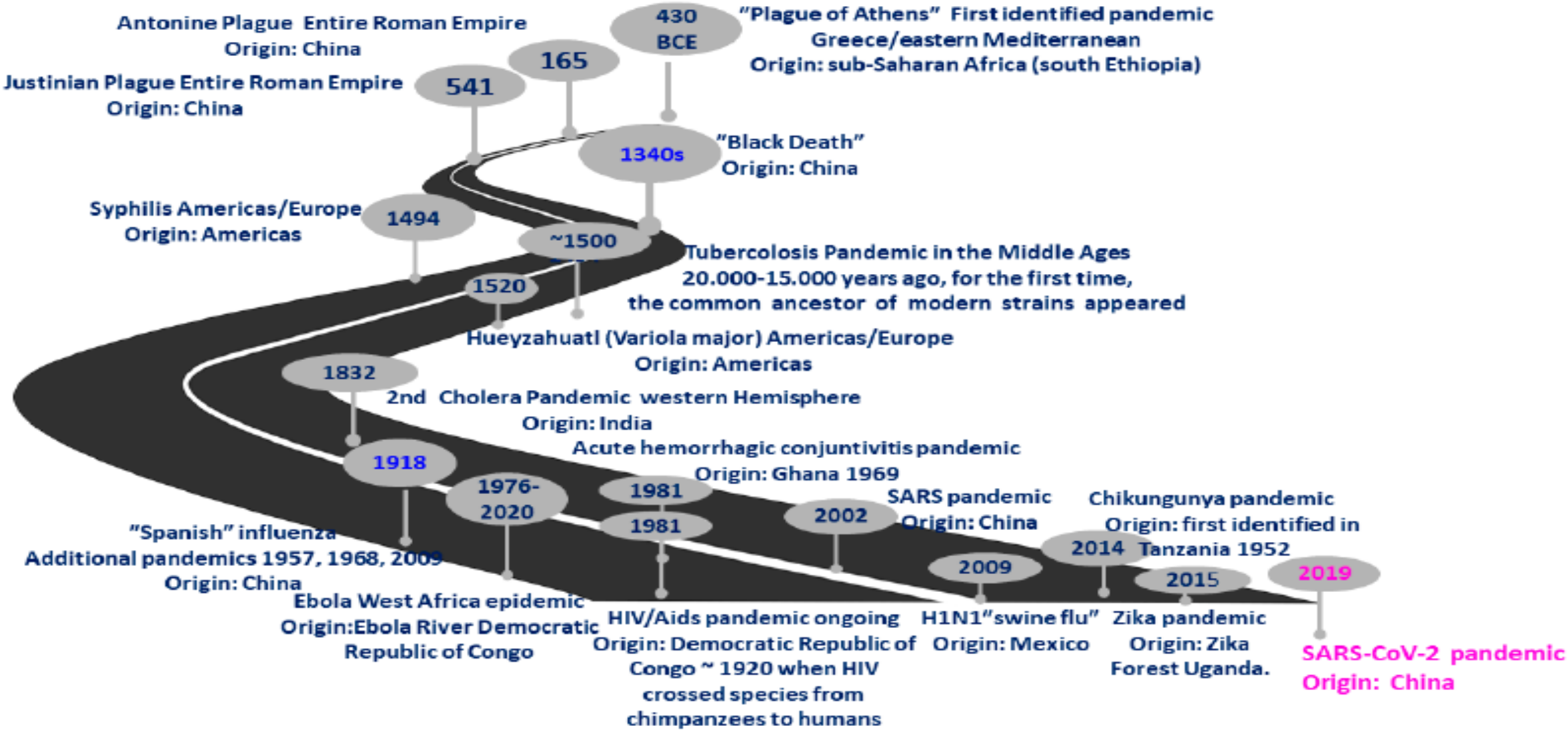
International air trav SARS epidemic (2002–2004)



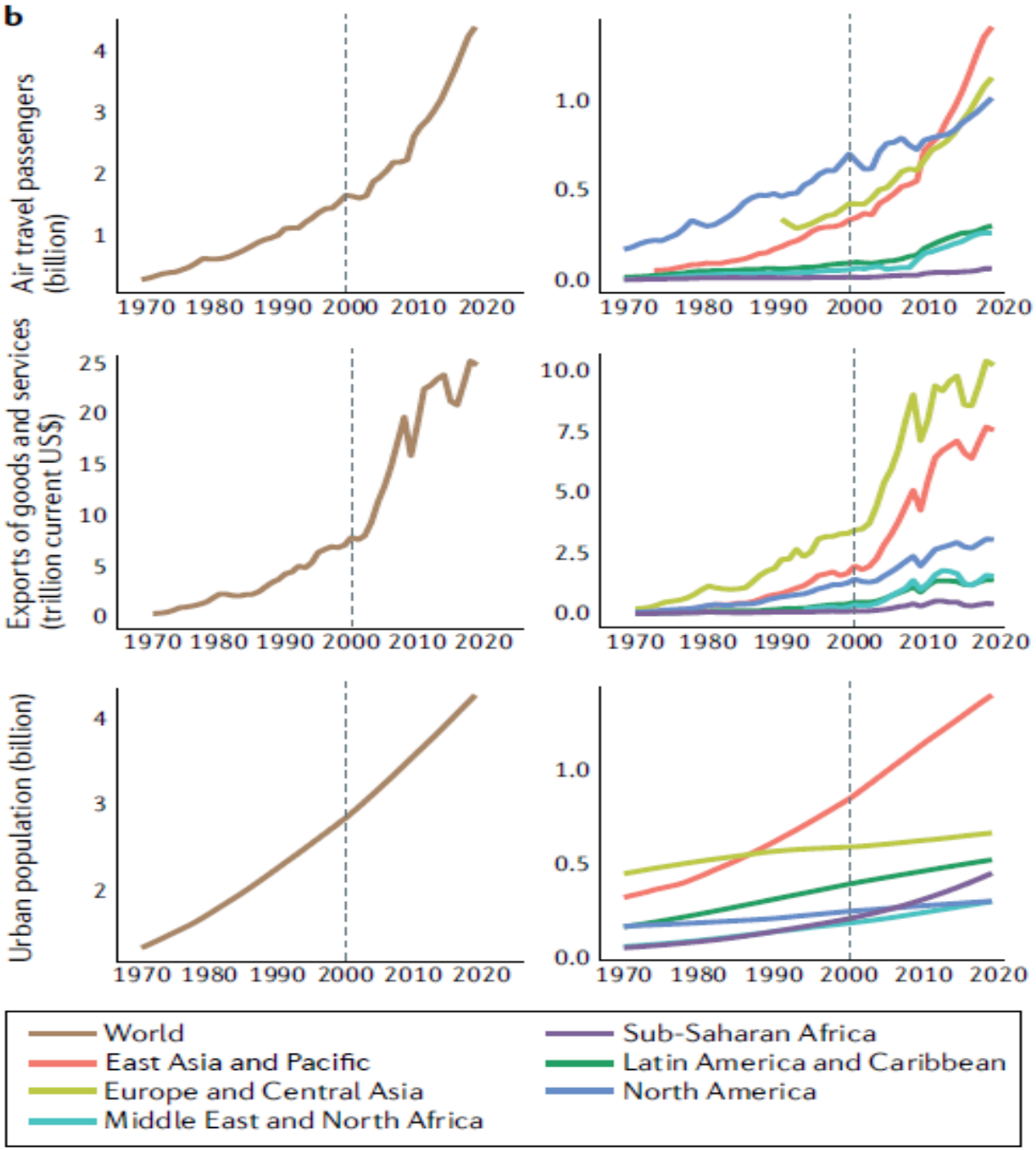
Baker RE et al. Nature Rev Microbiol 2022;20:193-205

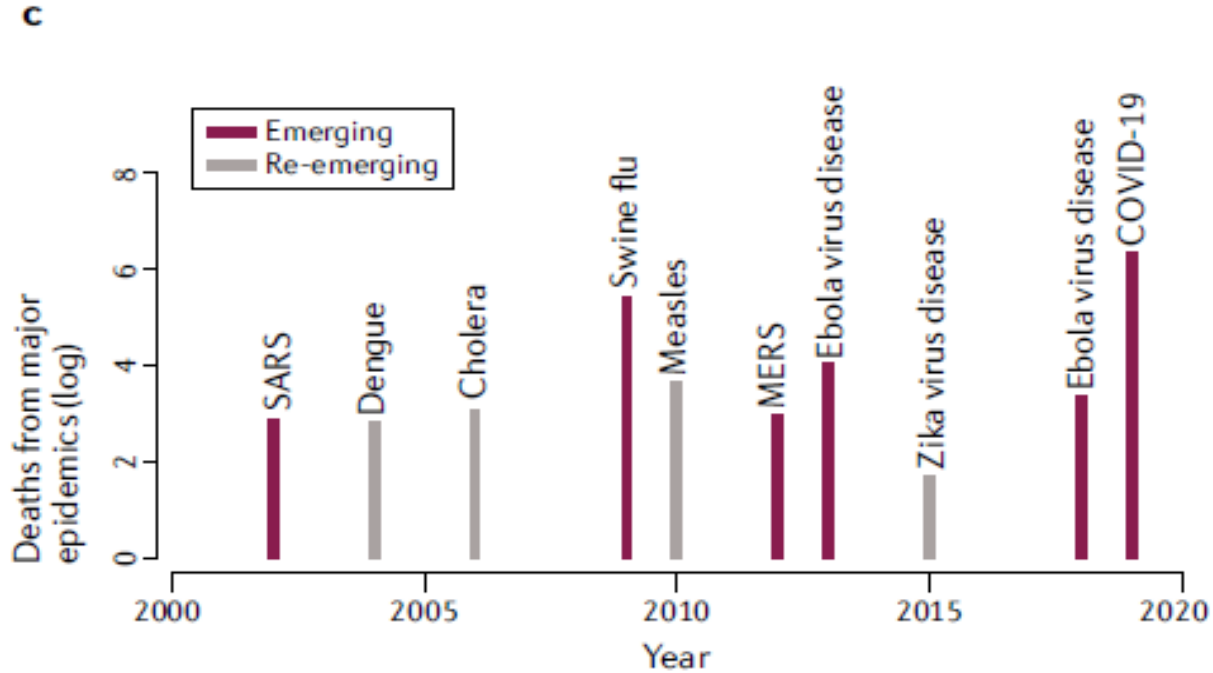


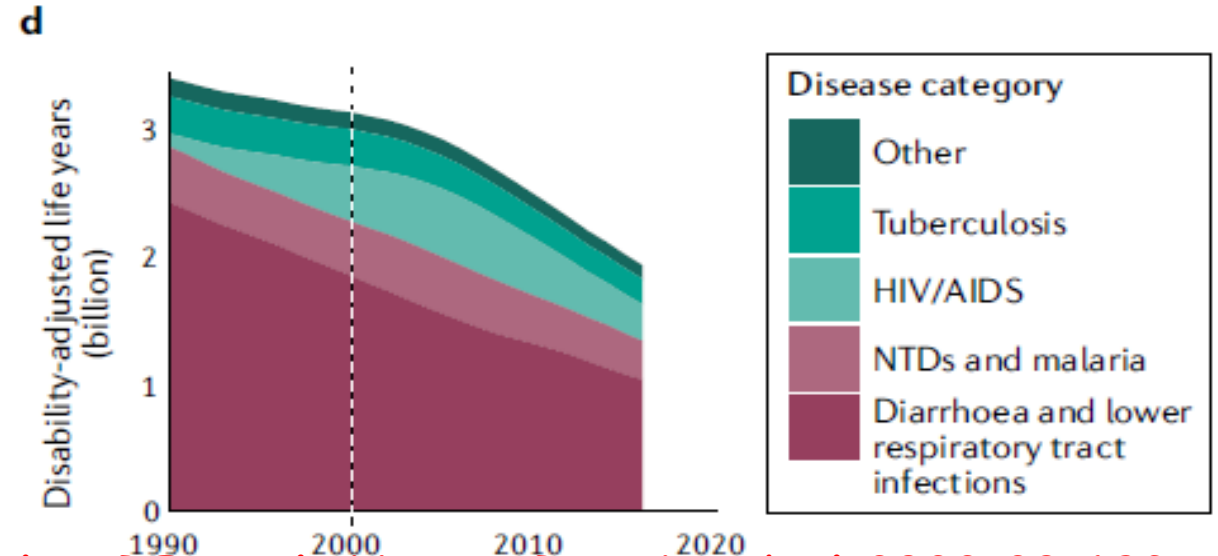
Vitiello L, et al. J Clin Med 2022; 11:1960



Vitiello L, et al. J Clin Med 2022; 11:1960

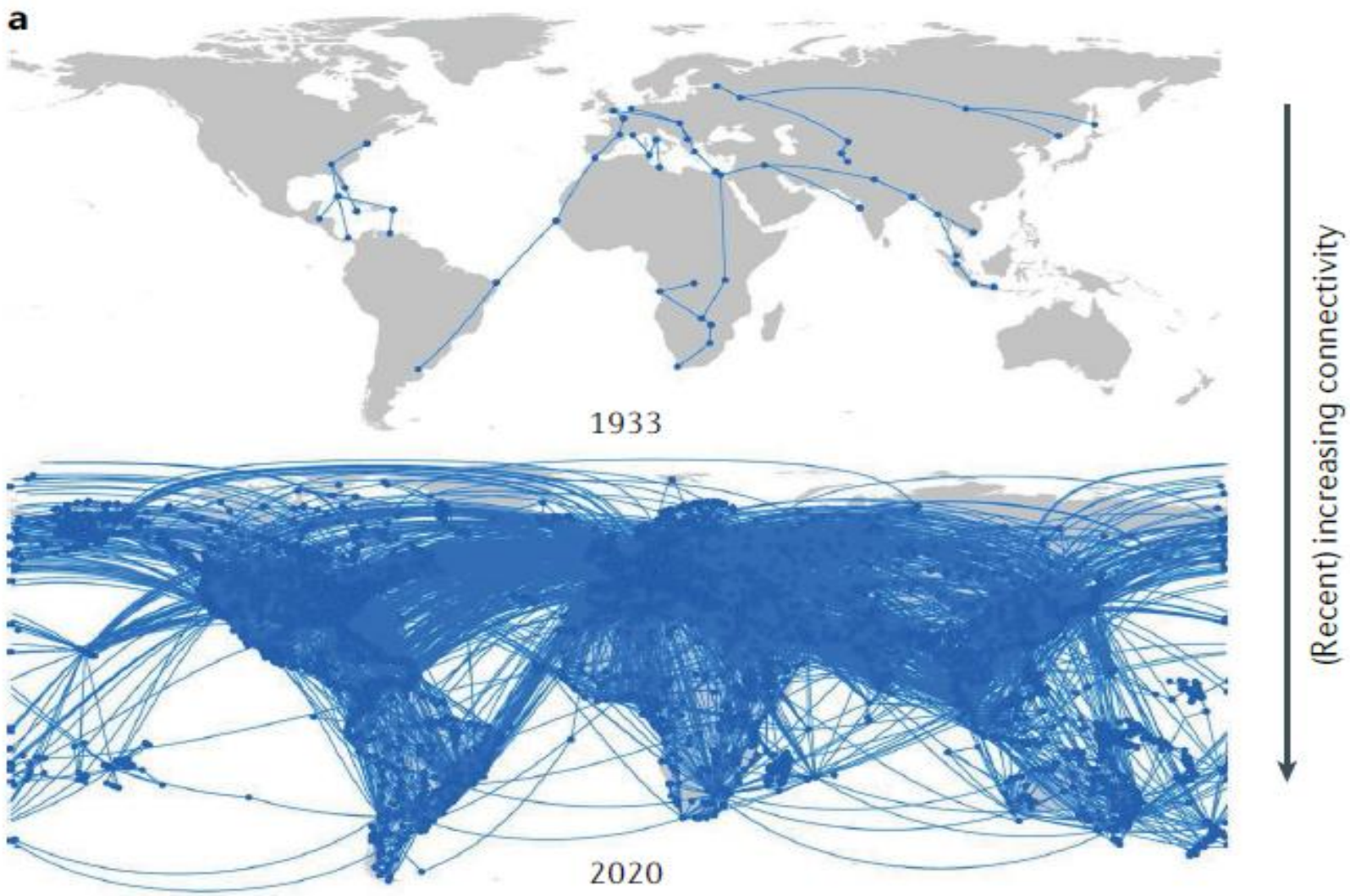






Baker RE et al. Nature Rev Microbiol 2022;20:193-205

The global international air travel network



Baker RE et al. Nature Rev Microbiol 2022;20:193-205

BMJ Global Health

Scoping future outbreaks: a scoping review on the outbreak prediction of the WHO Blueprint list of priority diseases

Jonkmans N, *et al. BMJ Global Health* 2021;6:e006623.

Box 1 2018 WHO Blueprint list of priority diseases

➢Ebola virus disease: the Ebola virus outbreak in West Africa in 2014–2016 primarily affected Sierra Leone, Guinea and Liberia. This outbreak caused 28 639 deaths, a loss of 2.2 billion dollars, a substantial loss in private and public sector growth, agriculture production, food security concerns and restrictions of movement, goods and services.[70 71]

➢Zika virus disease: Zika virus has infected millions in the Americas since 2014 and has caused an increase in medical sequelae in some populations (congenital disease, Guillain-Barré) as well as socioeconomic disparities.[72 73]

➢River Valley fever (RVF): RVF outbreaks in South and Eastern Africa impacted the economy and public health of multiple countries, leaving behind long-term societal consequences.[74]

➢Lassa fever: Lassa fever, a severe haemorrhagic fever transmitted through rats, is estimated to infect millions in West Africa each year, with 20% of those patients experiencing severe multisystemic disease.[75]

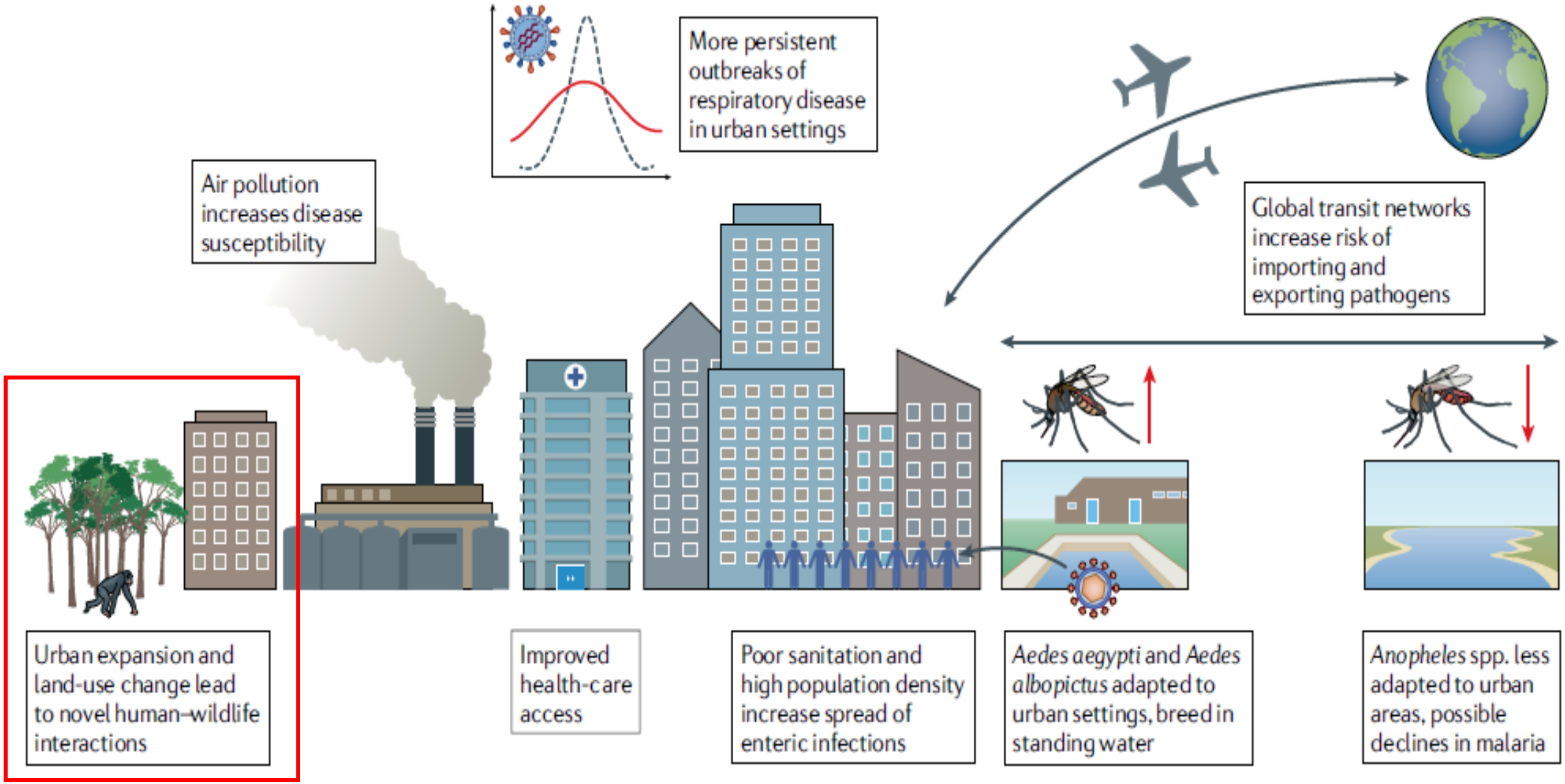
➢Nipah and henipaviral disease: Nipah virus, discovered in 1998, is isolated to Malaysia, Singapore, Bangladesh and India. However, Nipah continues to pose a significant threat as a bat-based zoonosis with yearly spillover events, significant morbidity and case fatality rates of up to 100%.[76]

➢Crimean-Congo haemorrhagic fever: CCHF, a widely distributed tick-borne zoonosis, infects domestic and wild vertebrates as hosts, resulting in severe human disease and high mortality, and poses a continued threat to central Africa, South-Western Russia and central Asia.[77]

➢Severe acute respiratory syndrome (SARS) due to SARS-CoV-1: a coronavirus causing SARS emerged in 2003 and rapidly spread from Southeast Asia to Canada. SARS causes severe atypical pneumonia, leading to high morbidity, mortality and major economic consequences.[78]

➢Middle East respiratory syndrome (MERS): another coronavirus, MERS-CoV, emerged in the Arabian Peninsula in 2012 and has been found in Europe, North America and Asian countries with a mortality of about 30%.[79]

➢Disease X: disease X is a term used to 'enable cross-cutting R&D preparedness that is relevant for currently unknown diseases'.[11] Disease X was included to stimulate research into emerging pathogens, before their formal discovery.

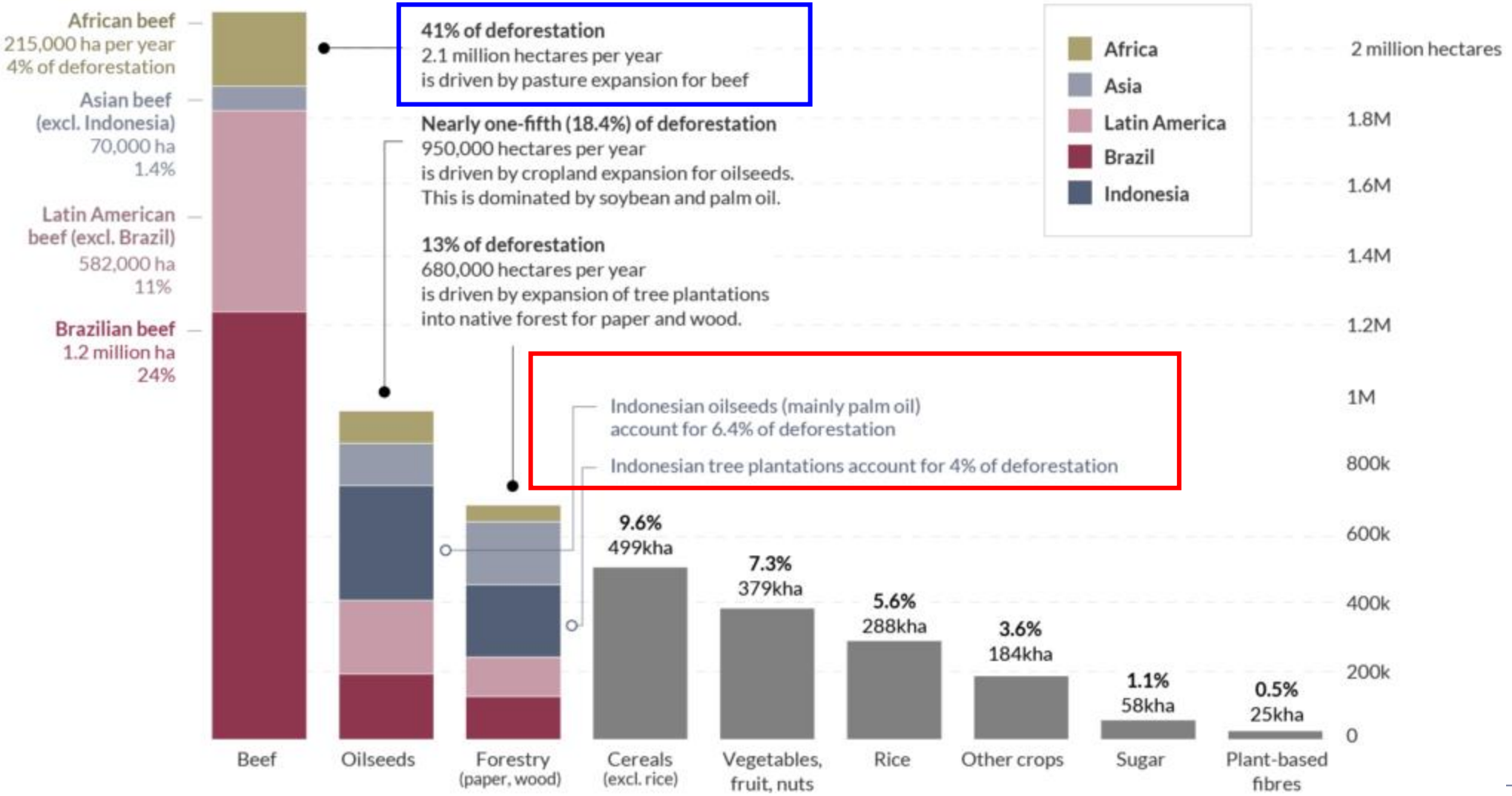


Baker RE et al. Nature Rev Microbiol 2022;20:193-205c

What are the drivers of tropical deforestation?

Our World in Data

Nearly all of global deforestation occurs in tropical and subtropical countries. 70% to 80% is driven by conversion of primary forest to agriculture or tree plantations. Shown is the breakdown of these drivers averaged over the years 2005 to 2013. Further observations since 2013 suggest that drivers have not changed substantially over this period.



Data source: Florence Pendrill et al. (2019). Deforestation displaced: trade in forest-risk commodities and the prospects for a global forest transition.

OurWorldinData.org – Research and data to make progress against the world's largest problems.

A large focus of naturally acquired *Plasmodium knowlesi* infections in human beings

Balbir Singh, Lee Kim Sung, Asmad Matusop, Anand Radhakrishnan, Sunita S G Shamsul, Janet Cox-Singh, Alan Thomas, David J Conway

Findings All DNA sequences were phylogenetically indistinguishable from those of *P knowlesi*, a malaria parasite of long-tailed macaque monkeys, but were significantly different from other malaria parasite species. By PCR assay, 120 (58%) of 208 people with malaria tested positive for *P knowlesi*, whereas none was positive for *P malariae*. *P knowlesi* parasites in human erythrocytes were difficult to distinguish from *P malariae* by microscopy. Most of the *P knowlesi* infections were in adults and we did not note any clustering of cases within communities. *P knowlesi* infections were successfully treated with chloroquine and primaquine.

Interpretation Naturally acquired *P knowlesi* infections, misdiagnosed by microscopy mainly as *P malariae*, accounted for over half of all malaria cases in our study. Morphological similarities between *P knowlesi* and *P malariae* necessitate the use of molecular methods for correct identification. Further work is needed to determine whether human *P knowlesi* infections in the Kapit division are acquired from macaque monkeys or whether a host switch to human beings has occurred.

Lancet 2004; **363:** 1017–24

Outbreak of human malaria caused by *Plasmodium simium* in the Atlantic Forest in Rio de Janeiro: a molecular epidemiological investigation

Lancet Glob Health 2017; 5: e1038–46

Patrícia Brasil, Mariano Gustavo Zalis*, Anielle de Pina-Costa, Andre Machado Siqueira, Cesare Bianco Júnior, Sidnei Silva, André Luiz Lisboa Areas, Marcelo Pelajo-Machado, Denise Anete Madureira de Alvarenga, Ana Carolina Faria da Silva Santelli, Hermano Gomes Albuquerque, Pedro Cravo, Filipe Vieira Santos de Abreu, Cassio Leonel Peterka, Graziela Maria Zanini, Martha Cecilia Suárez Mutis, Alcides Pissinatti, Ricardo Lourenço-de-Oliveira, Cristiana Ferreira Alves de Brito, Maria de Fátima Ferreira-da-Cruz, Richard Culleton, Cláudio Tadeu Daniel-Ribeiro*

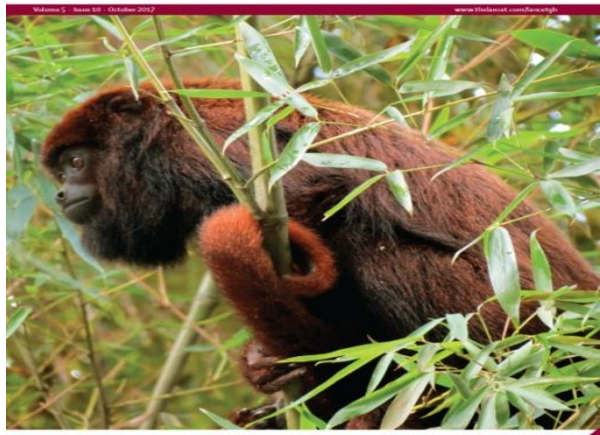
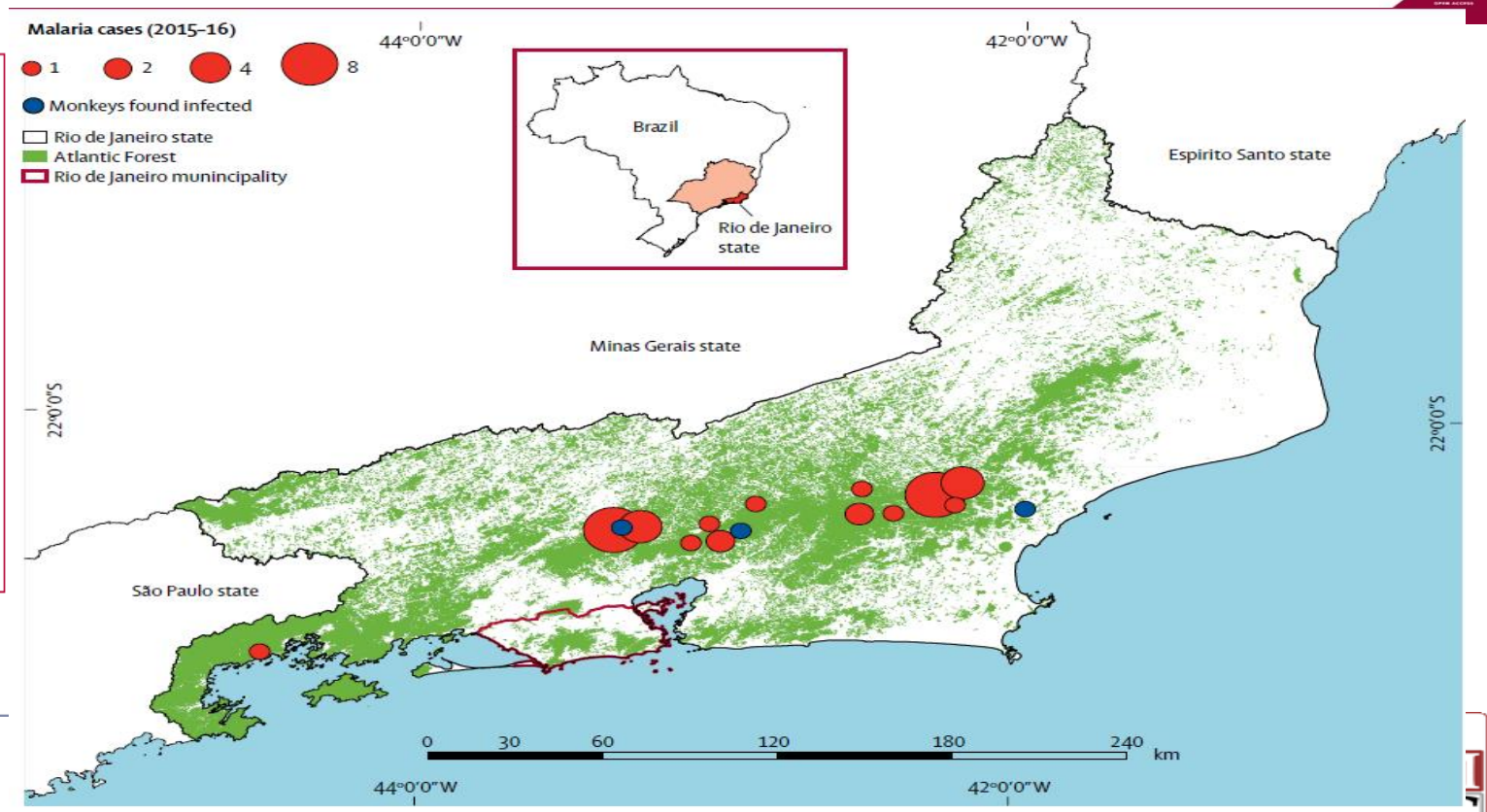


Figure 1: Historical series of autochthonous malaria cases in the state of Rio de Janeiro, Brazil, from 2006 to 2016



EBioMedicine 2 (2015) 1186–1192

Contents lists available at ScienceDirect

EBioMedicine

journal homepage: www.ebiomedicine.com

Research Paper

Natural infection of *Plasmodium brasilianum* in humans: Man and monkey share quartan malaria parasites in the Venezuelan Amazon

Albert Lalremruata [a], Magda Magris [b], Sarai Vivas-Martínez [b,d], Maike Koehler [a], Meral Esen [a], Prakasha Kempaiah [c], Sankarganesh Jeyaraj [a], Douglas Jay Perkins [c], Benjamin Mordmüller [a], Wolfram G. Metzger [a,b,*]

[a] Institute of Tropical Medicine, University of Tübingen, Tübingen, Germany
[b] Servicio Autónomo Centro Amazónico para la Investigación y Control de Enfermedades Tropicales 'Simón Bolívar' (SACAICET), Puerto Ayacucho, Estado Amazonas, Venezuela
[c] Center for Global Health, Department of Internal Medicine, University of New Mexico School of Medicine, Albuquerque, NM, USA
[d] Cátedra de Salud Pública, Escuela de Medicina Luis Razetti, Universidad Central de Venezuela, Caracas, Venezuela

EBioMedicine 2 (2015) 1023–1024

Contents lists available at ScienceDirect

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journal homepage: www.ebiomedicine.com

Commentary

Plasmodium malariae Malaria: From Monkey to Man?

Julian C. Rayner

Malaria Programme, Wellcome Trust Sanger Institute, Wellcome Genome Campus, Hinxton, Cambridge CB10 1SA, United Kingdom

The Journal of Infectious Diseases

MAJOR ARTICLE

Asymptomatic Natural Human Infections With the Simian Malaria Parasites *Plasmodium cynomolgi* and *Plasmodium knowlesi*

Mallika Imwong,[1,2] Wanassanan Madmanee,[2] Kanokon Suwannasin,[2] Chanon Kunasol,[2] Thomas J. Peto,[2,3] Rupam Tripura,[2,3] Lorenz von Seidlein,[2,3] Chea Nguon,[4] Chan Davoeung,[5] Nicholas P. J. Day,[2,3] Arjen M. Dondorp,[2,3] and Nicholas J. White[2,3]

Results. Asymptomatic malaria parasite infections were detected in 1361 of 14 732 samples (9.2%). Asymptomatic infections with nonhuman primate malaria parasites were found in 21 individuals living close to forested areas; *P. cynomolgi* was found in 11, *P. knowlesi* was found in 8, and *P. vivax* and *P. cynomolgi* were both found in 2. Only 2 subjects were female, and 14 were men aged 20–40 years. Geometric mean parasite densities were 3604 parasites/mL in *P. cynomolgi* infections and 52 488 parasites/mL in *P. knowlesi* infections. All *P. cynomolgi* isolates had wild-type dihydrofolate reductase genes, in contrast to the very high prevalence of mutations in the human malaria parasites. Asymptomatic reappearance of *P. cynomolgi* occurred in 2 subjects 3 months after the first infection.

Conclusions. Asymptomatic naturally acquired *P. cynomolgi* and *P. knowlesi* infections can both occur in humans.

CASE REPORT Open Access

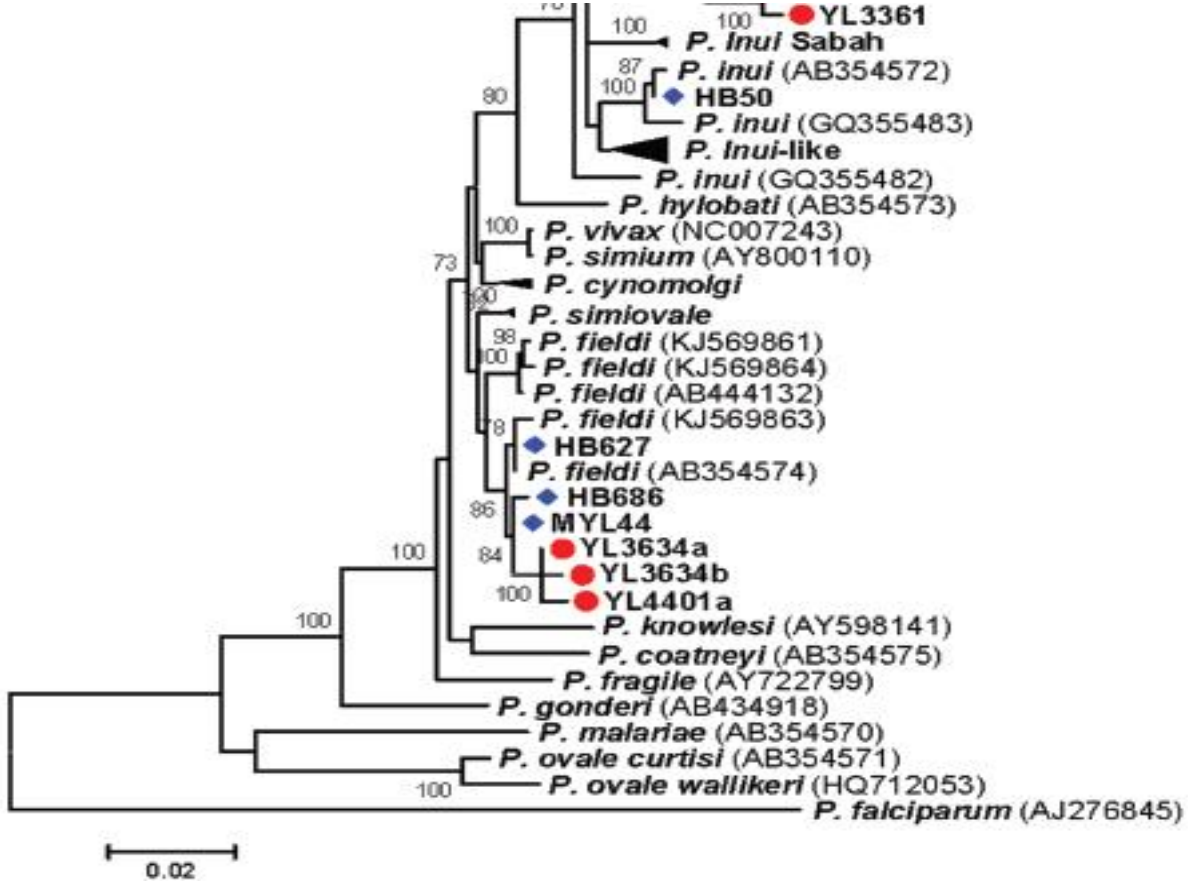
First case of a naturally acquired human infection with *Plasmodium cynomolgi*

Malaria Journal 2014, 13:68

Thuy H Ta[1], Shamilah Hisam[2], Marta Lanza[1], Adela I Jiram[2], NorParina Ismail[2] and José M Rubio[1*]

Cryptic *Plasmodium inui* and *Plasmodium fieldi* Infections Among Symptomatic Malaria Patients in Thailand

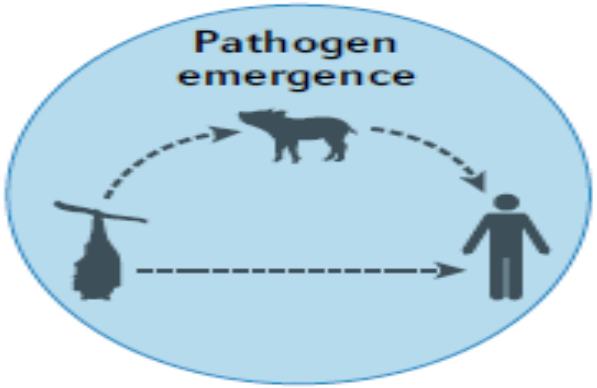
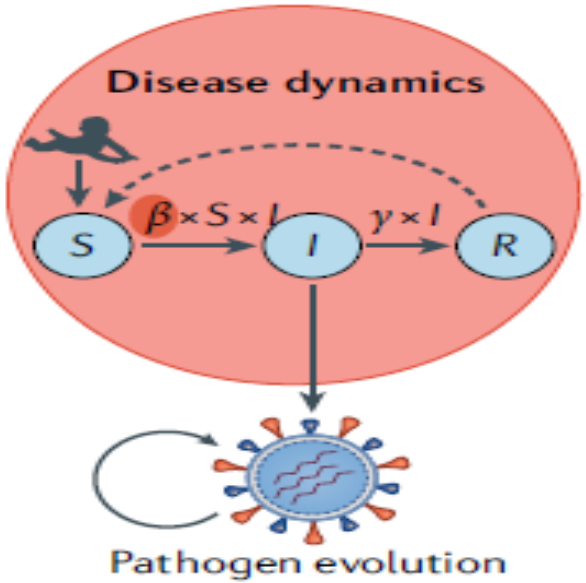
Chaturong Putaporntip,[1] Napaporn Kuamsab,[1] Sunee Seethamchai,[2] Urassaya Pattanawong,[1] Rattanaporn Rojrung,[1] Surasuk Yanmanee,[1] Chew Weng Cheng,[3] and Somchai Jongwutiwes[1]



DISCUSSION

Identifying *P. inui* and *P. fieldi* infections among symptomatic malaria patients in Thailand has expanded our knowledge of zoonotic malaria beyond *P. knowlesi* and *P. cynomolgi* [6–9]. The integrity of diagnosing *P. inui* and *P. fieldi* has been reaffirmed by species-specific PCR, sequencing of recombinant PCR products and deep amplicon sequencing, yielding concordant results. Furthermore, laboratory contamination of *P. inui* and *P. fieldi* in human blood samples can be excluded by the differences in the COX1 sequences from human- and macaque-derived blood samples. Meanwhile, a spurious detection of sporozoite-derived DNA in the patient's circulation without an established infection is unlikely due to a scarcity of sporozoites in circulation during the infection process. Therefore, to the best of our knowledge, this is the first identification of naturally acquired infections with *P. fieldi* in humans and *P. inui* among malaria patients in Thailand.

Although we did not perform a systematic assessment, *P. inui* was found in 19 patients, accounting for 0.45% of 4195 PCR-positive individuals which is almost comparable with those of *P. malariae* (0.55%), *P. knowlesi* (0.72%), and *P. cynomolgi* (0.5%). The presence of *P. inui* among malaria patients across

			
Climatic change	Drives range shifts for reservoir species	Affects transmission and susceptibility	Affects the geographical range of vectors
Technological change			
Transportation	Improved global surveillance		Air transit and high-speed rail affect pace and range of spread
Health care		Vaccination affects dynamics	Improved care reduces burden
Demographic change			
Population growth and land use	Increased contact with reservoir species	Population numbers affect evolution, birth rates affect dynamics	Larger population travelling
Urbanization	Depends on species	Density affects contact rate	Urban population more connected
Ageing	Imunosenescence affects spillover risk	Ageing population increases transmission	Possible larger burden

Baker RE et al. Nature Rev Microbiol 2022;20:193-205

JAMA Health Forum. JAMA Health Forum. 2022;3(9):e224062. d

JAMA Forum

Living in an Age of Pandemics—From COVID-19 to Monkeypox, Polio, and Disease X

Lawrence O. Gostin, JD

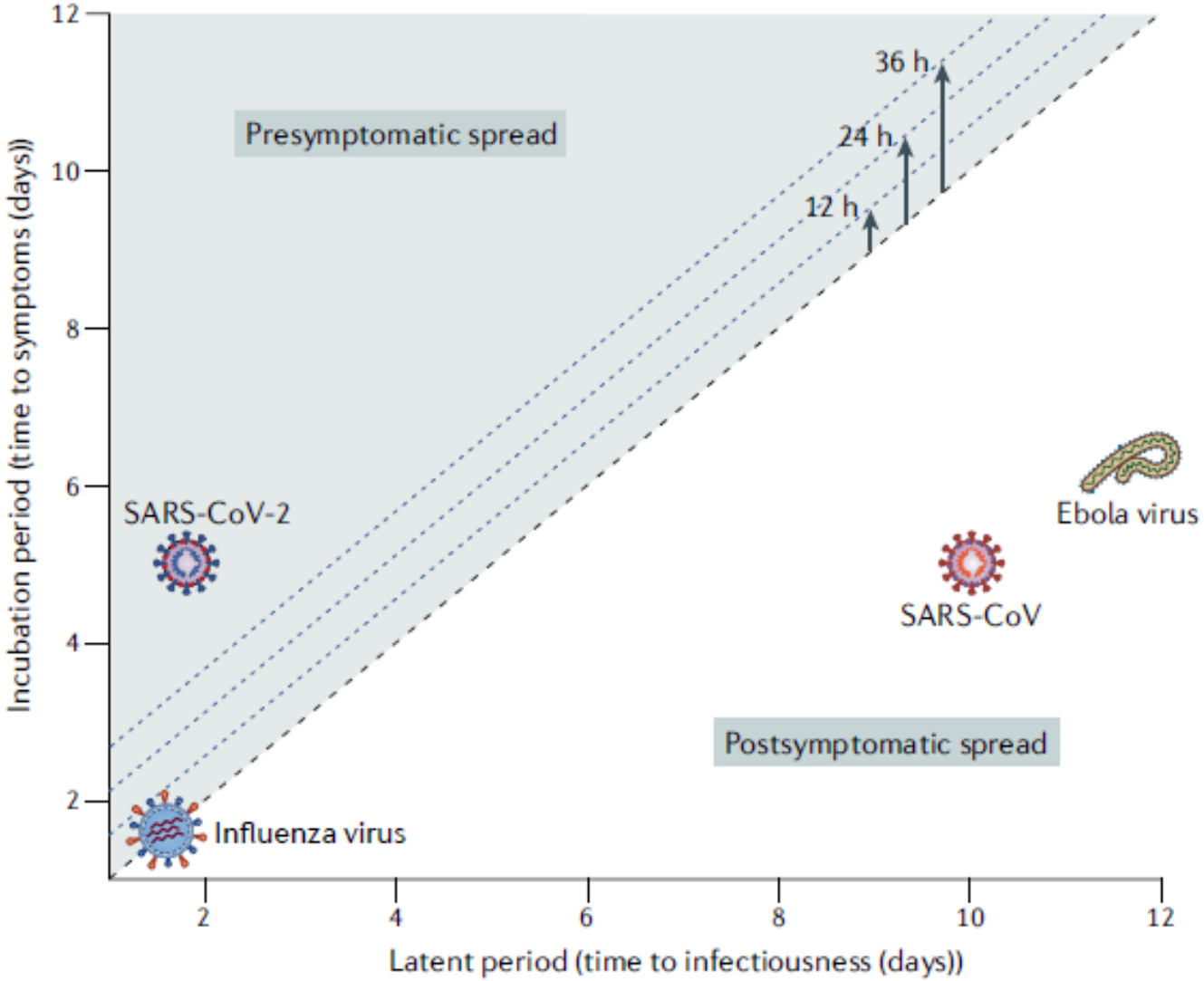
Pandemic Drivers

Zoonotic pathogens—such as those causing HIV, SARS, Ebola, monkeypox, and COVID-19—account for 60% of all communicable diseases and 70% of novel ones. Zoonotic spillovers are more frequent and resulting outbreaks are spreading more rapidly[2] due to human behavior. As humans encroach on wildlife environments at an alarming rate[3] for agriculture, natural resource extraction, and urban expansion, ecosystems are destroyed and wild species are displaced and placed under stress. Increased co-mingling of wildlife, humans, and livestock increases zoonotic spillovers. High-density livestock operations and international trafficking of wild animals pose high risks. The accumulated evidence suggests SARS-CoV-2 most likely originated at the Huanan Seafood Wholesale Market.

Anthropogenic climate change dramatically increases cross-species viral transmission because global warming makes some habitats less habitable.[4] Species, harboring pathogens, migrate to cooler latitudes, potentially across continents. Bats, in which scores of coronaviruses have been identified, can travel long distances. Climate change also expands pathogen vectors to new geographic areas, propelling mosquito-borne diseases.

Urbanization increases human population density, driving person-to-person spread of pathogens, and rapid transportation and mass migrations propel global outbreaks throughout the globe. The World Bank estimates that 56% of the world's population—4.4 billion people—live in cities, and 70% will do so by 2050. Mass migrations driven by food insecurity, climate change, and armed conflict are at all-time highs, with the International Migration Office estimating 281 million international migrants in 2020, encompassing 3.6% of the global population.

An unlucky situation



Baker RE et al. Nature Rev Microbiol 2022;20:193-205

Emergence of vaccine-derived poliovirus in high-income settings in the absence of oral polio vaccine use

Linked global cases of poliovirus a cause of concern

Genetically linked vaccine-derived poliovirus type 2 has been detected in environmental samples in three countries and in a case of paralytic poliomyelitis. Priya Venkatesan reports

In the USA, in July 2022, following surveillance, the New York State Department of Health (NYSDOH) reported a case of paralytic poliomyelitis in an unvaccinated individual in the area of Rockland County. Initial sequencing by the US Centers for Disease Control and Prevention indicated that the case resulted from VDPV2. Subsequently, on July 29, the Global Polio Eradication Initiative confirmed that the VDPV2 isolated from the individual in Rockland County was genetically linked to the VDPV2 detected in the London (UK) environmental samples earlier in the year, as well as to two Sabin-like type 2 isolates collected from environmental samples in early June in both New York and Greater Jerusalem, Israel. The Global Polio Laboratory Network reported that stool samples obtained from the individual in New York with paralytic poliomyelitis yielded a VP1 sequence with ten mutations from Sabin 2 that was genetically linked to the sewage sequences from New York (99·34% identity), and

In the UK, in June 2022, vaccine-derived poliovirus type 2 (VDPV2) was detected in several sewage samples from north and east London taken between February and May, 2022, as part of routine surveillance. The UK Health Security Agency (UKHSA) noted that it is normal for a few vaccine-like polioviruses to be detected each year in the UK through surveillance, usually from an individual vaccinated overseas with the oral live-attenuated Sabin poliovirus vaccine (OPV) who arrives in the UK and briefly sheds traces of the vaccine virus in their faeces. However, vaccine-derived polioviruses occur when excreted virus from an individual immunised with OPV spreads and mutates in underimmunised populations. Eventually, the virus can regain sufficient neurovirulence and transmissibility to cause paralytic poliomyelitis in an unvaccinated individual. UKHSA stated that detection

The changing epidemiology of human monkeypox—A potential threat? A systematic review

PLOS Neglected Tropical Diseases |

Eveline M. Bunge[1], Bernard Hoet[2]*, Liddy Chen[3], Florian Lienert[2], Heinz Weidenthaler[4], Lorraine R. Baer[5], Robert Steffen[6,7]

Fig 2. Number of confirmed, probable, and/or possible monkeypox cases between 1970–1979.

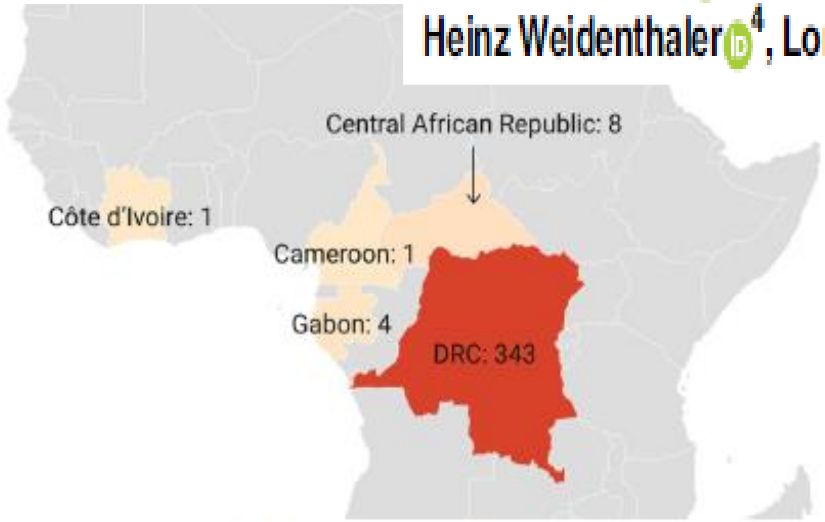


Fig 3. Number of confirmed, probable, and/or possible monkeypox cases between 1980–1989.

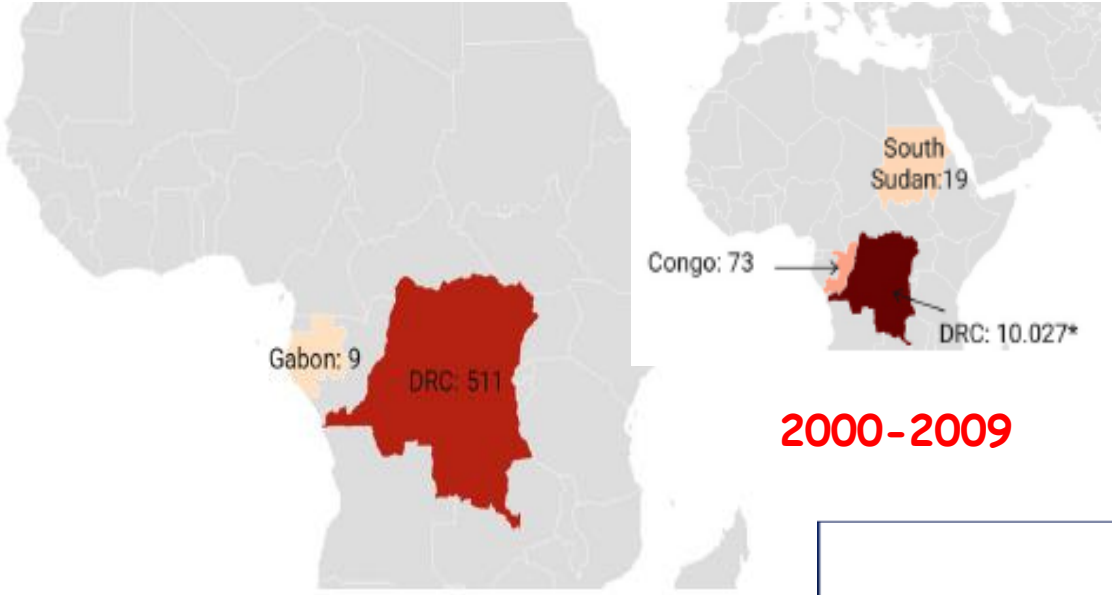
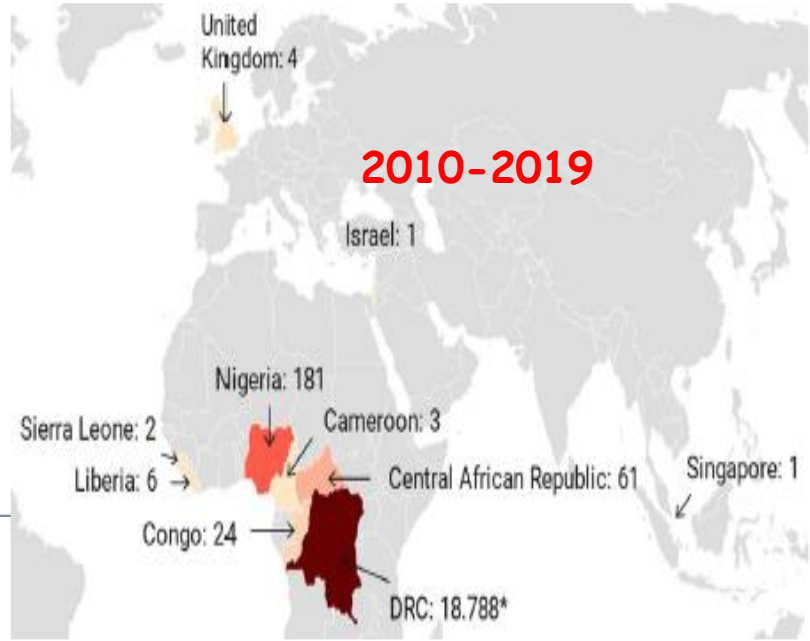
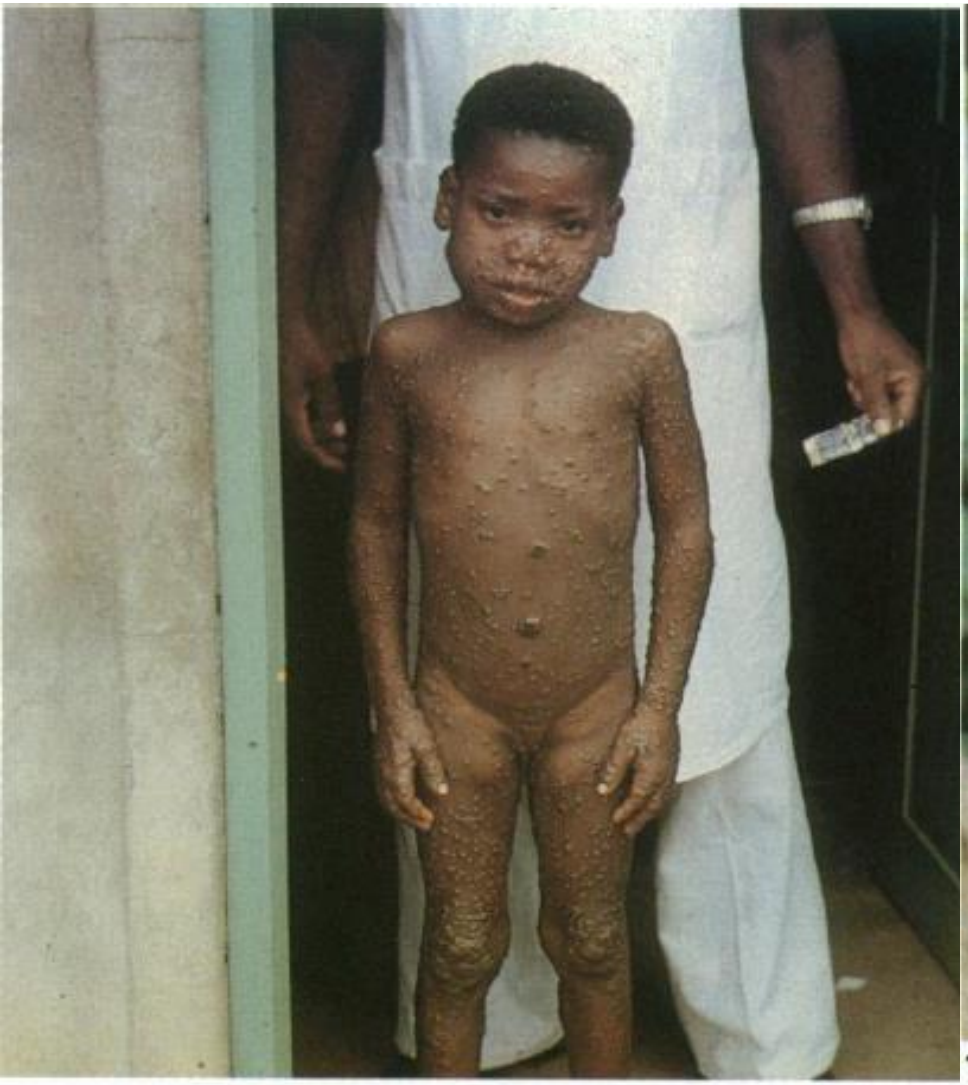


Fig 4. Number of confirmed, probable, and/or possible monkeypox cases between 1990–1999.

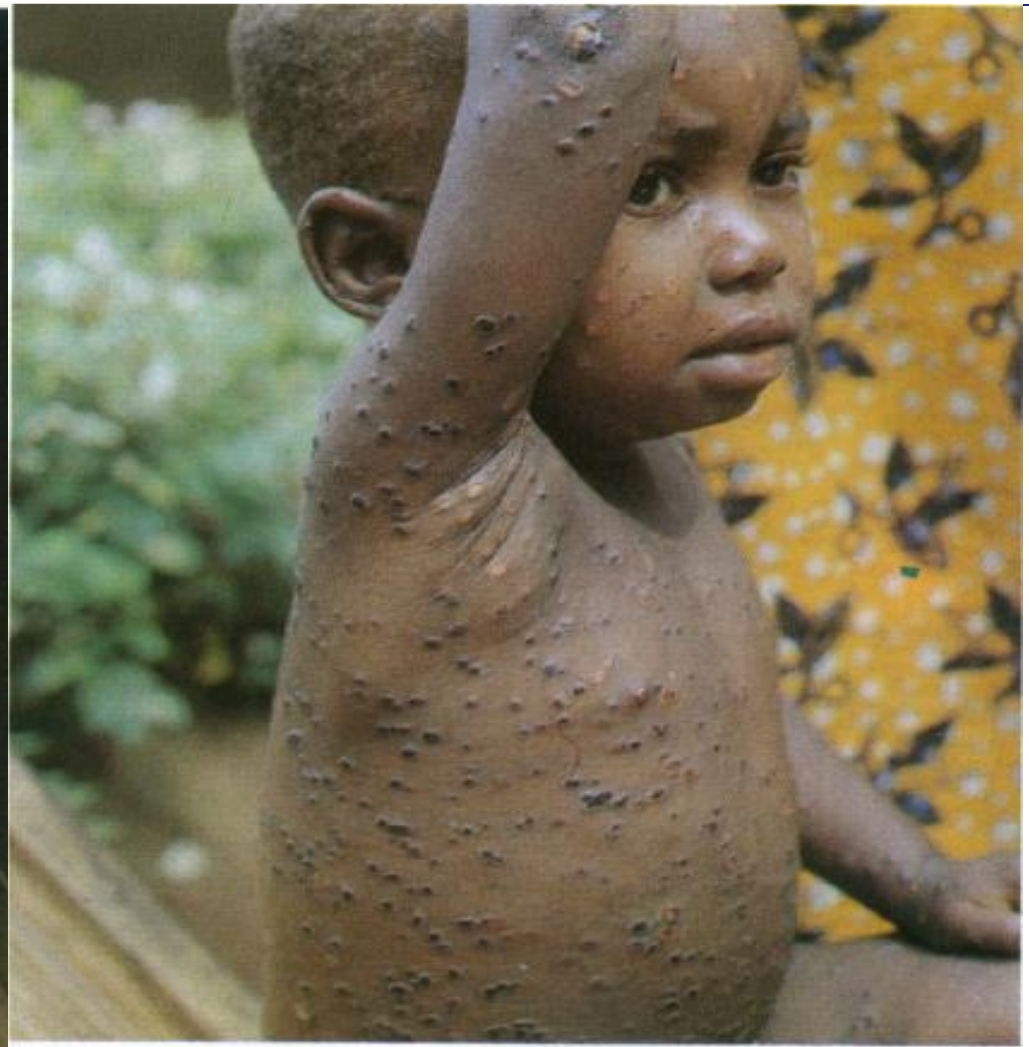


Bulletin of the World Health Organization, 62 (5): 703 – 713 (1984)

The current status of human monkeypox: Memorandum from a WHO Meeting*



1.1. Case 25, age 7 years. Day 7 of rash in the acute stage. Note distinct bilateral inguinal lymphadenopathy. There is also submaxillar lymphadenopathy on the right side.



1.3 Case 81, age 3 years. Rash in scabbing stage, approximately day 12. Note lymphadenopathy in armpit.

Bulletin of the World Health Organization, **58** (2): 165-182 (1980)

Human monkeypox, 1970–79*

J. G. BREMAN,[1] KALISA-RUTI,[2] M. V. STENIOWSKI,[3] E. ZANOTTO,[3]
A. I. GROMYKO,[1] & I. ARITA[1]

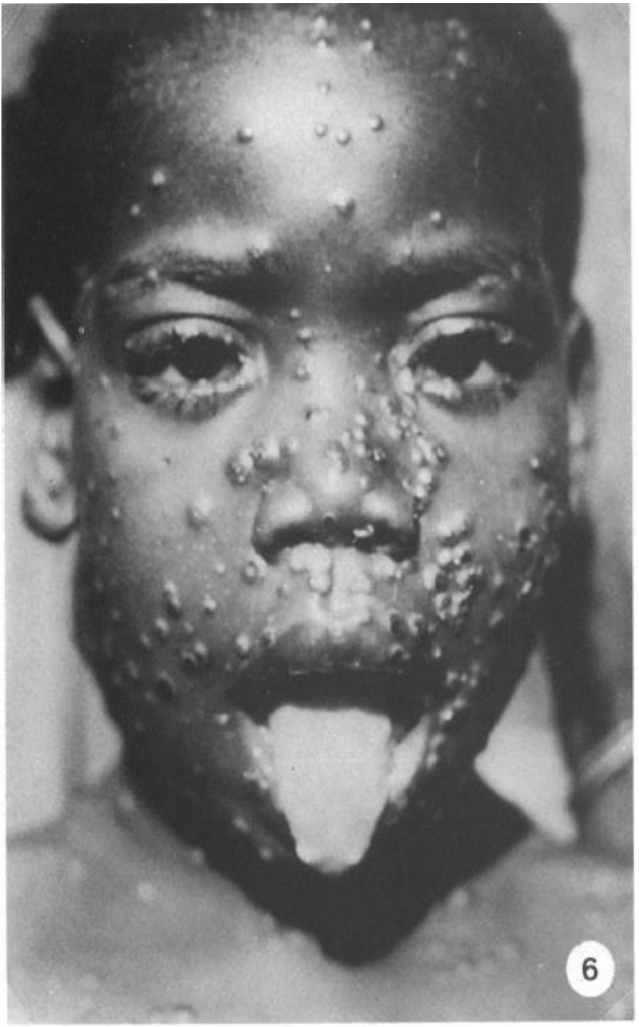


Fig. 6. Lesions on lips, tongue, and eyelid.

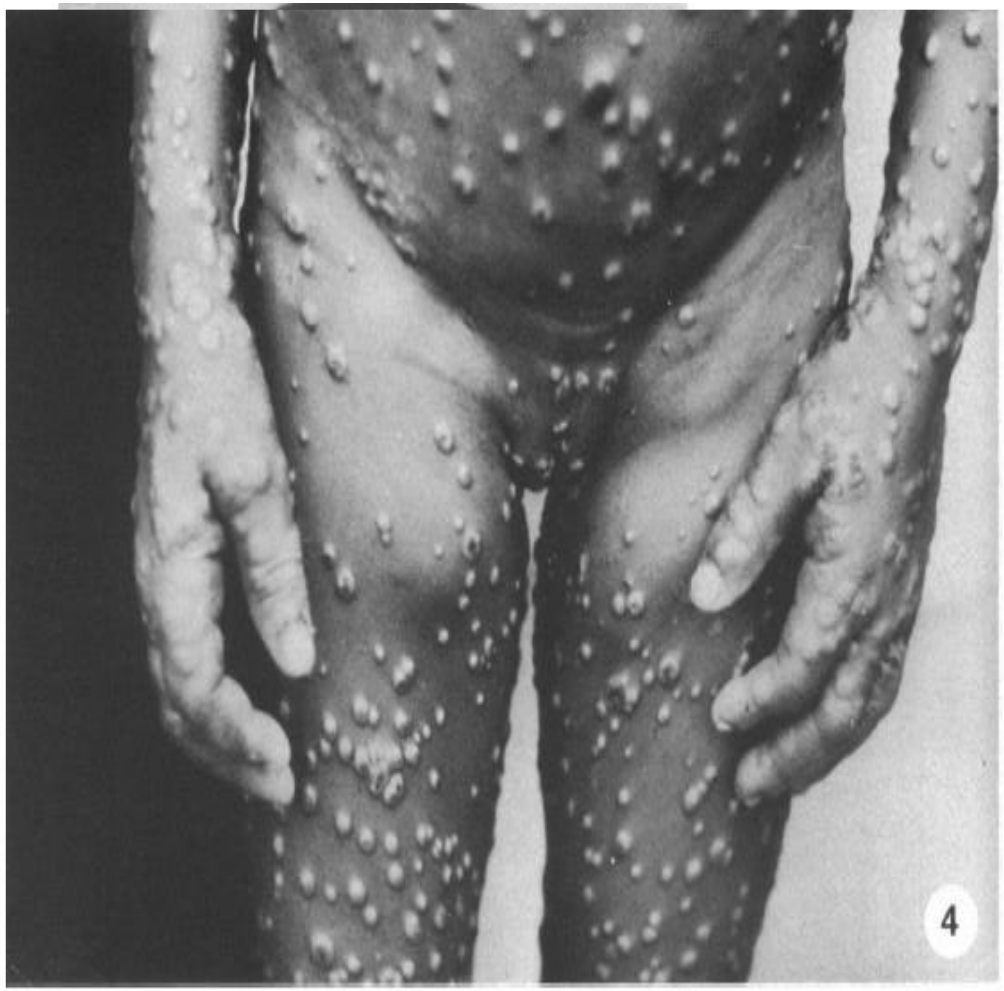
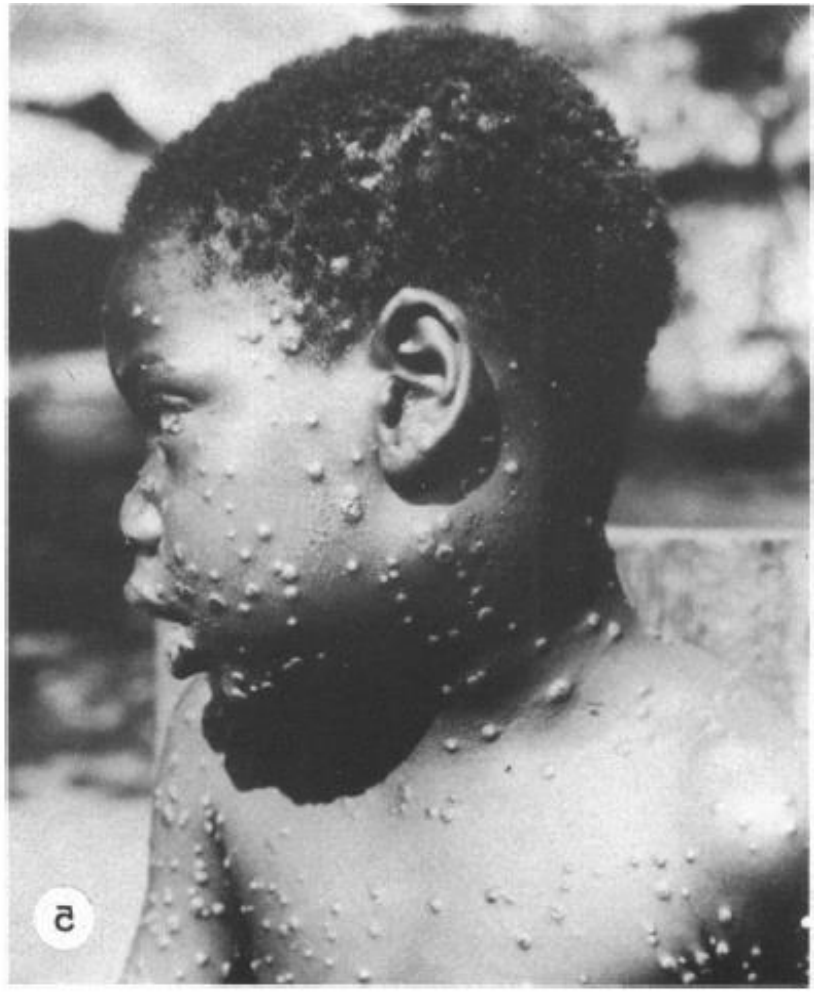


Fig. 4. Heavy concentration of lesions on the hands, inguinal lymphadenopathy, and pustules on genitalia.

lesions with shallow, pitting scars most prominent over bridge of nose.



swollen lower face and neck due to cervical and submandibular lymphadenop

Monkeypox virus in human body sites and fluids: evidence for transmission

With more than 50 000 cases worldwide in since May, 2022, and more than 95% of them in men who have sex with men, the monkeypox outbreak continues to represent a major medical and public health concern. Uncertainties persist regarding the transmission routes; together with epidemiological data, new insights are expected from the virological evaluation of the presence of monkeypox virus (MPXV) in different areas of the human body.

In this issue of *The Lancet Infectious Diseases*, Romain Palich and colleagues[1] report an extended evaluation of MPXV DNA in samples from skin, anus, throat, blood, urine, and semen from 50 French monkeypox cases. MPXV detection was more frequent in skin (44 [88%] of 50), anus (30 [71%] of 42), and throat (36 [77%] of 47) samples than from blood (13 [29%] of 45), urine (nine [22%] of 41), or semen (13 [54%] of 24) samples. Similar studies have been

Colavita F et al. Lancet Infect Dis 2022;September 29

Isolation of viable monkeypox virus from anal and urethral swabs, Italy, May to July 2022

www.eurosurveillance.org

Davide Moschese[1], Giacomo Pozza[2], Davide Mileto[3], Andrea Giacomelli[2], Miriam Cutrera[3], Maria Vittoria Cossu[1], Maddalena Matone[1], Martina Beltrami[2], Federica Salari[3], Spinello Antinori[4], Alessandra Lombardi[3], Giuliano Rizzardini[1]

Natural history of human Monkeypox in individuals attending a sexual health clinic in Milan, Italy

Davide Moschese*

Fig. 1. Rash was the first symptoms in half of individuals (50%), followed by fever (28.1%) and lymphadenopathy (9.4%). Other symptoms were common (71.9%), represented by fatigue, asthenia and malaise (62.5%), headache (21.9%), sore throat (18.7%) and back pain (15.6%).

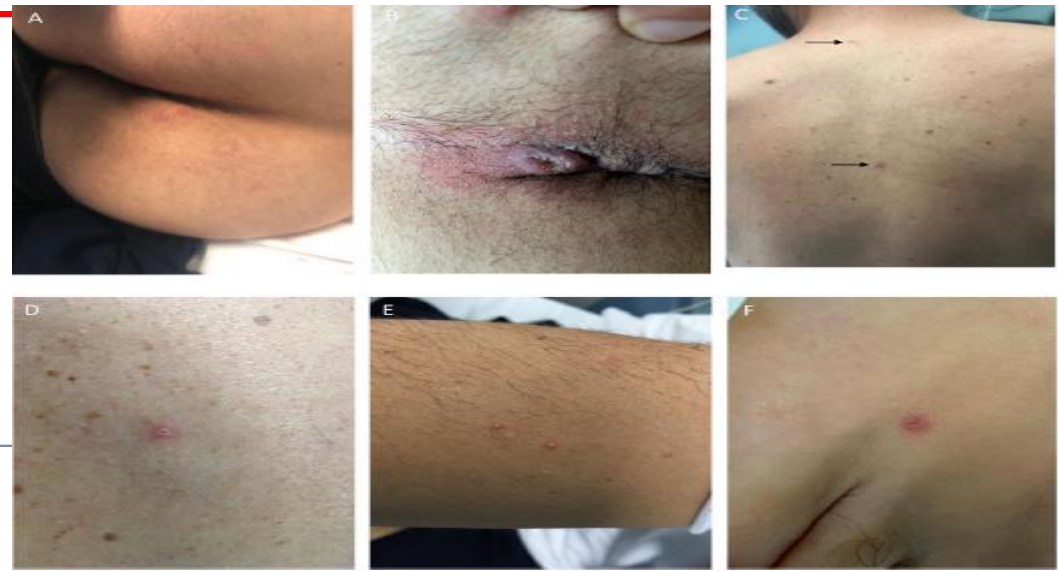
In 15 cases (46.9%) the rash started from the perianal region, in 13 cases (40.6%) started from the genital area and in three cases (9.4%) from face and oral cavity subsequently involving the perianal (56.2%) and genitals (46.9%) areas. All skin lesions were asynchronous classified as benign according to the rash extension (≤25 umbilicated vesicles evolving into pustules).

Fever was present in 75% of cases with a median duration of 3 days (IQR 2–4). Lymphadenopathy was present in 18 patients (56.2%), especially in inguinal area (n = 10, 55.6%).

New challenges in human monkeypox outside Africa: A review and case report from Italy

Travel Medicine and Infectious Disease 49 (2022) 102386

Davide Mileto[a], Agostino Riva[b,c], Miriam Cutrera[a], Davide Moschese[d], Alessandro Mancon[a], Luca Meroni[c], Andrea Giacomelli[c], Giovanna Bestetti[c], Giuliano Rizzardini[d], Maria Rita Gismondo[a,b], Spinello Antinori[b,c,*]



A Zoonotic Henipavirus in Febrile Patients in China

During sentinel surveillance of febrile patients with a recent history of animal exposure in eastern China, a phylogenetically distinct henipavirus, named Langya henipavirus (LayV), was identified in a throat swab sample from one patient by means of metagenomic analysis and subsequent virus isolation. The genome of LayV is composed of

Subsequent investigation identified 35 patients with acute LayV infection in the Shandong and Henan provinces of China, among whom 26 were infected with LayV only (no other pathogens were present). These 26 patients presented with fever (100% of the patients), fatigue (54%), cough (50%), anorexia (50%), myalgia (46%), nausea (38%), headache (35%), and vomiting (35%), accompanied by abnormalities of thrombocytopenia (35%), leukopenia (54%), and impaired liver (35%) and kidney (8%) function. A

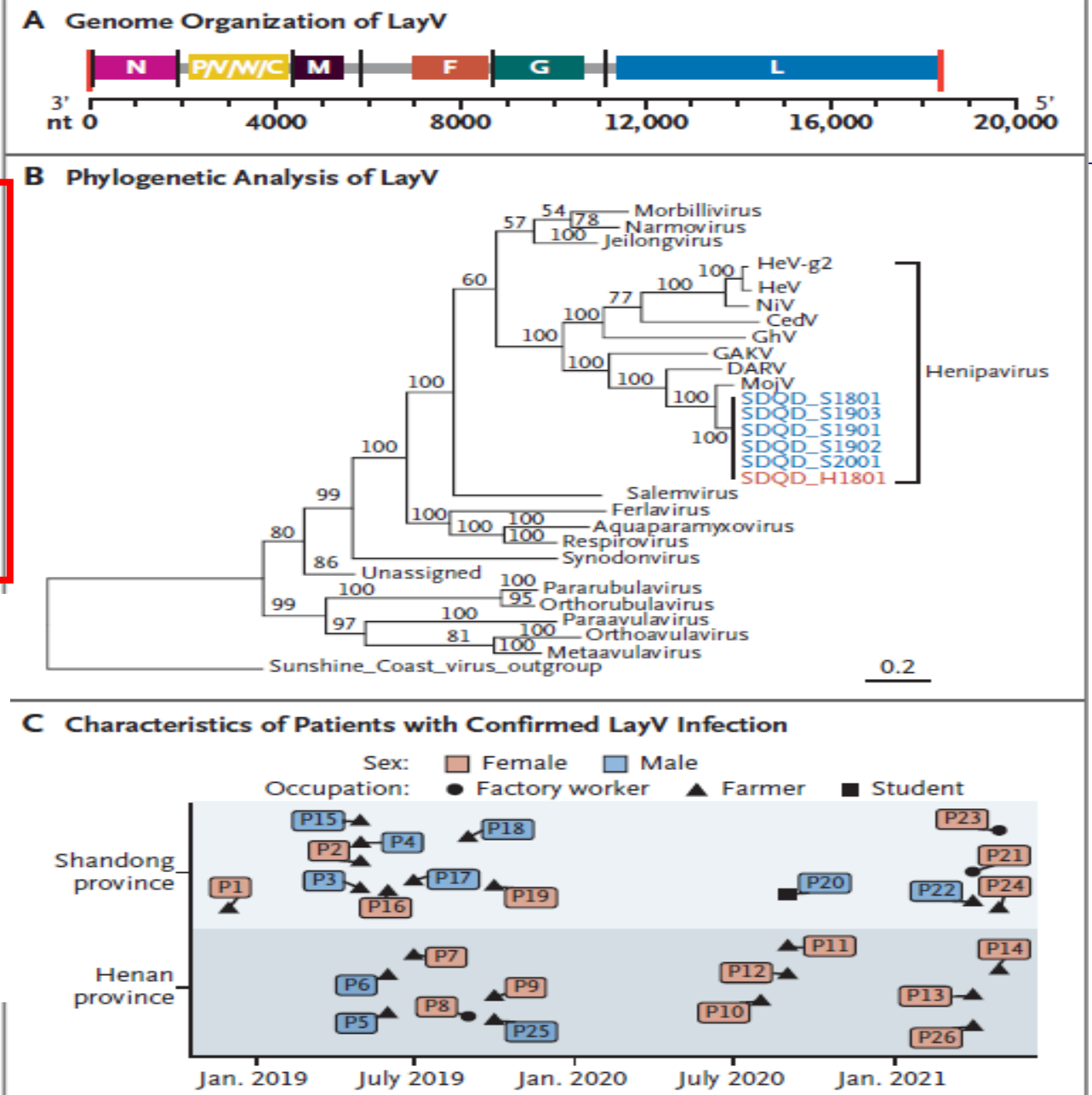
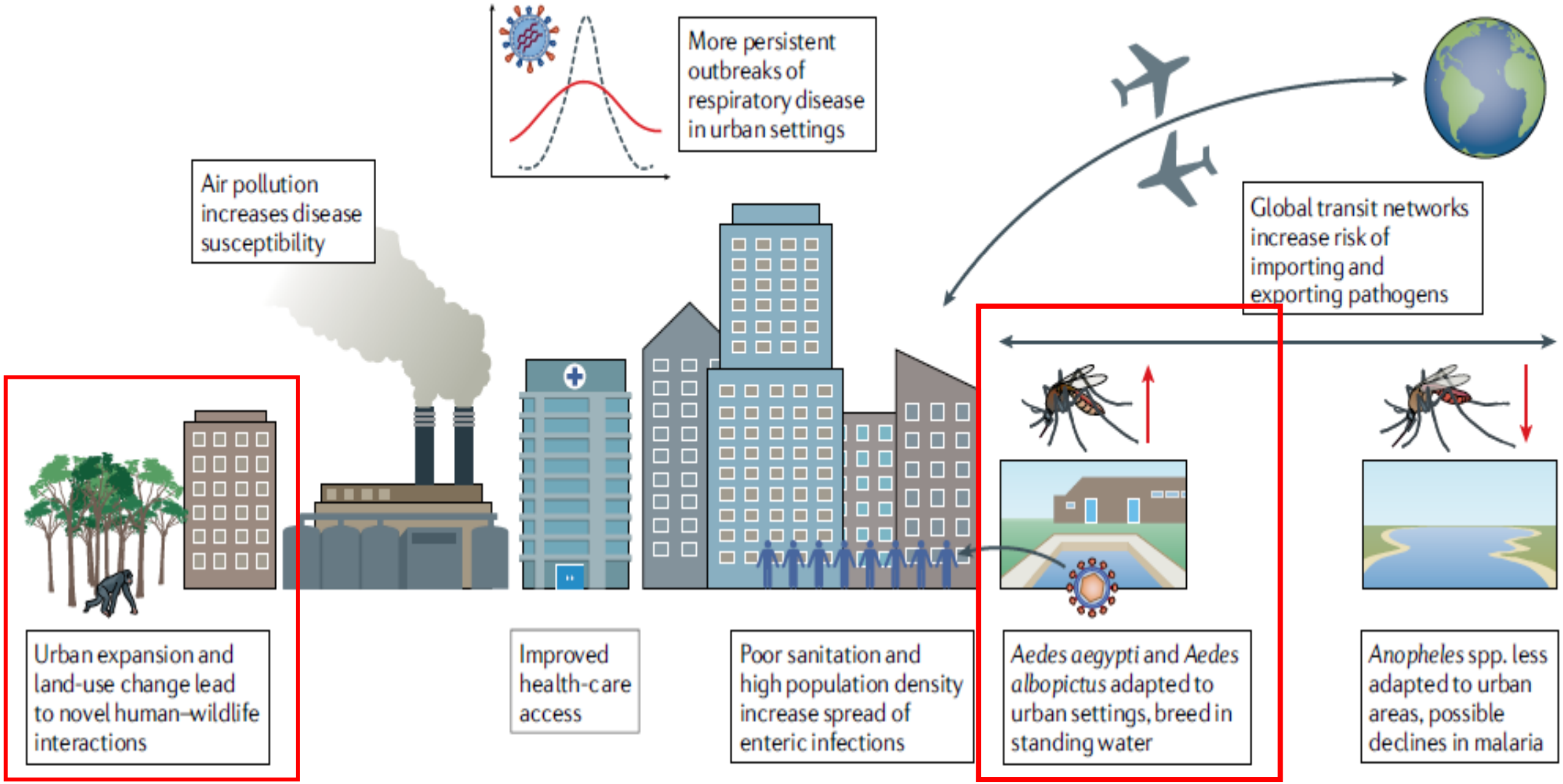


Figure 1. Genetic and Epidemiologic Characterization of LayV.

Ai-Zhang X et al, N Engl J Med 2022; 387: 470-72



Baker RE et al. Nature Rev Microbiol 2022;20:193-205c

Global risk mapping for major diseases transmitted by *Aedes aegypti* and *Aedes albopictus*

International Journal of Infectious Diseases 67 (2018) 25–35

Samson Leta[a,*], Tariku Jibat Beyene[a], Eva M. De Clercq[b], Kebede Amenu[a], Moritz U.G. Kraemer[c,d,e], Crawford W. Revie[f]

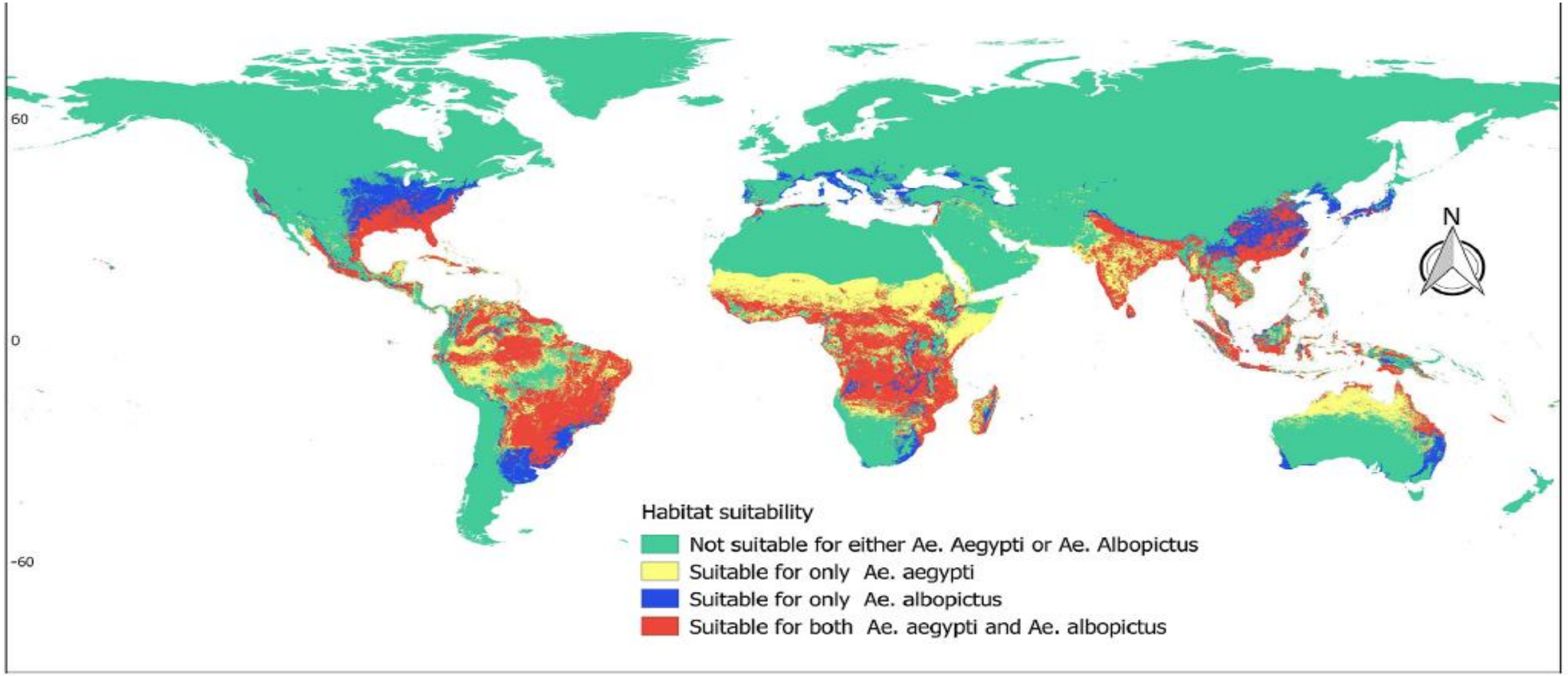


Figure 1. Global predicted habitat suitability of *Aedes aegypti* and *Aedes albopictus*.

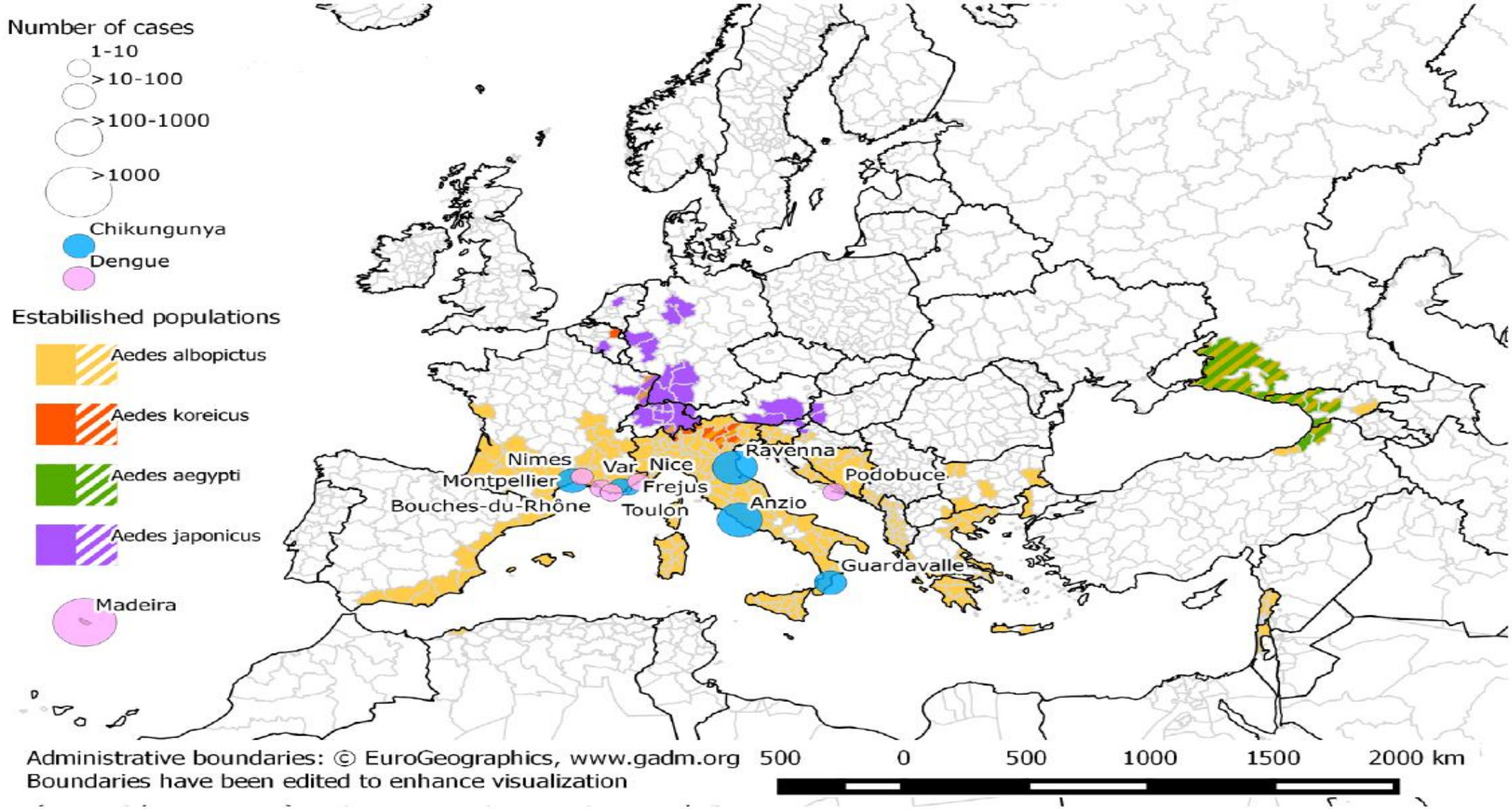
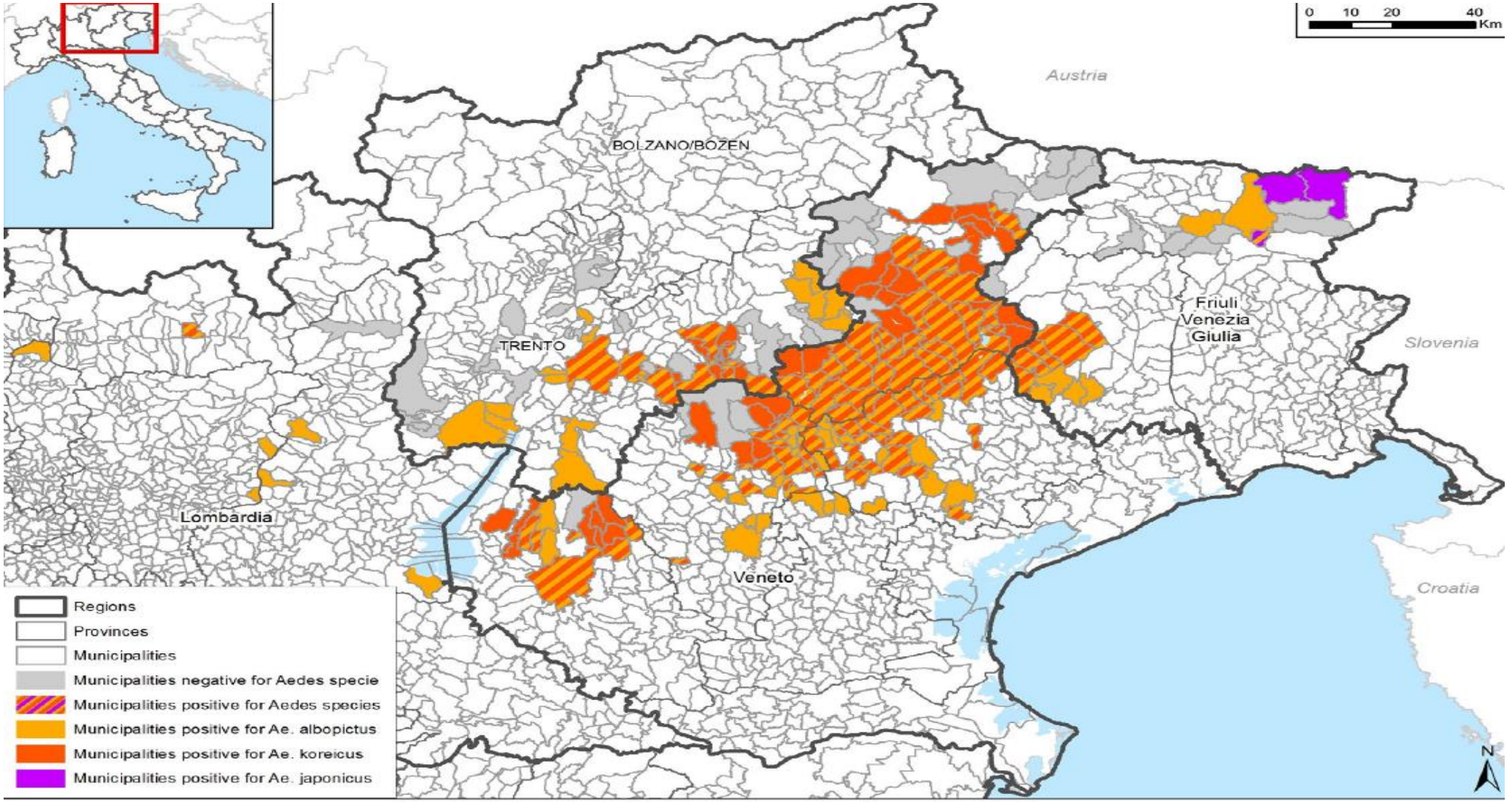


Figure 1. Distribution of invasive mosquito species in Europe (data collated from ECDC maps https://ecdc.europa.eu/en/disease-vectors/surveillance-and-disease-data/mosquito-maps) and locations and severity of autochthonous dengue and chikungunya outbreaks in Europe from 2007 [9,11,12,16,53–55,83–87]. Map created by Sandro Savino (University of Padua) and Silvia Ciocchetta (QIMR Berghofer).

The new European invader *Aedes* (*Finlaya*) *koreicus*: a potential vector of chikungunya virus

Silvia Ciocchetta[a,b], Natalie A. Prow[a], Jonathan M. Darbro[a], Francesca D. Frentiu[b], Sandro Savino[d], Fabrizio Montarsi[c], Gioia Capelli[c], John G. Aaskov[b] and Gregor J. Devine[a]

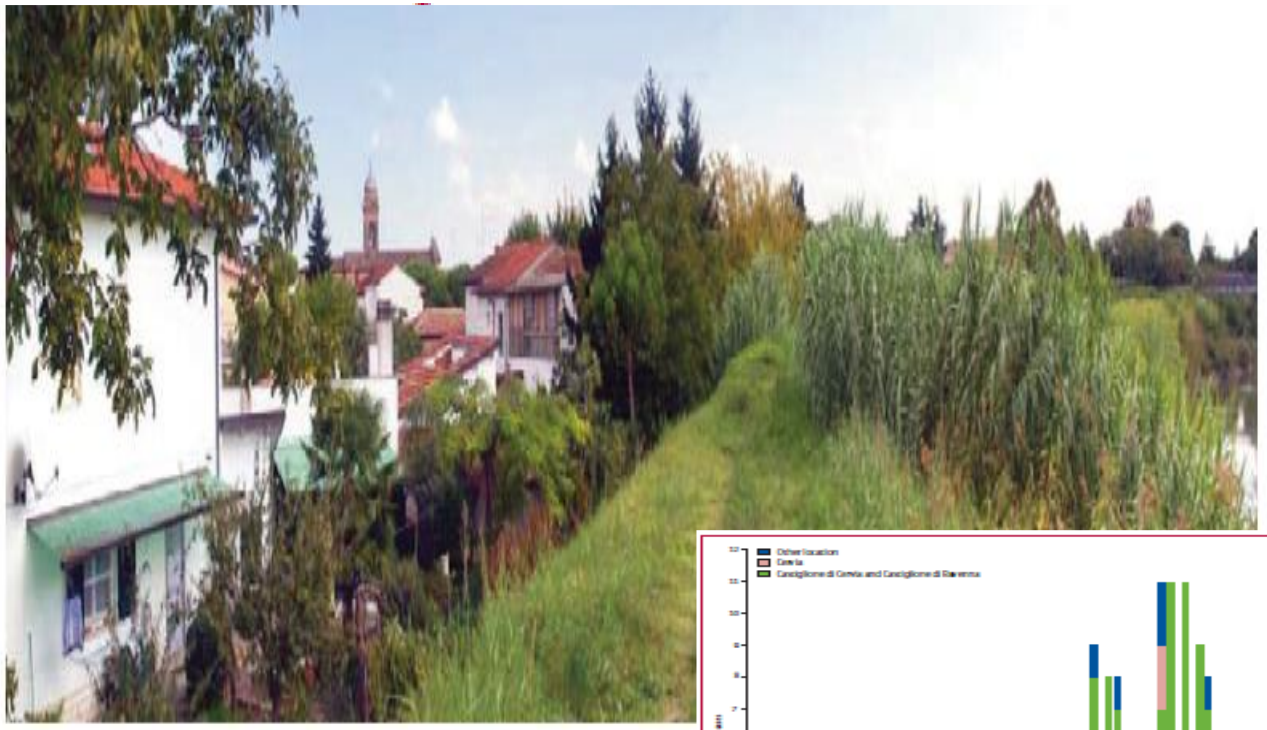


igure 2. Distribution of *Ae. koreicus*, *Ae. albopictus* and *Ae. japonicus* in northeastern Italy (data and map provided by Geograph
nformation Systems office, IZSVe).

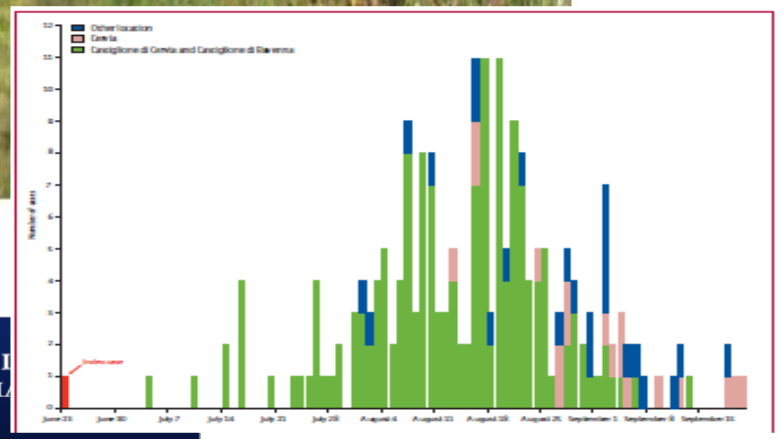
Infection with chikungunya virus in Italy: an outbreak in a temperate region

G Rezza*, L Nicoletti*, R Angelini, R Romi, A C Finarelli, M Panning, P Cordioli, C Fortuna, S Boros, F Magurano, G Silvi, P Angelini, M Dottori, M G Ciufolini, G C Majori, A Cassone, for the CHIKV study group†

Lancet 2007; 370: 1840–46



Riverbank, Castiglione di Cervia, province of Ravenna, 18 September 2007.



	Number of cases (%)
Fever*	205 (100%)
Joint pain†	199 (97%)
Fatigue	190 (93%)
Skin rash	106 (52%)
Headache	105 (51%)
Muscle pain	94 (46%)
Diarrhoea	48 (23%)
Itching	42 (20%)
Vomiting	40 (19%)
Photophobia	31 (15%)
Conjunctivitis	7 (3%)

*Mandatory in the case definition. †Not mandatory if diagnosis is laboratory confirmed.

Table 2: **Distribution of symptoms**

ITALIA: FOCOLAI AUTOCTONI DI INFEZIONE DA VIRUS CHIKUNGUNYA
(aggiornato al 26 settembre 2017)

186 casi notificati totali:

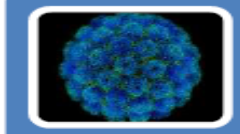
- 183 Regione Lazio
- 1 Regione Emilia-Romagna
- 1 Regione Marche
- 1 Paesi Europei (Francia)

112 casi confermati totali:

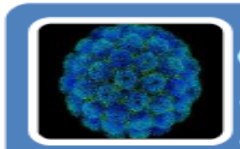
- 109 Regione Lazio
- 1 Regione Emilia-Romagna con legame epidemiologico Anzio
- 1 Regione Marche con legame epidemiologico Anzio
- 1 Paesi Europei (Francia) con legame epidemiologico Anzio

74 casi probabili totali:

- 74 Regione Lazio



- 91 (49 %) MASCHI
- 95 (51 %) FEMMINE



Gravità dell'infezione

- Ospedalizzati 26 (14 %)
- Deceduti 0

Chikungunya is back in Italy: 2007–2017

Giovanni Rezza*

Department of Infectious Diseases, Istituto Superiore di Sanità, Roma, Italy

Symptoms suggestive of chikungunya or dengue

↓

Travel to endemic area in the last two weeks or suspected autocthonous case

↓

<8 days after symptoms onset:
- PCR
- Serology (IgM) and PRNT
- Virus antigen (dengue virus)

≥8 days after symptoms onset:
- Serology (IgM/IgG) and PRNT
- Virus RNA in urine

Figure 2. Map of Italy with circles indicating the places where outbreaks of chikungunya occurred in 2007 (Emilia-Romagna Region) and in 2017 (Lazio and Calabria Region).

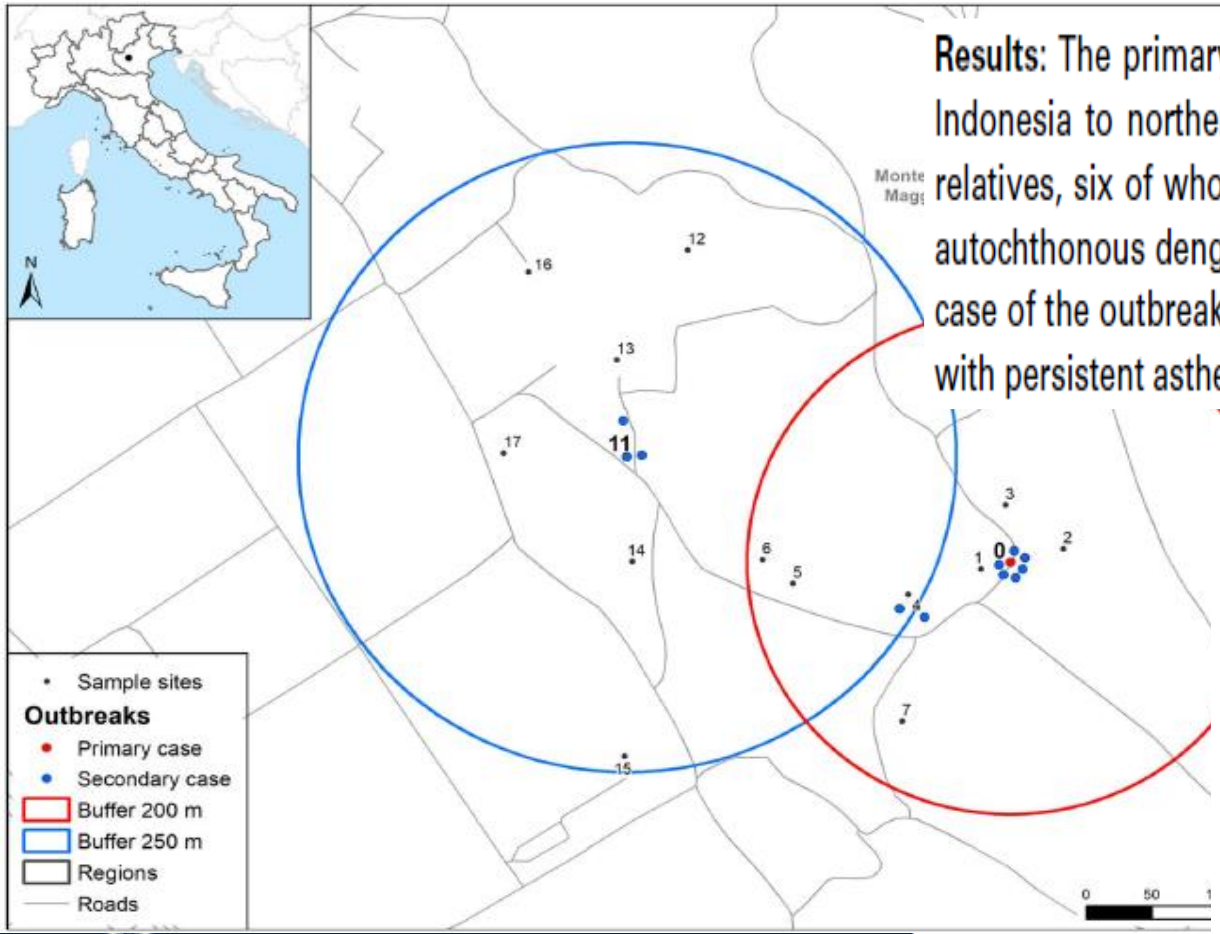
Journal of Travel Medicine, 2018, 1–4

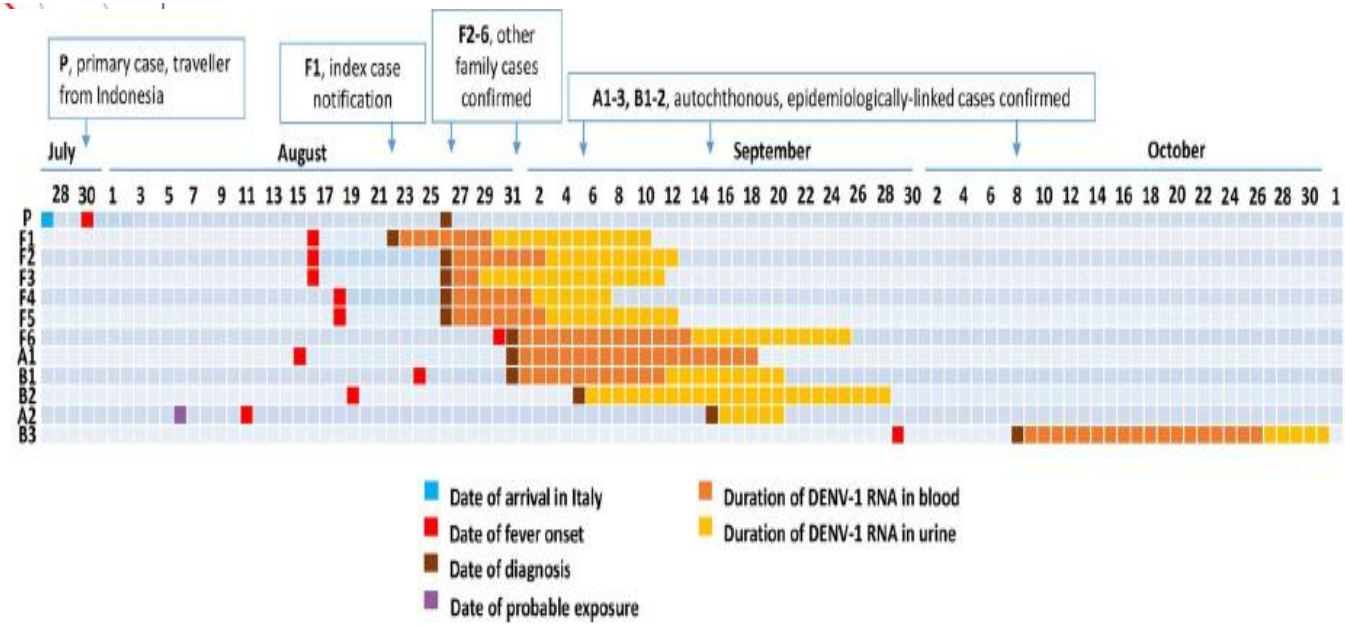
Journal of Travel Medicine
International Society of Travel Medicine
Promoting healthy travel worldwide
Established 1991
Journal of Travel Medicine, 2021, 1–9
https://doi.org/10.1093/jtm/taab130
Advance Access Publication Date: 18 August 2021
Original Article

Original Article

Autochthonous dengue outbreak in Italy 2020: clinical, virological and entomological findings

Results: The primary dengue case was identified in a young woman, who developed fever after returning from Indonesia to northern Italy, on 27 July 2020. She spent the mandatory quarantine for COVID-19 at home with relatives, six of whom developed dengue within two weeks. Epidemiological investigation identified further five autochthonous dengue cases among people who lived or stayed near the residence of the primary case. The last case of the outbreak developed fever on 29 September 2020. Dengue cases had a mild febrile illness, except one with persistent asthenia and myalgia. DENV-1 RNA was detected in blood and/or urine in all autochthonous cases,





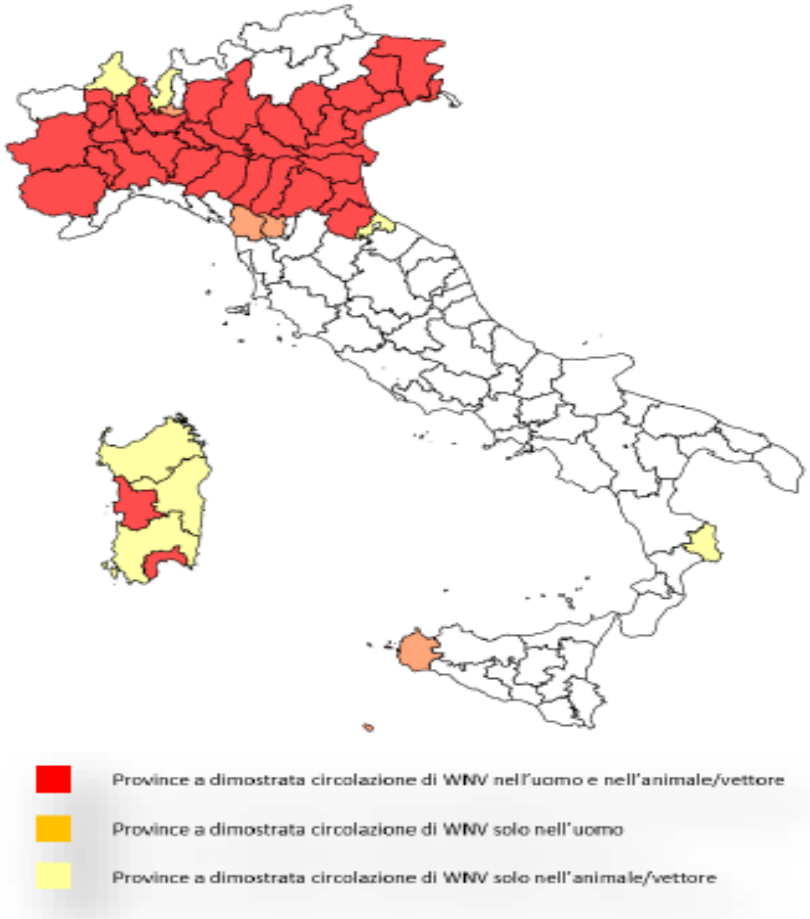
Sorveglianza integrata del West Nile e Usutu virus

Bollettino N. 15 del 28 settembre 2022
RISULTATI NAZIONALI

1. In Evidenza
2. Sorveglianza umana
3. Sorveglianza equidi
4. Sorveglianza uccelli bersaglio
5. Sorveglianza uccelli selvatici
6. Sorveglianza entomologica
7. Sorveglianza avicoli
8. Sorveglianza Usutu virus
9. Piano nazionale prevenzione, sorveglianza e risposta arbovirosi (PNA) 2020-2025

537 casi di 226 della forma neuro-invasiva, 80 casi in donatori di sangue, 180 casi di febbre, 1 caso importato, 28 decessi

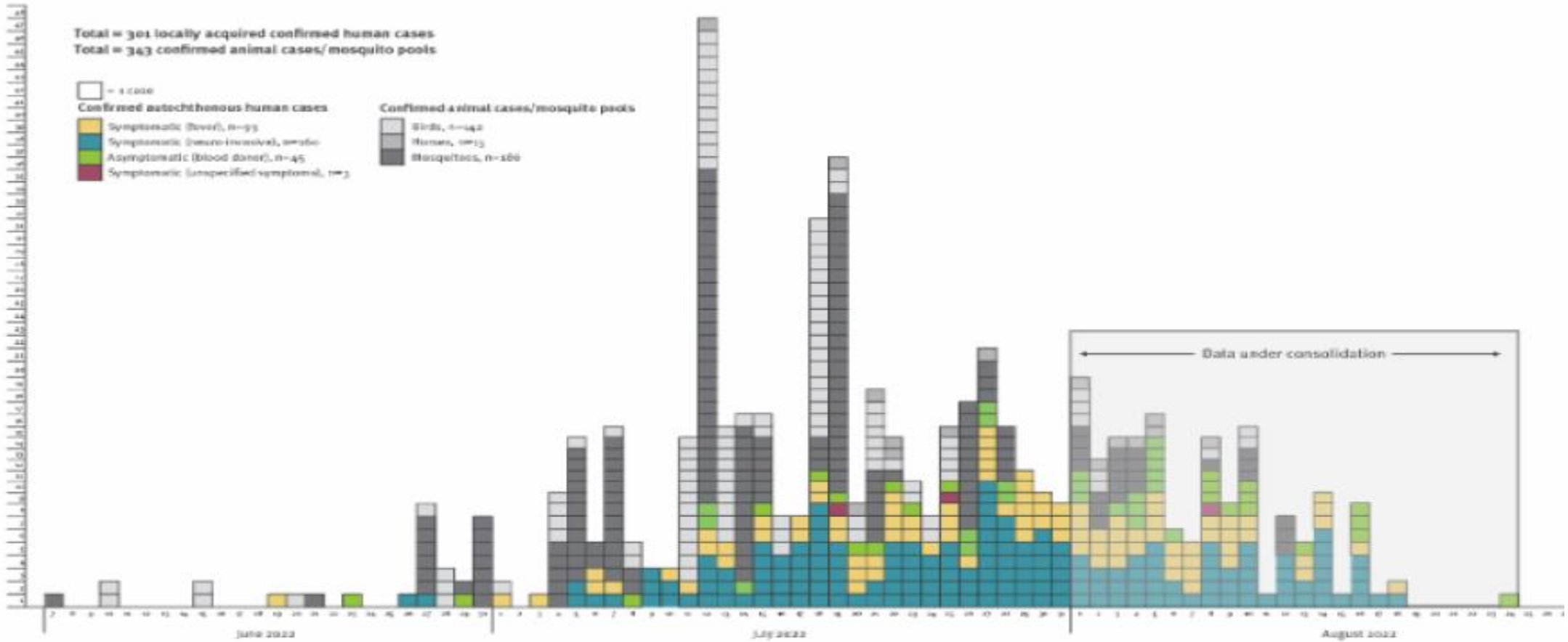
Figura 1. *Province con dimostrata circolazione di WNV in vettori, animali e uomo (donatori asintomatici, febbri e casi neuroinvasivi confermati)*



Rapid communication

Open Access

Rapid increase in neuroinvasive West Nile virus infections in humans, Italy, July 2022



Riccardo F et al. Euro Surveill 2022

Emerging and Reemerging Sexually Transmitted Infections

Deborah A. Williamson, M.D., Ph.D., and Marcus Y. Chen, M.D., Ph.D.

Table 1. Clinical Syndromes Caused by Major Emerging or Reemerging Sexually Transmissible Pathogens.

Clinical Syndrome	Pathogens
Enteritis or colitis	Shigella species Shiga toxin–producing *Escherichia coli* Campylobacter species *Entamoeba histolytica*
Urethritis	*Neisseria meningitidis* (unencapsulated) *Mycoplasma genitalium* *N. gonorrhoeae*
Proctitis	Lymphogranuloma venereum Enteric pathogens causing colitis
Systemic infections	*N. meningitidis* (capsulated) Zika virus Ebola virus *Treponema pallidum*

Table 2. Factors Contributing to the Emergence, Reemergence, and Spread of Sexually Transmissible Infections.*

Factor	Contributions
Pathogen	Antimicrobial resistance Infectiousness Virulence
Environment	Access to biomedical interventions (e.g., HIV PrEP) Behavioral aspects (e.g., chemsex†, condomless sex) International travel Access to testing and treatment Social media and use of online dating apps
Host	Previous immunity (e.g., to hepatitis A, *N. meningitidis*) Coinfection with other sexually transmissible pathogens Coexisting conditions (e.g., HIV infection)

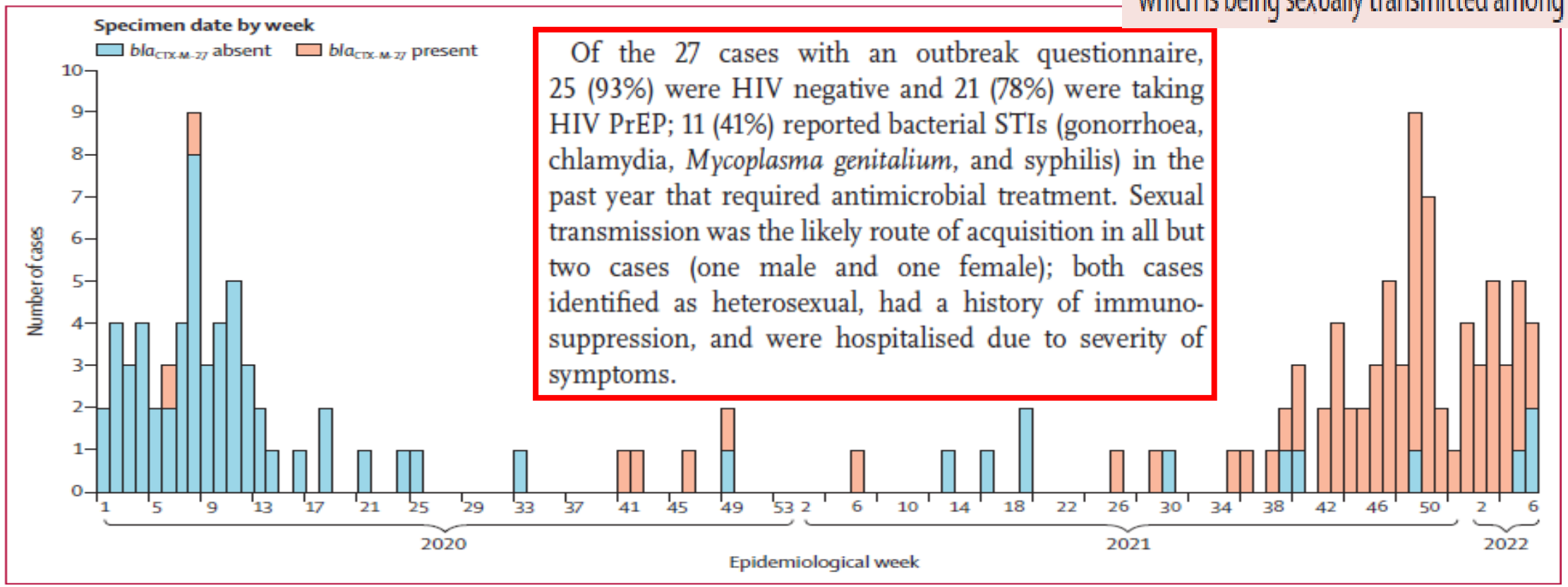
N Engl J Med 2020;382:2023-32

Outbreak of sexually transmitted, extensively drug-resistant *Shigella sonnei* in the UK, 2021–22: a descriptive epidemiological study

Hannah Charles, Mateo Prochazka, Katie Thorley, Adam Crewdson, David R Greig, Claire Jenkins, Anais Painset, Hele
Paul Cabrey, Robert Smith, Daniel Richardson, Laura Waters, Katy Sinka, Gauri Godbole, on behalf of the Outbreak C

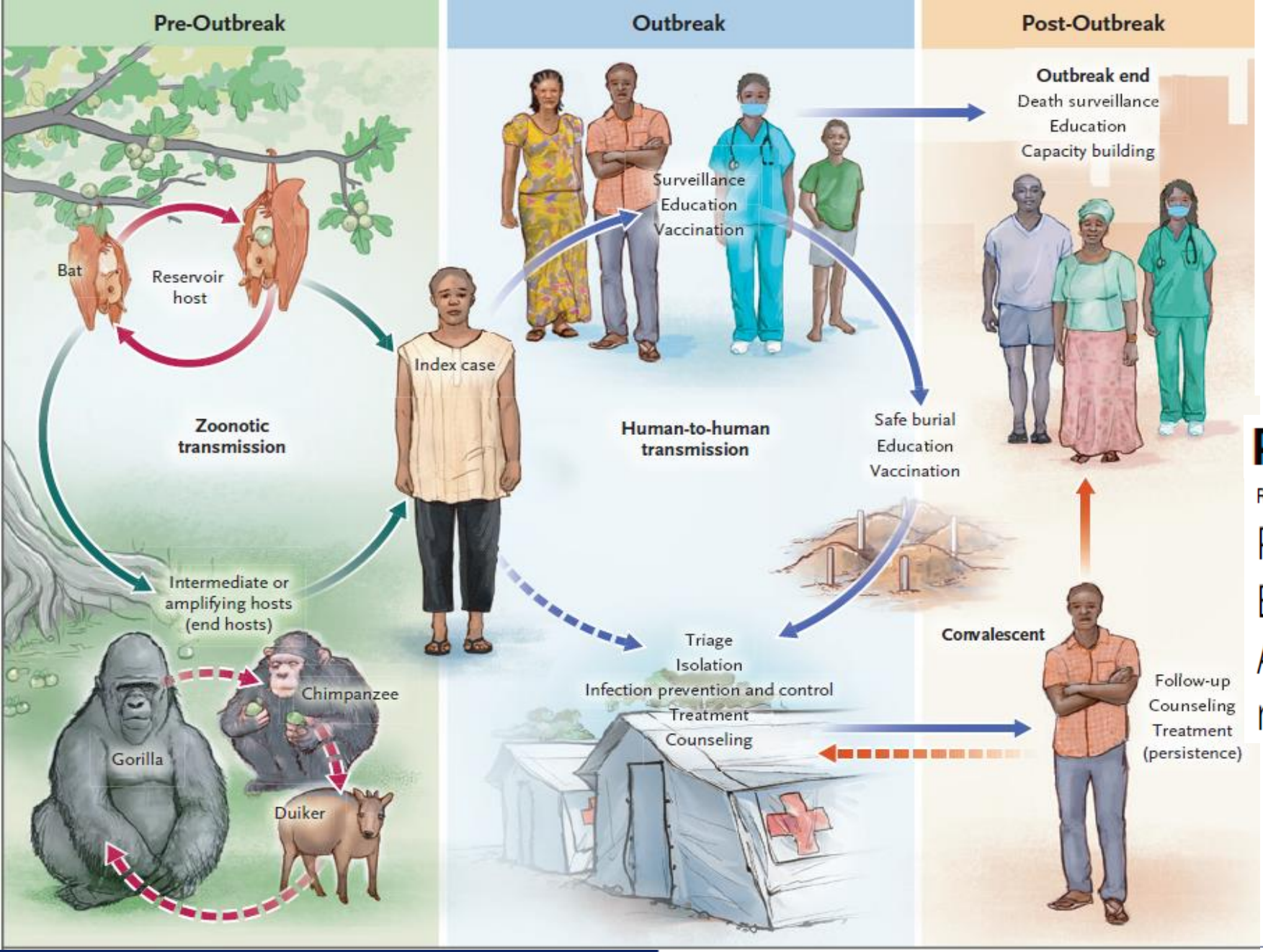
Implications of all the available evidence

Our findings contribute to understanding the emergence and dissemination of plasmid-mediated ESBL-producing S sonnei, which is being sexually transmitted among MSM. We identify



Of the 27 cases with an outbreak questionnaire, 25 (93%) were HIV negative and 21 (78%) were taking HIV PrEP; 11 (41%) reported bacterial STIs (gonorrhoea, chlamydia, *Mycoplasma genitalium*, and syphilis) in the past year that required antimicrobial treatment. Sexual transmission was the likely route of acquisition in all but two cases (one male and one female); both cases identified as heterosexual, had a history of immuno-suppression, and were hospitalised due to severity of symptoms.

Figure 1: Cases of *Shigella sonnei* clade 5 CC152 t10.377 in the UK by presence or absence of $bla_{CTX-M-27}$ and specimen date



The NEW ENGLAND JOURNAL of MEDICINE

BRIEF REPORT

Molecular Evidence of Sexual Transmission of Ebola Virus

PLOS MEDICINE

RESEARCH ARTICLE

Persistence of Ebola virus in semen among Ebola virus disease survivors in Sierra Leone: A cohort study of frequency, duration, and risk factors

20% a 1 anno

Lessons from the pandemic: Responding to emerging zoonotic viral diseases—a Keystone Symposia report

Lessons From COVID-19

- Global information sharing and collaborations are essential
- Existing clinical trial infrastructure should be utilized
- Prior scientific advances enable rapid vaccine development
- Prototype and priority pathogen approaches enable pandemic preparedness
- Continued surveillance of the human/animal interface is critical
- Longstanding systemic health and social inequities drive pandemic disparities
- Misinformation is the enemy of pandemic control

Ann NY Acad Sci 2022;1-17

Lessons from the pandemic: Responding to emerging zoonotic viral diseases—a Keystone Symposia report

EARLY WARNING AND REPORTING FOR EMERGING ZOONOTIC DISEASES

Event-based surveillance and informal data sources for early epidemic awareness

In 1981, *MMWR* published what would become the sentinel report of the HIV/AIDS pandemic.[15] However, it would later be determined that HIV had been circulating since the 1930s, with widespread occurrences of AIDS in West Africa.

Event-based, informal surveillance systems have increasingly been used to complement more traditional public health reporting systems to identify emerging outbreaks early. Madoff focused on the Program for Monitoring Emerging Diseases (ProMED), an electronic outbreak reporting service established in 1994.[18] ProMED has been the first outlet to publish reports of several outbreaks and epidemics, including cases of undiagnosed pneumonia in Wuhan, China based on social media and media outlets that would later be recognized as the beginning of the COVID-19 pandemic,[19] as well as cases related to the SARS-CoV-1 epidemic based on information from a reader who had read concerning information in a teacher chat room.[20] In addition to ProMED, other event-based surveillance systems include HealthMap, OIE-WAHIS, EMPRES-i+, and GISAID. These surveillance systems can

Ann NY Acad Sci 2022;1-17

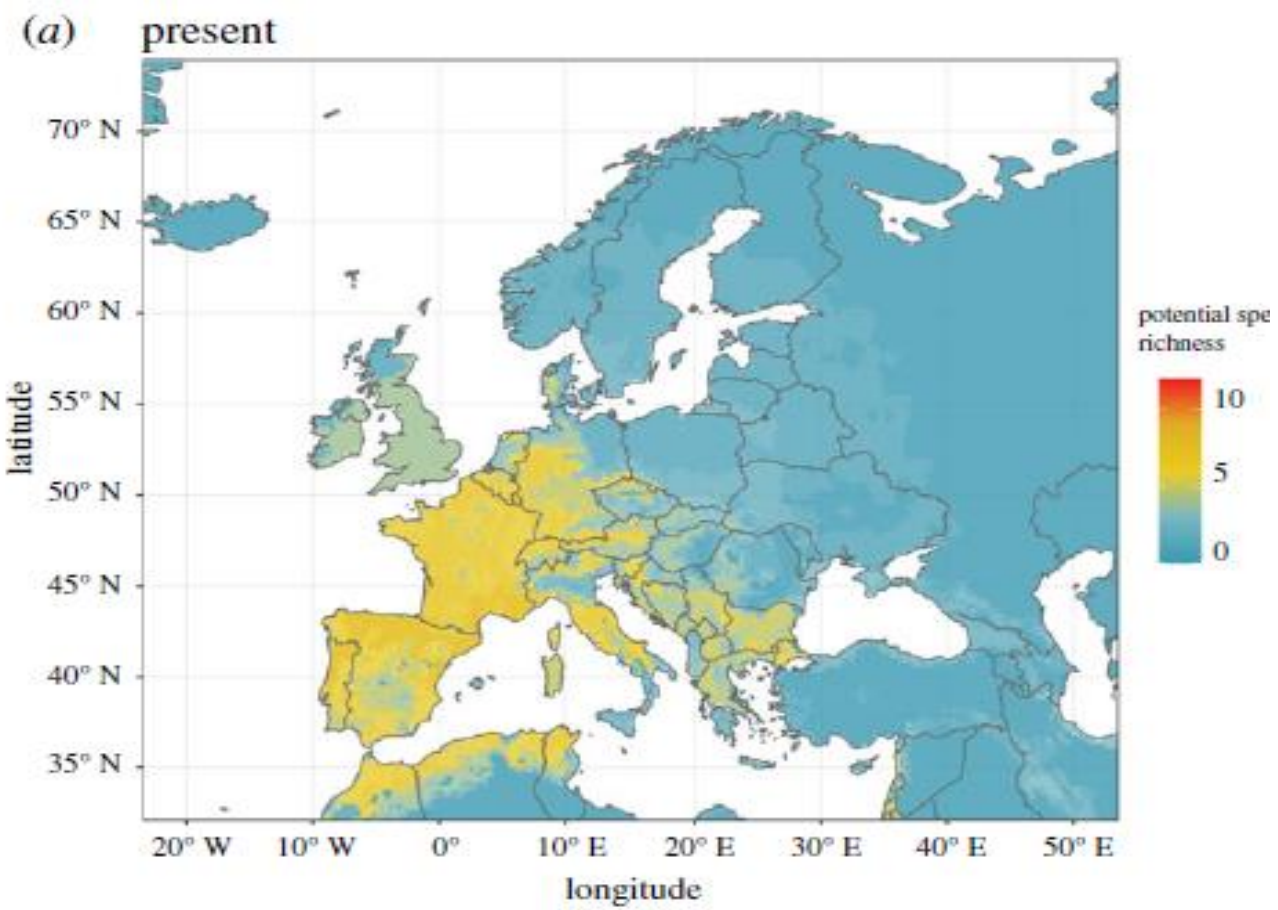
Lessons from the pandemic: Responding to emerging zoonotic viral diseases—a Keystone Symposia report

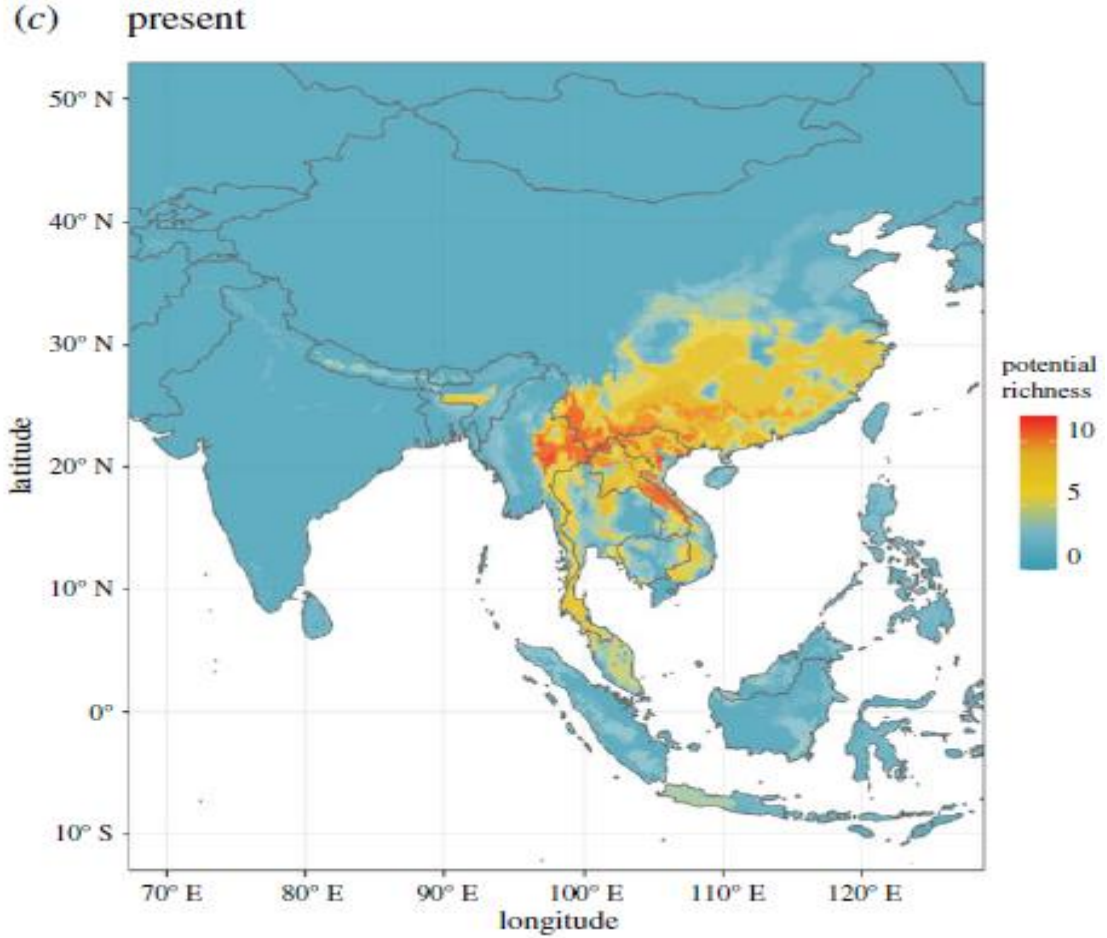
Preparing for the next coronavirus epidemic

Lin-Fa Wang from Duke–NUS Medical School discussed whether the world is prepared for the (nearly) inevitable emergence of a SARS-CoV-3 outbreak. Wang presented two possible scenarios for the next coronavirus outbreak—spillover from a natural animal reservoir, similar to what occurred with previous coronavirus epidemics, or reverse zoonotic transmission of SARS-CoV-2 from humans to animals and back to humans, which would be a unique event.[22] The chances of another sarbecovirus jumping from animals to humans is relatively high. Since 2020, more than a dozen new bat-borne coronaviruses related to SARS-CoV-2 have been identified in Asia.[23] Given that the bat species that harbors these viruses is found throughout Asia, Europe, and southern Africa, it seems only a matter of time until another virus spreads to humans. In the case of reverse zoonotic transmission, much of the focus has been on a theoretical transmission

Ann NY Acad Sci 2022;1-17

Present and future distribution of bat hosts of sarbecoviruses: implications for conservation and public health





Muylaert RL, et al. Pro R Soc B 2022;289:20220397

Present and future distribution of bat hosts of sarbecoviruses: implications for conservation and public health

Table 1. Highest national maximum *Sarbecovirus* host richness values (i.e. hotspots) predicted through SDMs.

country	subregion	hosts	median sampling rate (mean ± s.d.)
Myanmar	Southeast Asia	13	0.033 (0.053 ± 0.061)
China	East Asia	12	0.024 (0.051 ± 0.064)
Lao PDR	Southeast Asia	12	0.052 (0.063 ± 0.041)
Thailand	Southeast Asia	12	0.087 (0.102 ± 0.067)
Vietnam	Southeast Asia	12	0.086 (0.107 ± 0.074)
Cambodia	Southeast Asia	8	0.112 (0.127 ± 0.076)
India	South Asia	8	0.069 (0.09 ± 0.078)
France	West Europe	8	0.128 (0.144 ± 0.076)
Italy	South Europe	8	0.146 (0.152 ± 0.079)
Malaysia	Southeast Asia	8	0.051 (0.074 ± 0.072)

Muylaert RL, et al. Pro R Soc B 2022;289:20220397

BMJ Global Health

Scoping future outbreaks: a scoping review on the outbreak prediction of the WHO Blueprint list of priority diseases

Jonkmans N, *et al. BMJ Global Health* 2021;6:e006623.

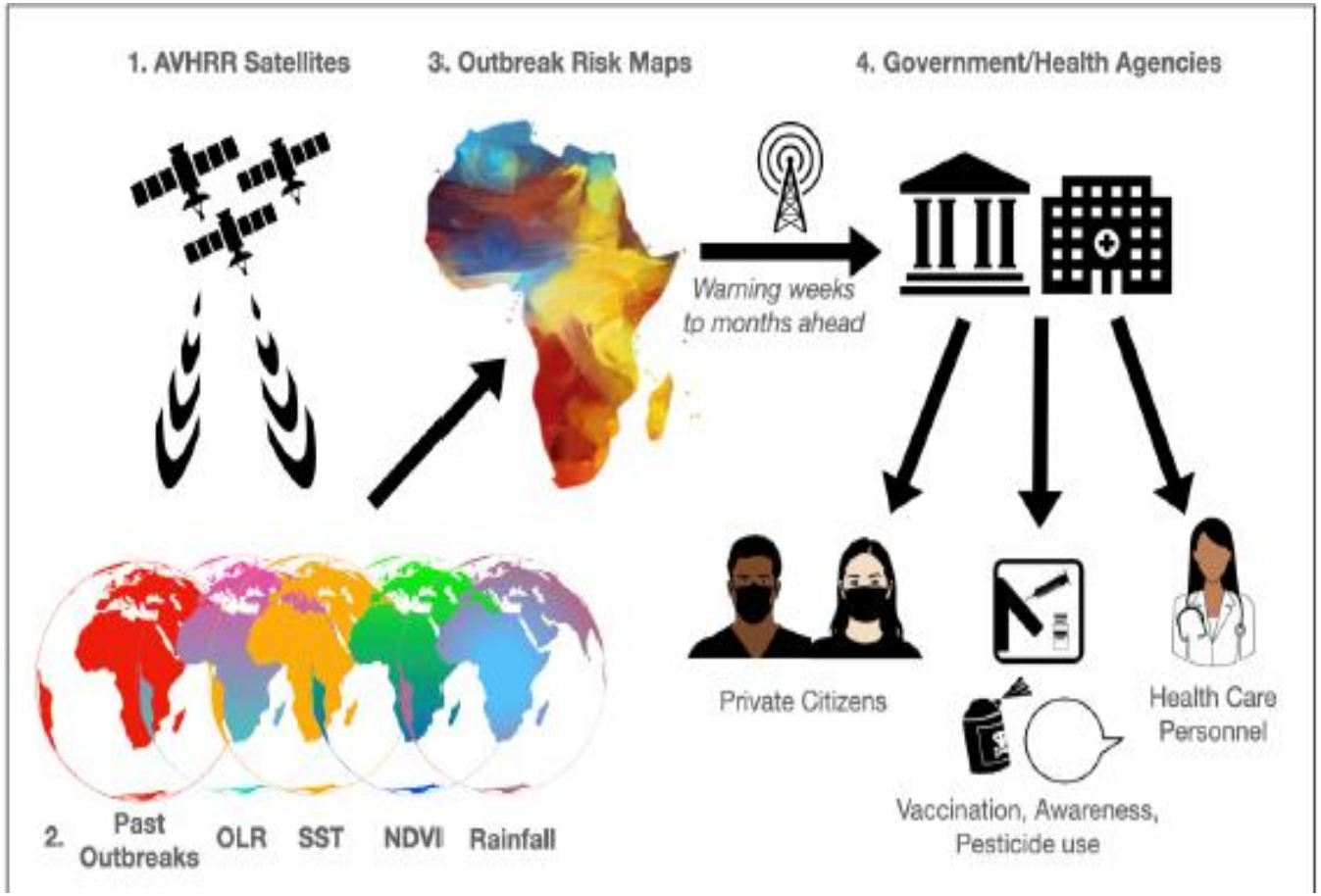


Figure 2 Example case study of Rift Valley fever (RVF) outbreak prediction. Illustration adapted from prediction strategies devised by Anyamba *et al*[43] : (1) advanced very high resolution radiometers (AVHRR) on satellites measure observations of various global to subregional variables; (2) outgoing longwave radiation (OLR), sea surface temperature (SST), normalised difference vegetation index (NDVI) and rainfall together with coordinates of previous outbreaks are integrated into outbreak risk maps; (3) risk map predictions are associated to persistent anomalies in NDVI over specific locations, for example, predicting RVF outbreaks during future time periods and enabling warnings with time lags weeks to months ahead. Warnings are transmitted as part of an early warning system to different agencies (4), which lead pre-emptive measures: information to private citizens and health personnel, vaccination drives, awareness campaigns and vector control through pesticides.

Table 2. Technology priorities for advancing global health security

Technology priority	Rationale
Platform vaccines	The rapid development of COVID-19 vaccines is due to several years of concerted research effort as well as international public-private partnerships aimed at the development of platform technologies: a technology that can be rapidly repurposed for multiple vaccines, such as mRNA vaccines [44].
Prototype pathogen research in advance	Similarly, the prototype pathogen approach suggests that with sustained effort, candidate vaccines and therapeutics could be generated for all categories of pandemic pathogens in advance [45,46].
Rapid point-of-person/point-of-care diagnostics	In future epidemics which may be more contagious than COVID-19, presenting to a centralized testing facility can be dangerous. Diagnostics that can be completed at home, cheaply and quickly, can be distributed directly to homes and repeated frequently, thereby reducing community spread.
Rapidly scalable diagnostics, vaccine and therapeutics manufacturing	In a pandemic, manufacturing capabilities will need to be rapidly scaled in order to meet global demand. This article outlines advancements in cheap, platform diagnostics such as the SHERLOCK system as well as platform mRNA vaccines. Therapeutics pose a more difficult challenge, as small molecules and antibodies face manufacturing bottlenecks.
Widespread sequencing capabilities	This article discusses cutting edge advancements in on-the-ground sequencing used during the Ebola epidemic for molecular epidemiology. However, continued simplicity and affordability of sequencing is needed to facilitate widespread pathogen surveillance including metagenomic surveillance, particularly in low-income settings.
Needle-free, shelf-stable vaccines	The National Institutes of Health have begun to adopt needle-free administration in epidemic vaccine clinical trials, such as the use of PharmaJet [10] in trials for Zika vaccine. Further advancements in, for example, needle microarray patches would eliminate the need for vaccine cold-chain storage, trained healthcare personnel for administration, and could be delivered to patient homes.
Advanced PPE	Present PPE cannot comfortably be worn for long periods of time, cannot be worn during risky social interactions such as eating or drinking, and impacts communication by physically covering the mouth or eyes.
Built environment improvements	Advancements in air filtration and sterilization, such as with UVC light, could make public indoor environments such as transportation hubs and event venues, less likely to contribute to super-spreader events.
Technological deterrence of bad actors	With advancements in biotechnology, bad actors may be able to engineer biosecurity threats accidentally for malicious purposes. To mitigate this, genetic engineering attribution techniques should be developed. Genetic attribution aims to be able to identify lab-of-origin of an engineered sequence [47,48].

Pannu J et al.Curr Opin Infect Dis 2022;34:401-8

Intercepting pandemics through genomics

W. John Kress[a,1], Jonna A. K. Mazet[b], and Paul D. N. Hebert[c]

Hence, there is an urgent need to establish a global, genomic-based biosurveillance platform, a development which would be of immense value to biosecurity, biodefense, and the economy. If implemented, this "pandemic interception system" would hugely advance our understanding of the natural world.

Three major research programs are poised to support this effort: BIOSCAN, the Earth BioGenome Project (EBP), and the Global Virome Project (GVP). Each of these global programs is now working to develop approaches in comparative genomics that are needed to discover all species and to reveal their interactions. The diversity of infectious agents involved

Broadly speaking, two strategies exist for preventing a global pandemic: Either we curb the spread of viral infections once they have started, or we proactively prevent infections by understanding the causes and processes behind pathogen transfers. The latter strategy is more desirable medically, economically, socially, and scientifically. Both actions may be necessary into the foreseeable future.

PNAS 2020; 117:13852-13855

The future of zoonotic risk prediction

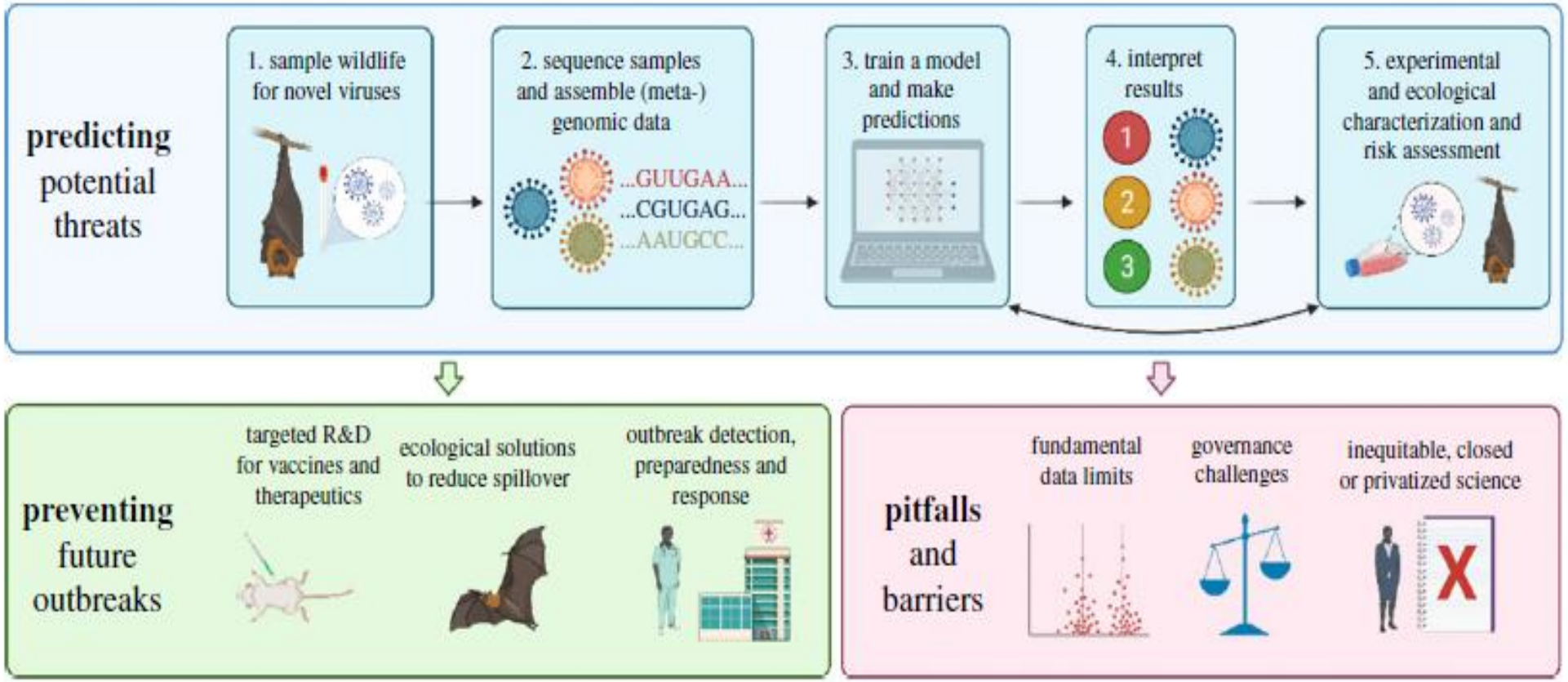


Figure 1. Zoonotic risk technology can be part of a broader scientific pipeline that connects viral discovery and wildlife disease surveillance to the development of biomedical and ecological solutions to predict, prevent and prepare for future outbreaks. Created with BioRender.com. (Online version in colour.)

Carlson CJ et al. Phil Trans R Soc B 2021;376:20200358

Conclusioni

La recente pandemia da COVID-19 e il continuo emergere di vecchie e nuove patologie infettive rappresentano una crescente sfida per l'infettivologia

La tecnologia oggi disponibile declinata in tutte le possibili applicazioni costituisce un importante ausilio per confrontarsi con queste nuove sfide ma non può rappresentare l'unica soluzione

Sono indispensabili interventi urgenti sul clima, sulle condizioni di vita, sull'equità economica e sanitaria a livello globale e su tutti gli attori che contribuiscono alla salute non solo dell'uomo ("One Health")