La Importancia del Diagnóstico de Laboratorio en la Aproximación de Una Sola Salud: El Modelo de las Zoonosis

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Committee on Tropical Medicine, Zoonoses and Travel Medicine, **Colombian Association of Infectious Diseases** (ACIN).

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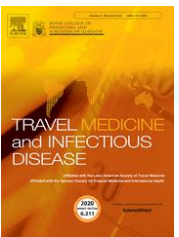

Disclosures/Conflicts of interests/Acknowledgments

- Sanofi Pasteur (USA/Braz/Mex/Col)
  - Member, Scientific Experts Panel for the Development of Zika virus vaccines, 2016
- Johnson & Johnson (Brazil)
  - Member, Latin-American Panel of Experts on Human Significant Arboviruses (Johnson & Johnson, 2016).
- Global Disease Research (USA)
  - Member of the Scientific Advisory Board (2016)
- National Academy of Sciences – Medicine (USA)
  - Member, Zika Virus Outbreak Expert Panel of the National Academies of Sciences, Engineering, and Medicine, NAS, 2016).
- Sanofi (USA)
  - Member of the Advisory Board for the development of Chikungunya virus antibody therapy, Sanofi Pasteur, 2017.
- Abbott (Colombia) – Consultant/Advisor (2019-2022) - POCTs
- WHO-TDR/SDC/IDRC/STPH grant (WHO Registration 2017/730668-1)
  - Project: Integrated strategies for the prevention and control of VBDs within the context of eco-bio-social approaches
- 2017-N-108041 CDC/BAA
  - Zika Diagnostic Development: 7/2017–6/2022 (Serologic diagnosis of recent and remote Zika infections in flavirirus-endemic regions)
- Thrasher Early Career Development
  - Project: Serologic risk for congenital Zika syndrome
- Universidad Tecnologica de Pereira (CI-2018/CI2019) – Colciencias (JTP-2019-Contrato 762/Subc. 5459, 5460, 5464, 5465)
  - Project: "Evaluación de la función y el fenotipo de linfocitos T como indicador de exposición a Zika *in-utero*", Código 5-18-3 [2018-2020].
  - Project: "Evaluación de la respuesta inmune adaptativa de memoria específica durante el embarazo, contra arbovirus endémicos, en un grupo de pacientes embarazadas de La Virginia, Risaralda, Colombia", Código 5-19-3 [2019-2021]
- Takeda (Col)
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- Amgen (Speaker COVID-19 Vaccines)
- AstraZeneca (Speaker COVID-19 Vaccines)
- Merck Sharp and Dohme (Speaker Arbovirus)
- Valneva (Consultant COVID-19 Vaccines; Speaker Chikungunya)

Contents

- Socio-environmental overview of Latin America: importance of climate change, OneHealth approach and determinants
- Arboviruses in the region
- We have not just mosquitoes, but many rodents involved in emerging viral infections in the region: Mammarenaviruses and Orthohantaviruses
- Cocirculation during COVID-19 pandemic, mpox, and avian influenza
- Some conclusions - mitigation

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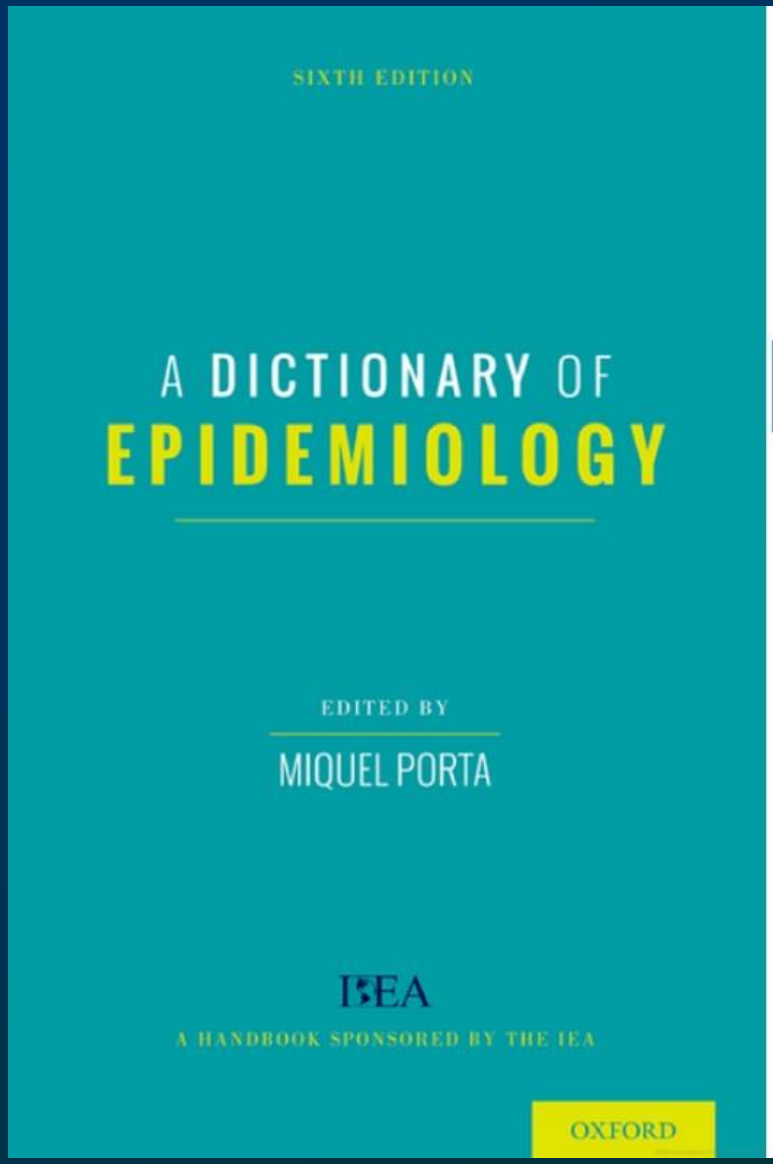
- Some conclusions - mitigation

Let's think on arboviral diseases: Most of them, zoonotic

Figure 1. Conditions prone for arboviral *Aedes* vectors proliferation. Area endemic for Zika and other arbovirus cocirculation and coinfections, La Virginia Risaralda, Colombia.

Sánchez-Duque JA, Rodriguez-Morales AJ, Trujillo AM, Cardona-Ospina JA, Villamil-Gómez WE. Cocirculation and Coinfection Associated to Zika Virus in the Americas. In: Rodriguez-Morales AJ. (Editor). Current Topics in Zika. ISBN 978-1-78923-271-4. InTech, United Kingdom, June 2018. Chapter 5: 71-83. Available at: https://www.intechopen.com/books/current-topics-in-zika/cocirculation-and-coinfection-associated-to-zika-virus-in-the-americas



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GUSTAVO A. SILVA
Geneve, Sweden

ISABEL DOS SANTOS SILVA
London, England, UK

CHITR SITTHI-AMORN
Bangkok, Thailand

2014

EMERGING INFECTIONS (Syn: emerging pathogens) Infectious diseases that have recently been identified and taxonomically classified. Many of them are capable of causing dangerous epidemics. They include human immunodeficiency virus (HIV) infection, Ebola virus disease, hantavirus pulmonary syndrome and other viral hemorrhagic fevers, *Campylobacter* infection, transmissible spongiform encephalopathies, Legionnaires' disease, and Lyme disease. Some appear to be new diseases of humans (e.g., HIV infection). Others, such as the viral hemorrhagic fevers, may have existed for many centuries and have been recognized only recently, because ecological or other environmental and demographic changes have increased the risk of human infection. *Reemerging infections* are certain "old" diseases, such as tuberculosis and syphilis, that have experienced a resurgence because of changed host-agent-environment conditions.[56,69,217-219,367,368]

Z

ZOONOSIS A DISEASE, INFECTION, OR INFESTATION transmitted under natural conditions from vertebrate animals to humans. Examples include rabies and plague. May be enzootic or epizootic.[20-22]

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World Health Organization

f. 1948

Pan-American Sanitary Bureau (1902),
Office International d'Hygiène Publique (1907),
Health Organization of the League of Nations (1920).

Public Health Emergency of International Concern (PHEIC)

- The declaration is publicized by an Emergency Committee (EC) made up of international experts operating under the IHR (2005), which was developed following the SARS 2002/2003 outbreak.

1. **SARS** outbreak of 2002/2003
2. the 2009 **H1N1 (or swine flu)** pandemic,
3. the 2014 polio declaration,
4. the 2014 outbreak of **Ebola** in Western Africa,
5. the 2015–16 **Zika** virus epidemic[6] and,
6. as of 17 July 2019, the Kivu **Ebola** epidemic which began in 2018.
7. **SARS-CoV-2** (Mar 2020-May 2023), later becoming pandemic.
8. **Monkeypox** (Jul 2022-May 2023)

Zoonoses:

- **Viruses**
- **Bacteria**
- **Parasites**
- **Fungal**
- **Prion**

World Health Organization | Europe

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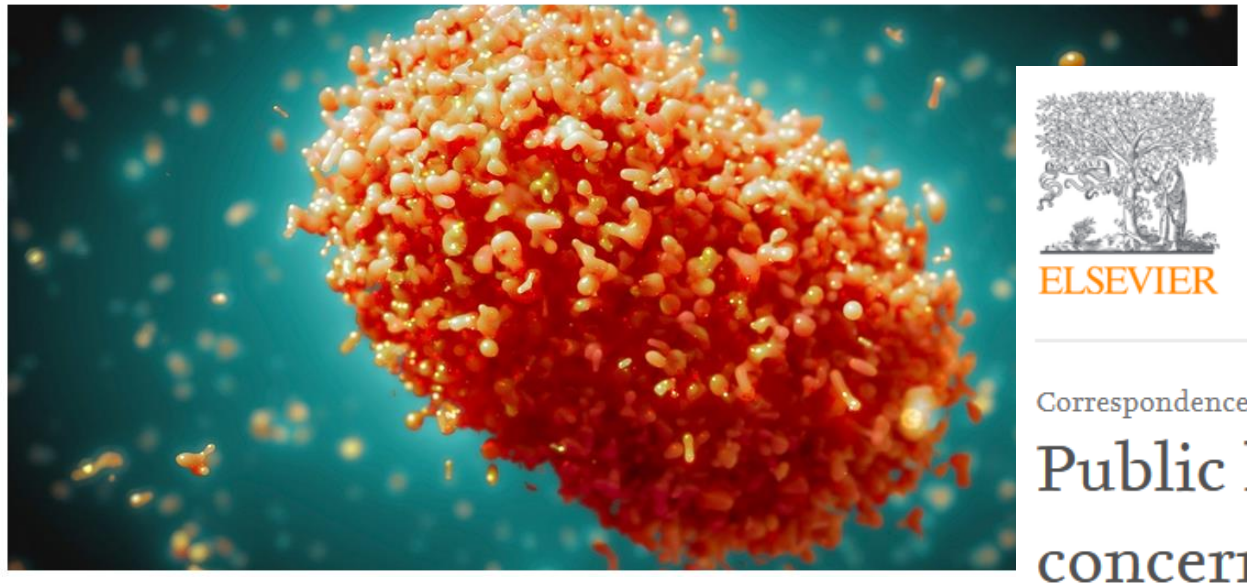
WHO Director-General declares the ongoing monkeypox outbreak a Public Health Emergency of International Concern



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Public health emergencies of international concernin the 21st century

Ranjit Sah ✉, Abdullah Reda ✉, Basant Ismail Lashin ✉, Aroop Mohanty ✉, Abdelaziz Abdelaal ✉, Alfonso J. Rodriguez-Morales ✉

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Le Infezioni in Medicina, n. 1, 3-5, 2020

EDITORIAL

History is repeating itself: Probable zoonotic spillover as the cause of the 2019 novel Coronavirus Epidemic

Alfonso J. Rodriguez-Morales[1,2,3], D. Katterine Bonilla-Aldana[1,4], Graciela Josefina Balbin-Ramon[3,5], Ali A. Rabaan[6], Ranjit Sah[7], Alberto Paniz-Mondolfi[8,9,10], Pasquale Pagliano[11], Silvano Esposito[11]

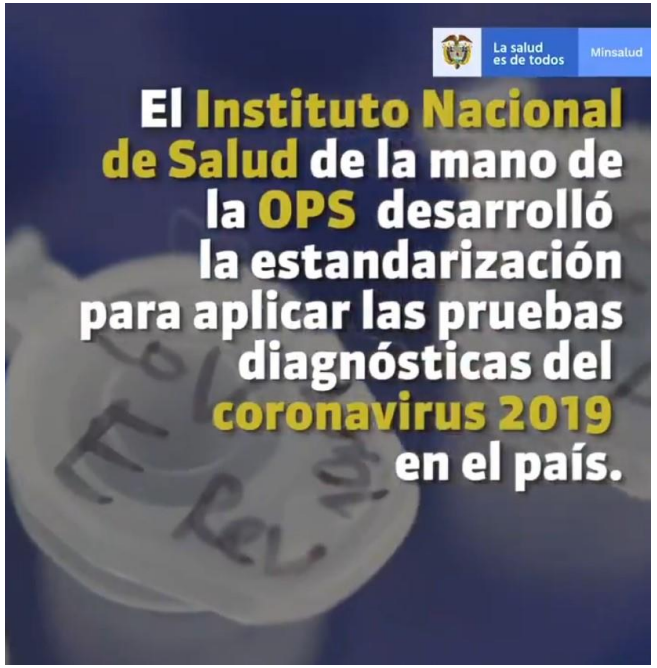
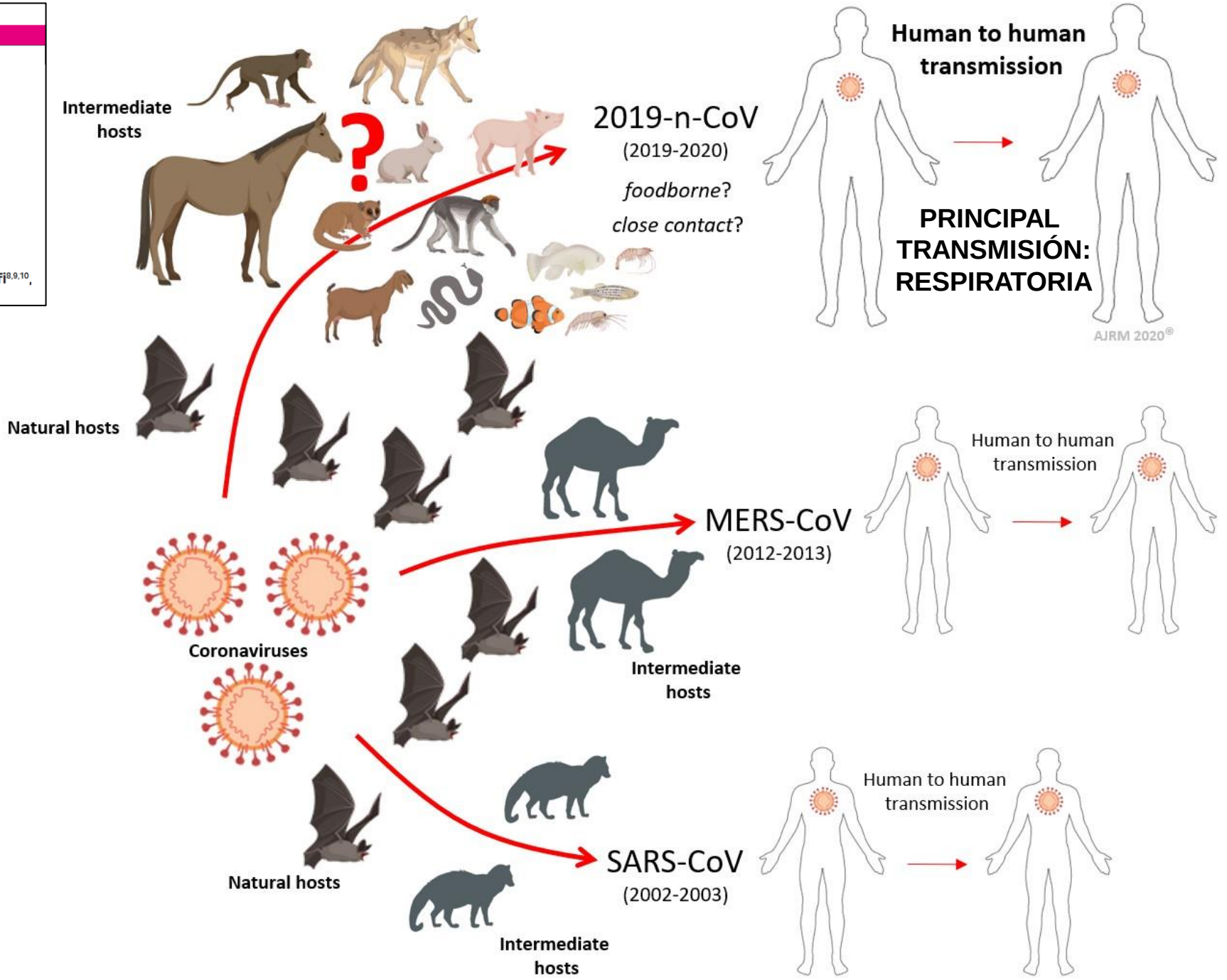


Figure 1 - Potential animal origins of human coronaviruses.



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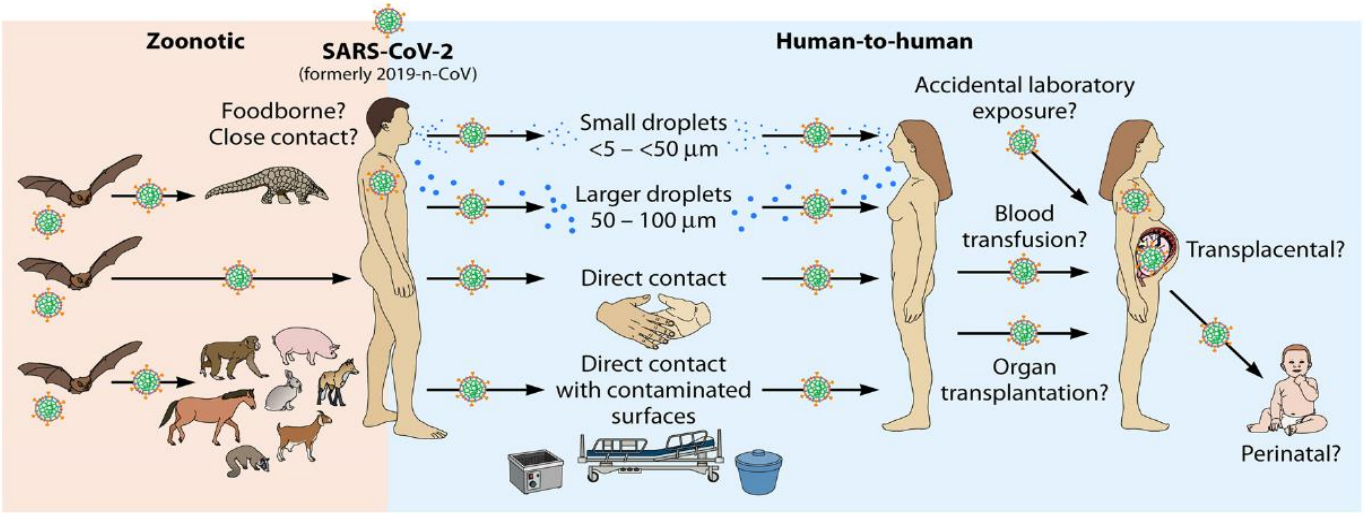


FIG 6 Potential transmission routes for SARS-CoV-2.

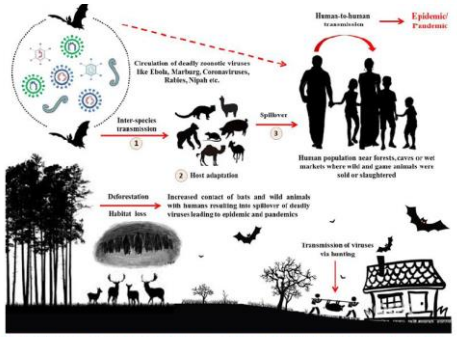


Fig. 1. Bat interactions, selected associated diseases, and the potential spillover to humans in the context of anthropogenic landscape changes and other related environmental and social factors

NEXT PANDEMIC

when?

Climate change

Migration

Deforestation

Contamination

Animal-human

Travel

War

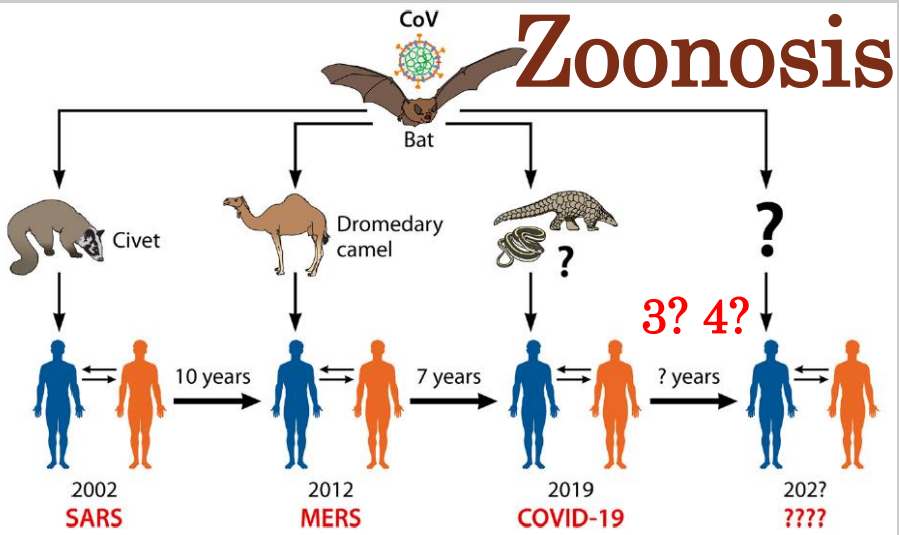
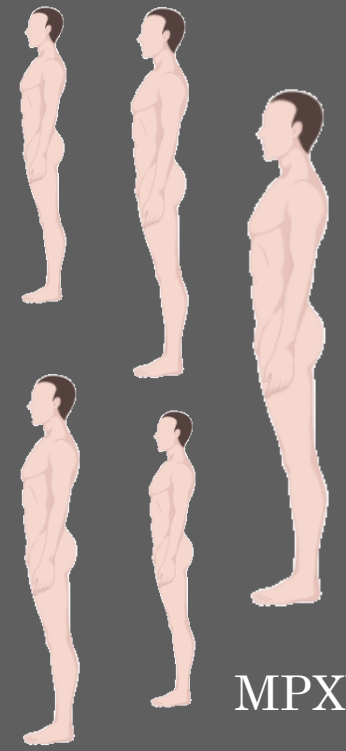


FIG 7 Coronavirus origins. Coronavirus is the most prominent example of an emerging virus that has crossed the species barrier from wild animals to humans, like SARS and MERS. The origin of SARS-CoV-2 is also suspected to be from an intermediate animal host. The possibility of crossing the species barrier again for the fourth time cannot be ruled out.

Bonilla-Aldana DK, Jimenez-Diaz SD, Patel SK, Dhama K, Rabaan AA, Sah R, Sierra M, Zambrano LI, Arteaga-Livias K, **Rodriguez-Morales AJ. Importance of Bats in Wildlife: Not Just Carriers of Pandemic SARS-CoV-2 and Other Viruses**. *J Pure Appl Microbiol* 2020 May, 14(Suppl 1):709-712. doi: 10.22207/JPAM.14.SPL1.05

SARS-CoV-2

MERS-CoV



MPXV

Cocirculation

Coinfections

Adenovirus

Hepatitis?

Dhama K, Sharun K, Tiwari R, Sircar S, Bhat S, Malik YS, Singh KP, Chaicumpa W, **Bonilla-Aldana DK, Rodriguez-Morales AJ. Coronavirus Disease 2019 – COVID-19.** *Clin Microbiol Rev* 2020; 33(4):e00028-20. https://doi.org/10.1128/CMR.00028-20

Editorial > Travel Med Infect Dis. 2023 Jun 8;54:102606. doi: 10.1016/j.tmaid.2023.102606.
Online ahead of print.

The global challenges of the long COVID-19 in adults and children

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Affiliations + expand

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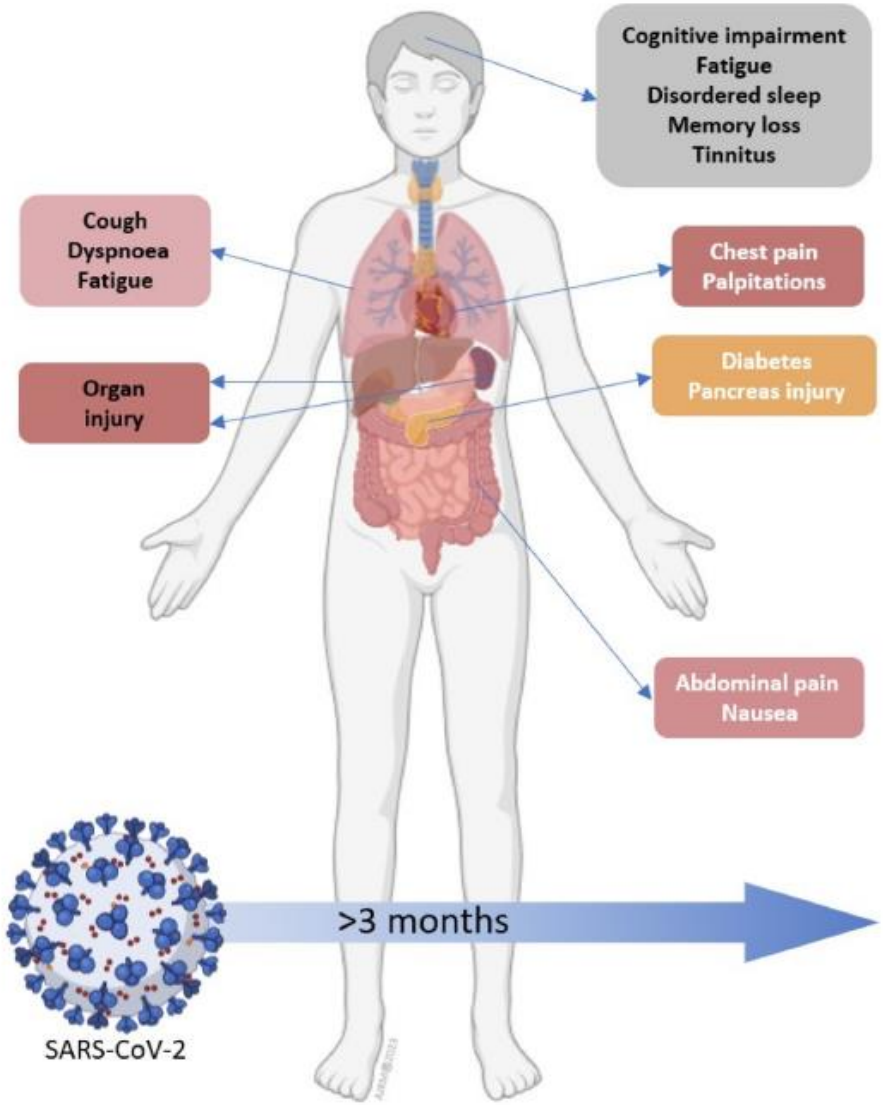

Fig. 1. Some of the clinical findings associated with long COVID-19, modified from Davis et al. [63].

A.J. Rodriguez-Morales et al. Travel Medicine and Infectious Disease 54 (2023) 102606

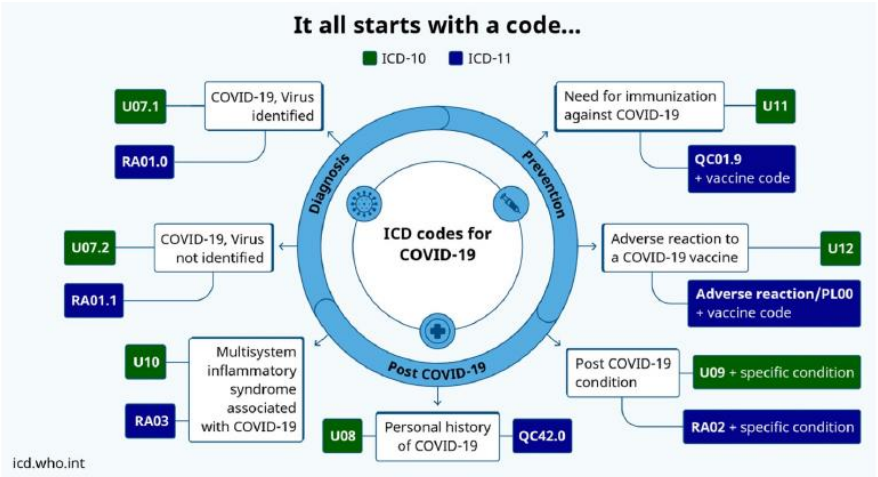

Fig. 2. ICD codes for COVID-19, according the WHO (https://www.who.int/standards/classifications/classification-of-diseases/emergency-use-icd-codes-for-covid-19-disease-outbreak).

Rodriguez-Morales AJ, Lopez-Echeverri MC, Perez-Raga MF, Quintero-Romero V, Valencia-Gallego V, Galindo-Herrera N, López-Alzate S, Sánchez-Vinasco JD, Gutiérrez-Vargas JJ, Mayta-Tristan P, Husni R, Moghnieh R, Stephan J, Faour W, Tawil S, Barakat H, Chaaban T, Megarbane A, Rizk Y, Sakr R, Escalera-Antezana JP, Alvarado-Arnez LE, Bonilla-Aldana DK, Camacho-Moreno G, Mendoza H, Rodriguez-Sabogal IA, Millán-Oñate J, Lopardo G, Barbosa AN, Cimerman S, Chaves TDSS, Orduna T, Lloveras S, Rodriguez-Morales AG, Thormann M, Zambrano PG, Perez C, Sandoval N, Zambrano L, Alvarez-Moreno CA, Chacon-Cruz E, Villamil-Gomez WE, Benites-Zapata V, Savio-Larriera E, Cardona-Ospina JA, Risquez A, Forero-Peña DA, Henao-Martínez AF, Sah R, Barboza JJ, León-Figueroa DA, Acosta-España JD, Carrero-Gonzalez CM, Al-Tawfiq JA, Rabaan AA, Leblebicioglu H, Gonzales-Zamora JA, Ulloa-Gutiérrez R. The global challenges of the long COVID-19 in adults and children. Travel Med Infect Dis. 2023 Jun 8;54:102606. doi: 10.1016/j.tmaid.2023.102606. Epub ahead of print. PMID: 37295581; PMCID: PMC10247301.

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Annals of Clinical Microbiology and Antimicrobials

EDITORIAL Open Access

Monkeypox outbreaks during COVID-19 pandemic: are we looking at an independent phenomenon or an overlapping pandemic?

Ramadan Abdelmoez Farahat[1*], Abdelaziz Abdelaal[2,3], Jaffer Shah[4,5], Sherief Ghozy[6,7], Ranjit Sah[8], D. Katterine Bonilla-Aldana[9,10], Alfonso J. Rodriguez-Morales[9,11,12,13*], Timothy D. McHugh[14] and Hakan Leblebicioglu[15]

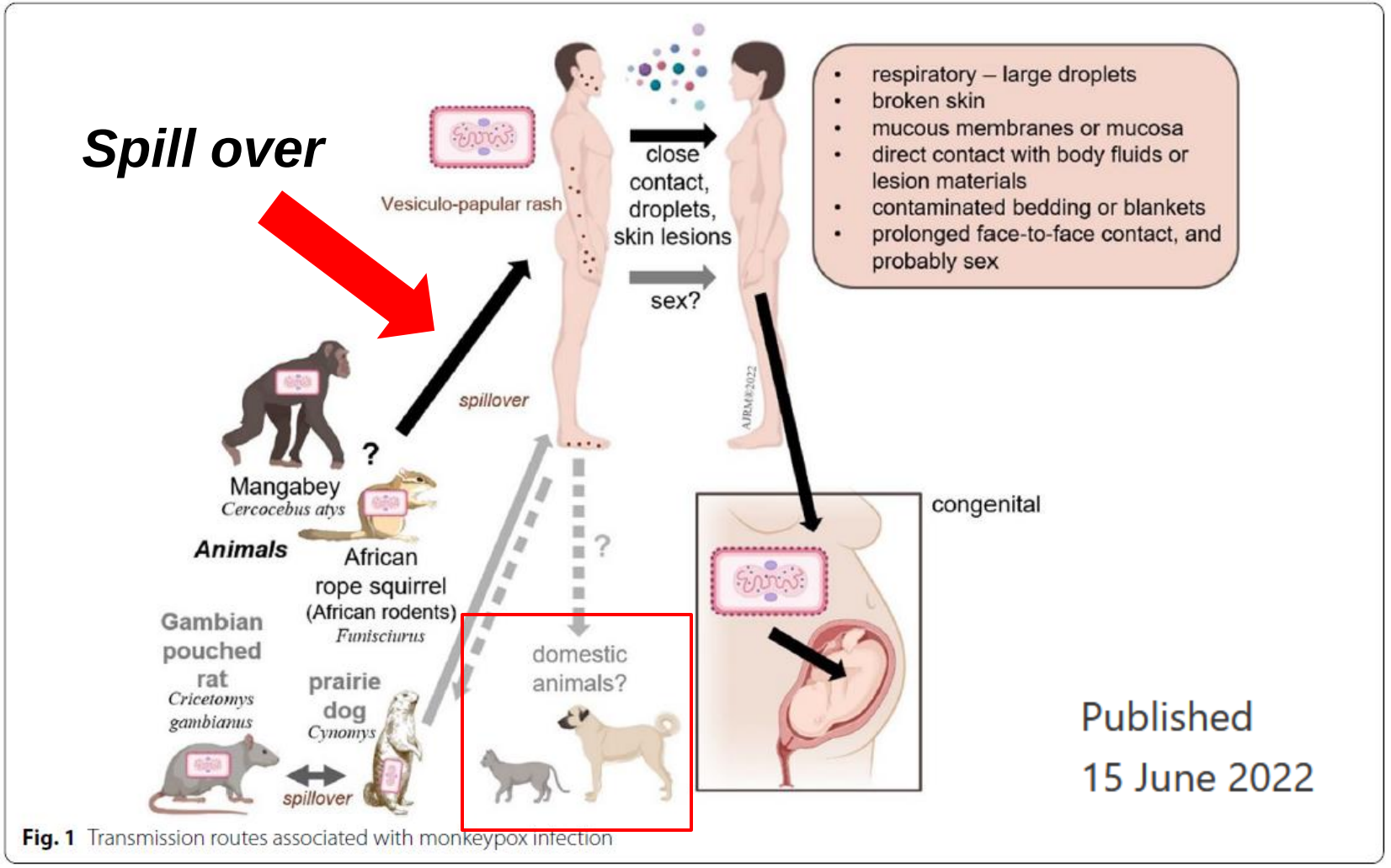

Fig. 1 Transmission routes associated with monkeypox infection

Evidence of human-to-dog transmission of monkeypox virus

Human monkeypox virus is spreading in Europe and the USA among individuals who have not travelled to endemic areas.[1] On July 23, 2022, monkeypox was declared a Public Health Emergency of International Concern by WHO Director-General Tedros Adhanom Ghebreyesus.[2] Human-to-human transmission of monkeypox virus usually occurs through close contact with the lesions, body fluids, and respiratory droplets of infected people or animals.[3] The possibility of sexual transmission is being investigated, as the current outbreak appears to be concentrated in men who have sex with men and has been associated with unexpected anal and genital lesions.[3,4] Whether domesticated cats and dogs could be a vector for monkeypox virus is unknown. Here we describe the first case of a dog with confirmed monkeypox virus infection that might have been acquired through human transmission.

Two men who have sex with men attended Pitié-Salpêtrière Hospital, Paris, France, on June 10, 2022 (appendix). One man (referred to as patient 1 going forward) is Latino, aged 44 years, and lives with HIV with undetectable viral loads on antiretrovirals; the second man (patient 2) is White, aged 27 years, and HIV-negative. The men are non-exclusive partners living in the same household. They each signed a consent form for the use of their clinical and biological data, and for the publication of anonymised photographs. The men had presented with anal ulceration 6 days after sex with other partners. In patient 1, anal ulceration was followed by a vesiculopustular rash on the face, ears, and legs; in patient 2, on the legs and back. In both cases, rash was associated with asthenia, headaches, and fever 4 days later (figure A, B).

Monkeypox virus was assayed by real-time PCR (LightCycler 480 System; Roche Diagnostics, Meylan, France). In patient 1, virus was detected in skin and oropharynx samples; whereas in patient 2, virus was detected in anal and oropharynx samples.

12 days after symptom onset, their male Italian greyhound, aged 4 years and with no previous medical disorders, presented with mucocutaneous lesions, including abdomen pustules and a thin anal ulceration (figure C, D; appendix). The dog tested positive for monkeypox virus by use of a PCR protocol adapted from Li and colleagues[5] that involved scraping skin lesions and swabbing the anus and oral cavity. Monkeypox virus DNA sequences from the dog and patient 1 were compared by next-generation sequencing (MinION; Oxford Nanopore Technologies, Oxford, UK). Both samples contained virus of the hMPXV-1 clade, lineage B.1, which has been spreading in non-endemic countries since April, 2022, and, as of Aug 4, 2022, has infected more than 1700 people in France, mostly concentrated in Paris, where the dog first developed symptoms. Moreover, the virus that infected patient 1 and the virus that infected the dog showed 100% sequence homology on the 19·5 kilobase pairs sequenced.

The men reported co-sleeping with their dog. They had been careful to prevent their dog from contact with other pets or humans from the onset of their own symptoms (ie, 13 days before the dog started to present cutaneous manifestations).

In endemic countries, only wild animals (rodents and primates) have been found to carry monkeypox virus.[6] However, transmission of monkeypox virus in prairie dogs has been described

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See Online for appendix

For monkeypox cases in France see https://www.santepubliquefrance.fr/les-actualites/2022/cas-de-variole-du-singe-point-de-situation-au-4-aout-2022

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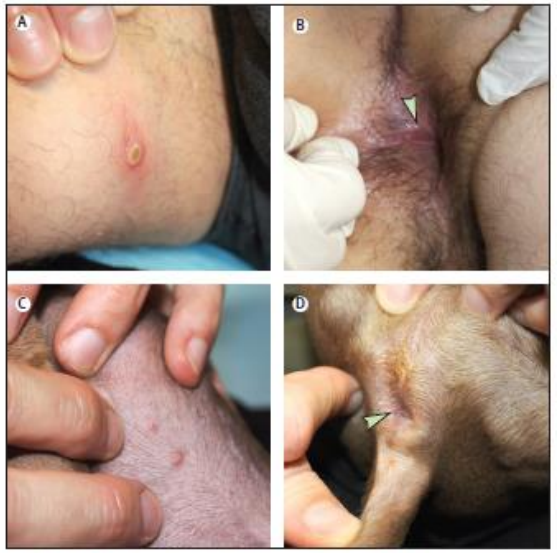
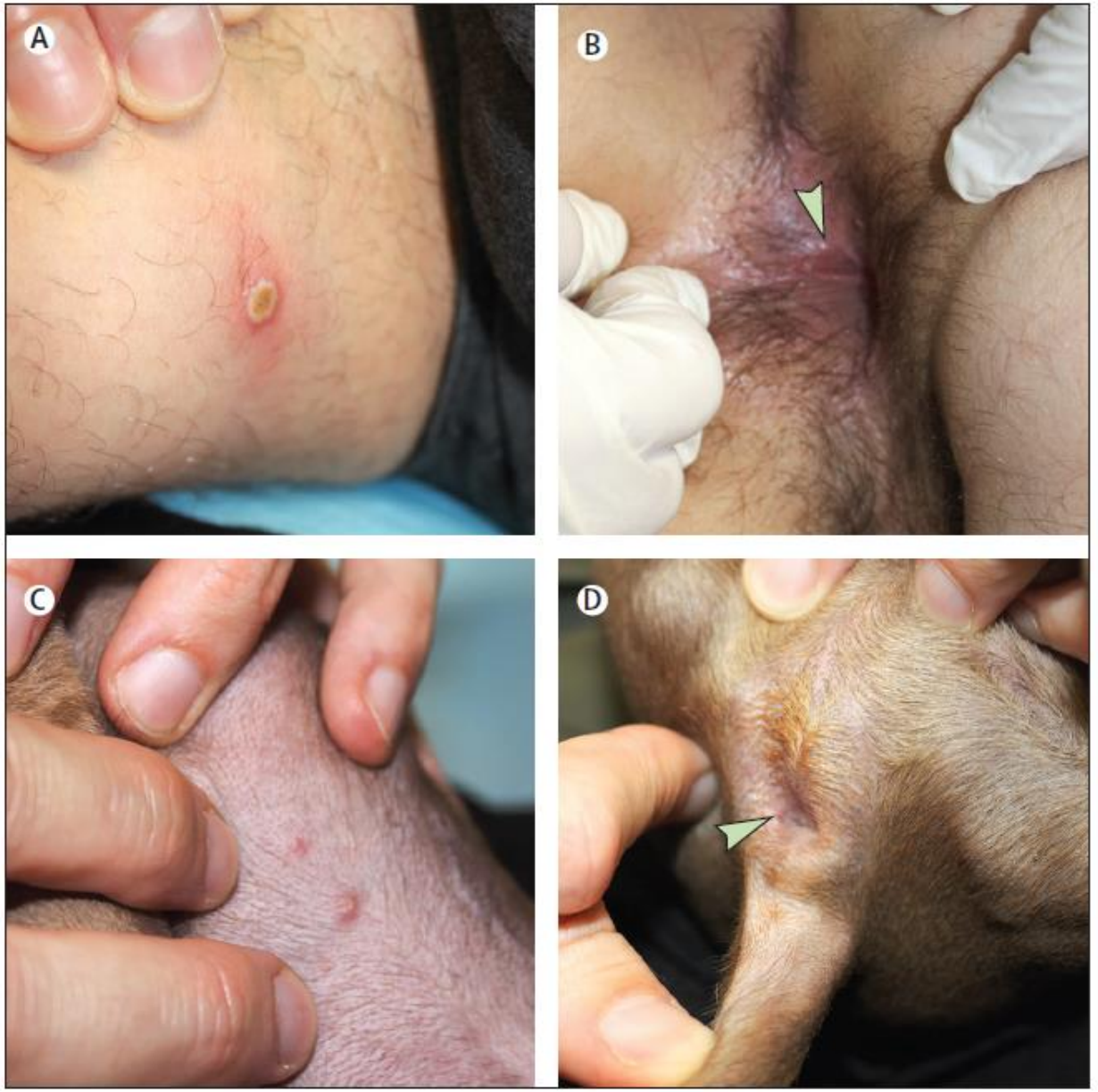


Figure: Skin and mucosal lesions in two male patients and their dog with confirmed monkeypox virus
(A) Pustular lesion of the thigh, with central umbilication and the onset of necrosis, in patient 1. (B) Erosive and pustular anal lesions in patient 2. (C) Two slightly crusty erythematous papules in the dog. (D) Millimetric erosive anal lesion in the dog.



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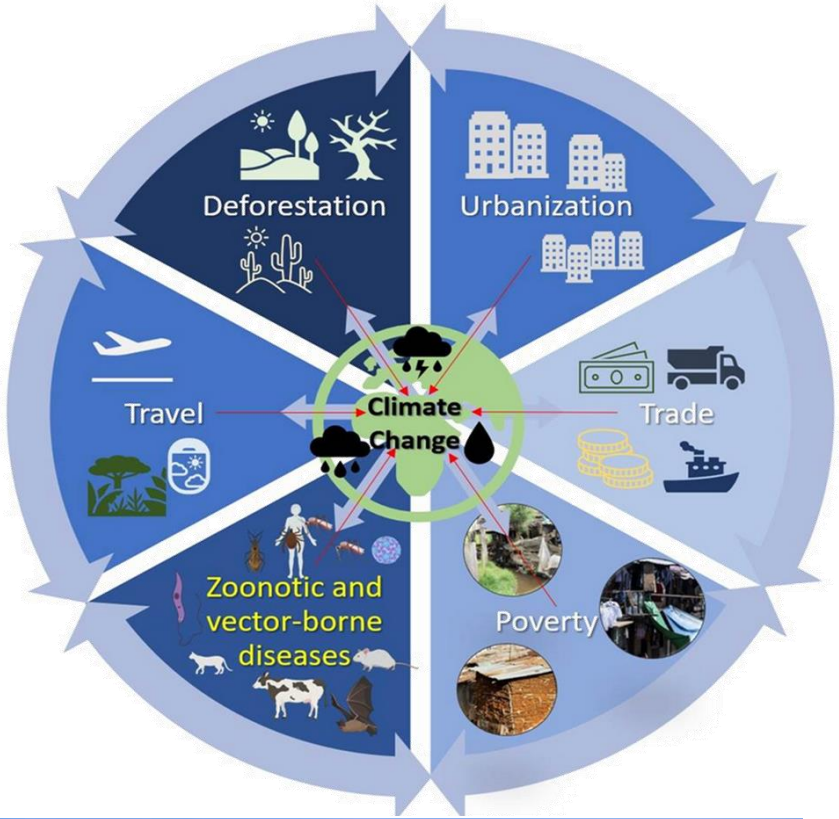
Bonilla-Aldana DK, Faccini-Martínez ÁA, Vallejo-Timaran DA, Bocanegra-Viteri FdeM, Ruiz-Saenz J, Paniz-Mondolfi AE, Rodriguez-Morales AJ, and Suárez JA (2021).

The Grass Was Greener - Climate Change, One Health, and the High Hopes to Mitigate COVID-19, Avian Influenza, and other Zoonotic Emerging Diseases.

World Vet. J., 11 (2): 313-316.



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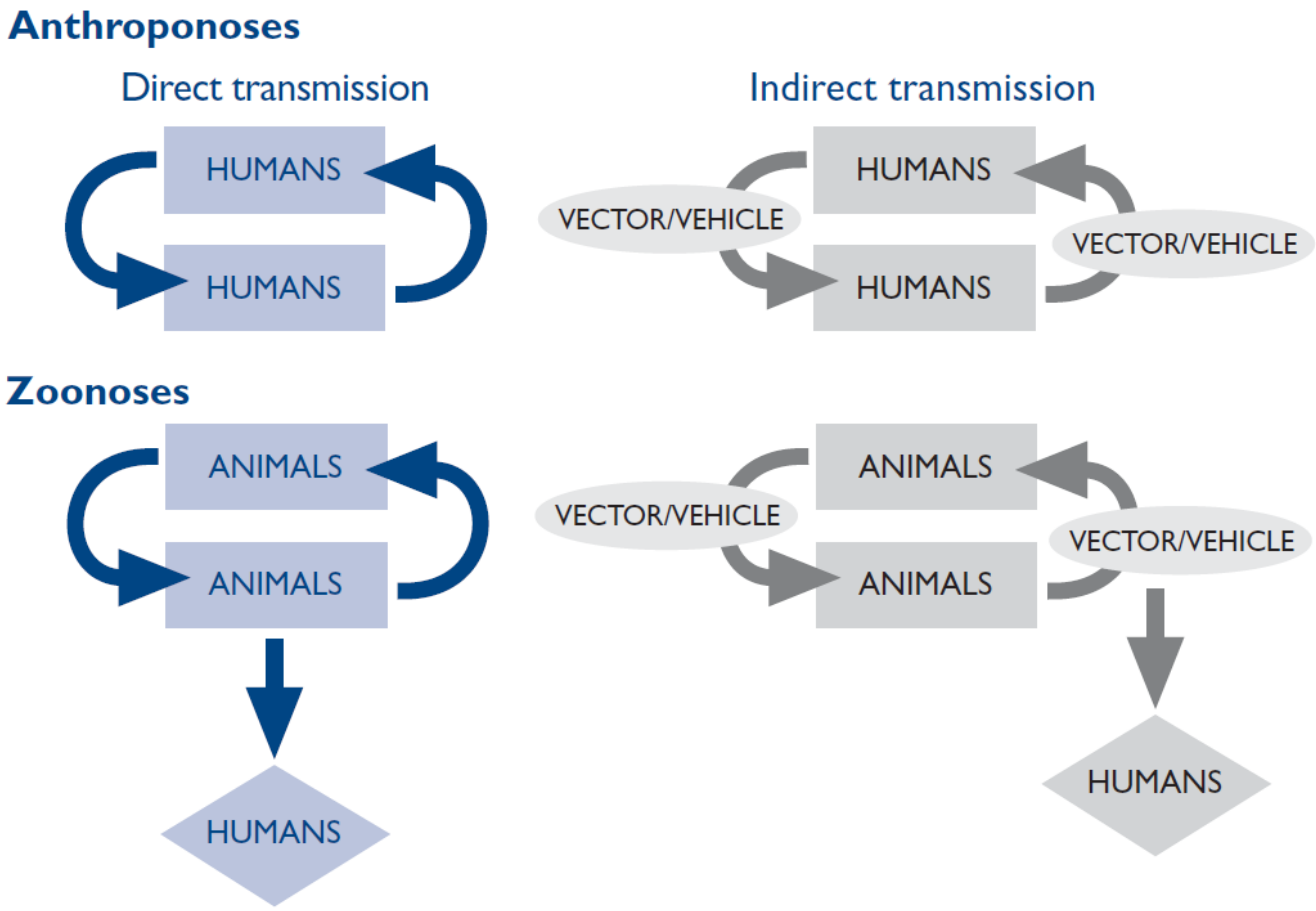
Cambio Climático y Enfermedades Infecciosas



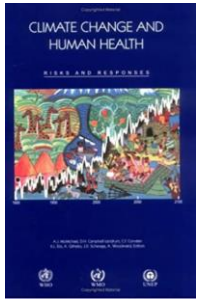


FIGURE 6.1 Four main types of transmission cycle for infectious diseases.

Source: reproduced from reference 3.

OPEN ACCESS
Advances in Animal and Veterinary Sciences

Editorial

Revisiting the One Health Approach in the Context of COVID-19: A Look into the Ecology of this Emerging Disease

D. Katterine Bonilla-Aldana[1,2], Kuldeep Dhama[3], Alfonso J. Rodriguez-Morales[2,4*]

[1]Incubator in Zoonosis (SIZOO), Biodiversity and Ecosystem Conservation Research Group (BIOECOS), Fundación Universitaria Autónoma de las Américas, Sede Pereira, Pereira, Risaralda, Colombia.; [2]Public Health and Infection Research Group, Faculty of Health Sciences, Universidad Tecnológica de Pereira, Pereira, Risaralda, Colombia; [3]Division of Pathology, ICAR-Indian Veterinary Research Institute, Izatnagar 243 122, Bareilly, Uttar Pradesh, India; [4]Grupo de Investigación Biomedicina, Faculty of Medicine, Fundación Universitaria Autónoma de las Américas, Pereira, Risaralda, Colombia.

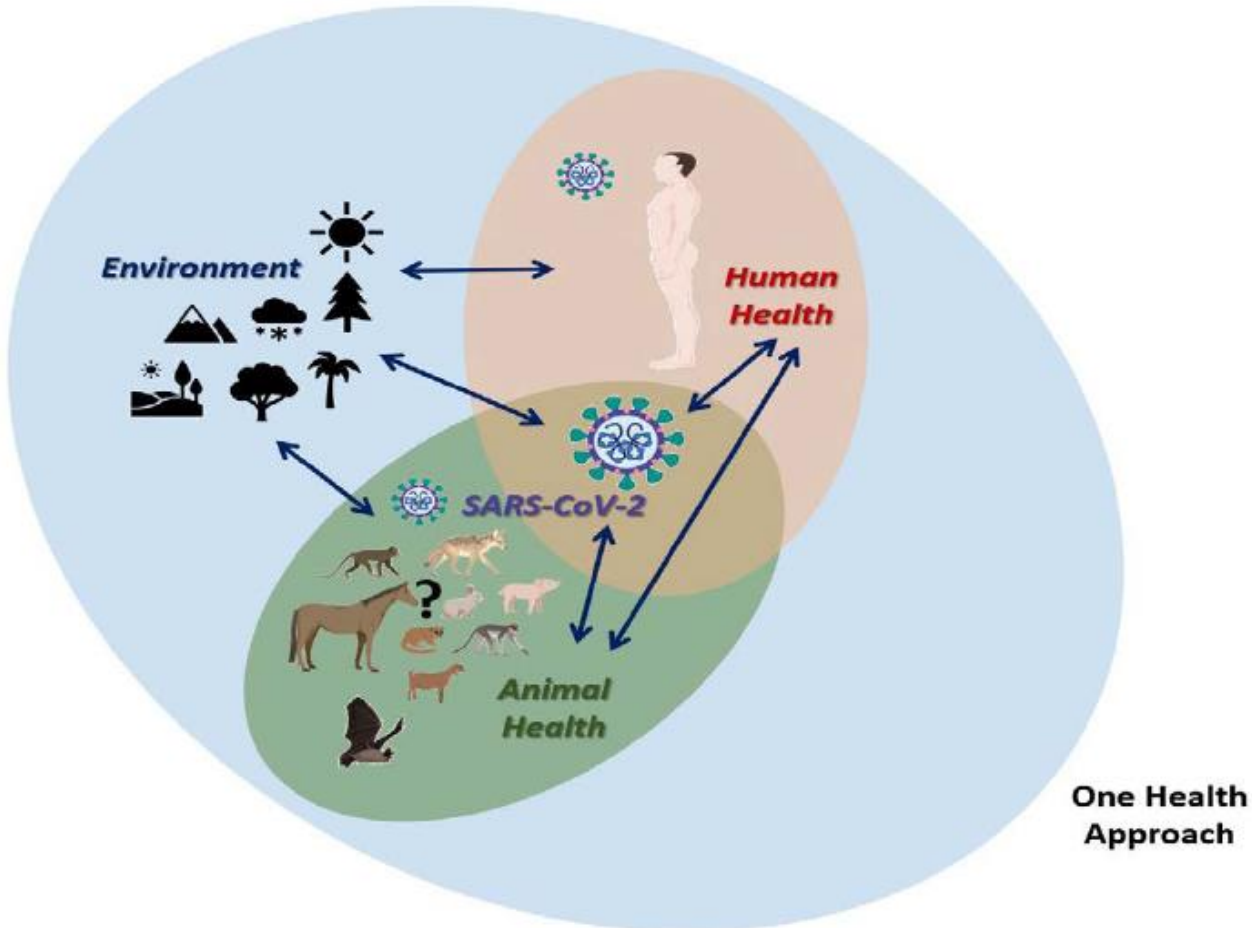


Figure 1: One health approach in the context of coronavirus disease 2019 (COVID-19) caused by the SARS-CoV-2.

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Una Sola Salud

Salud Humana

Salud Ambiental

Salud Animal

Centers for Disease Control and Prevention
National Center for Emerging and Zoonotic Infectious Diseases

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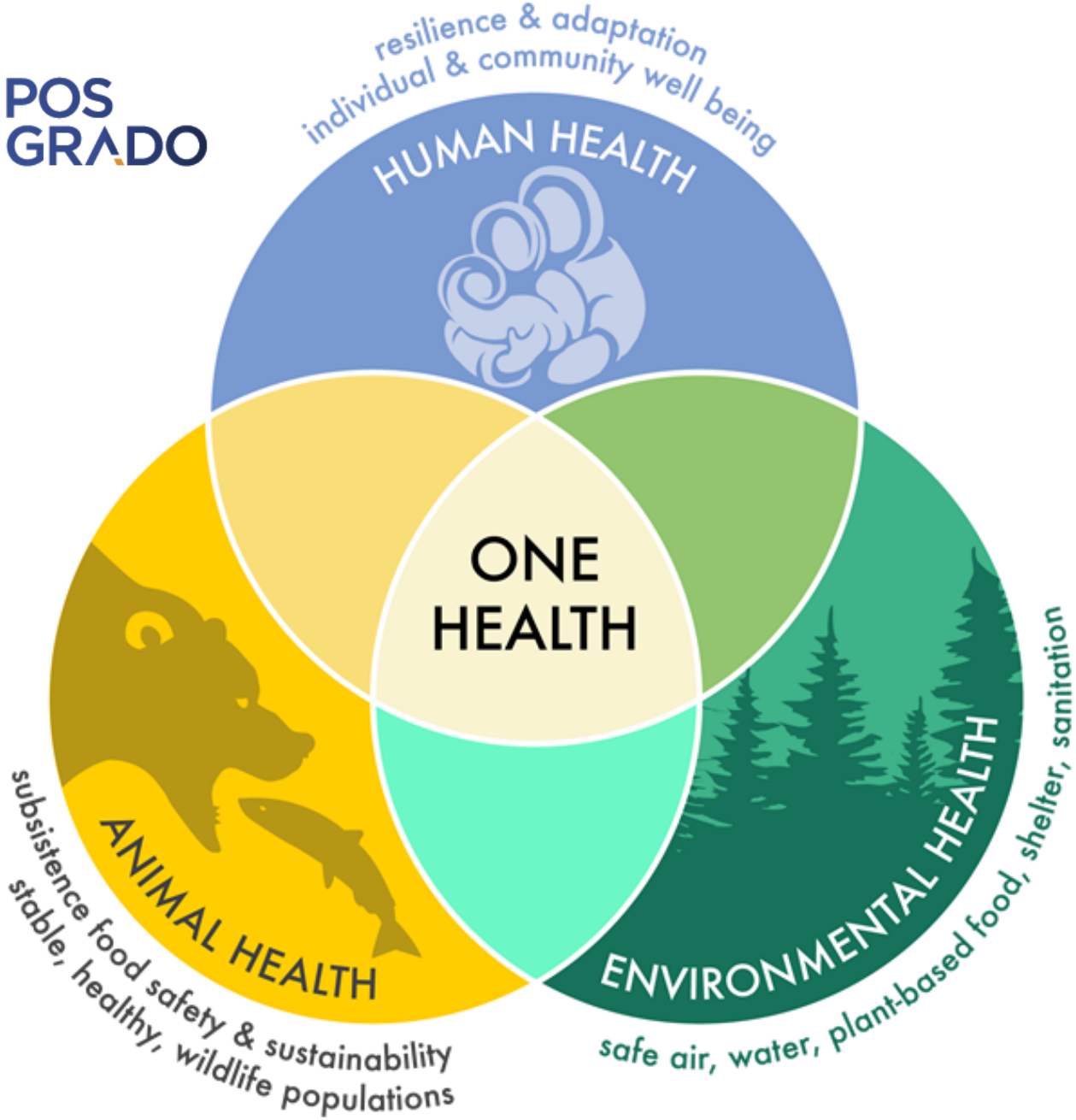

CDC Centers for Disease Control and Prevention
National Center for Emerging and Zoonotic Infectious Diseases

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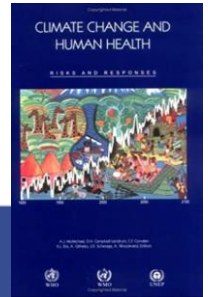
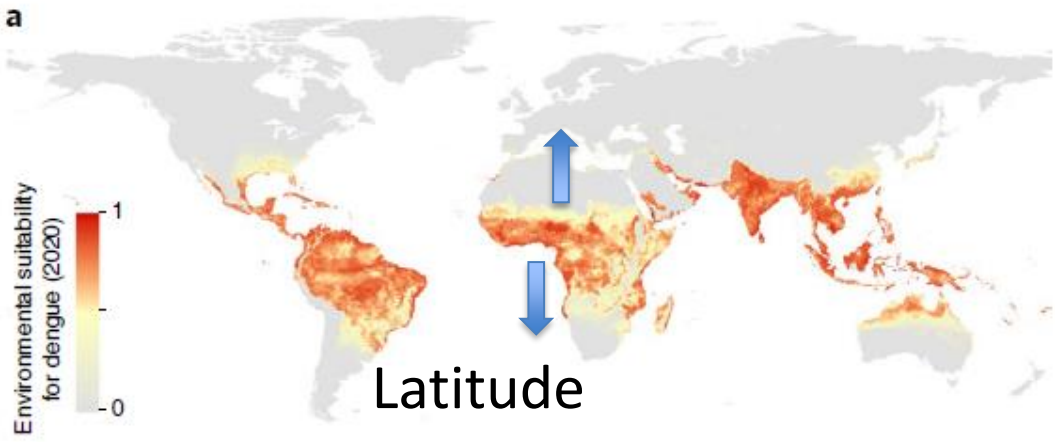
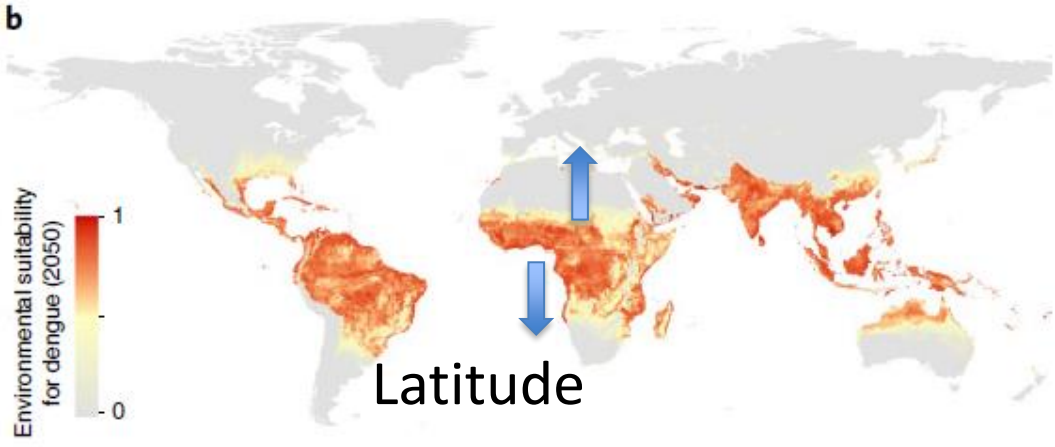
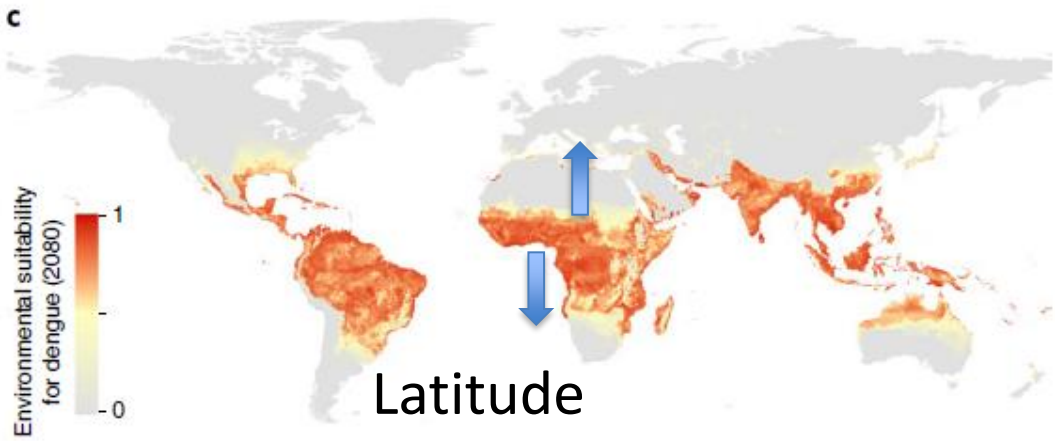
Pathogen

- decreased incubation period of pathogens at higher temperatures
- changes in transmission season
- **changes in distribution**









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frontiers in PHYSIOLOGY
REVIEW ARTICLE
published: 02 August 2012
doi: 10.3389/fphys.2012.00315

Malaria in East African highlands during the past 30 years: impact of environmental changes

Yousif E. Himeidan[1]* *and Eliningaya J. Kweka*[2]

[1] Entomology Unit, Faculty of Agriculture and Natural Resources, University of Kassala, New Halfa, Sudan
[2] Mosquito Section, Division of Livestock and Human Health Vector Control, Tropical Pesticides Research Institute, Arusha, Tanzania

Pathogen

- decreased incubation period of pathogens at higher temperatures
- changes in transmission season
- **changes in distribution**

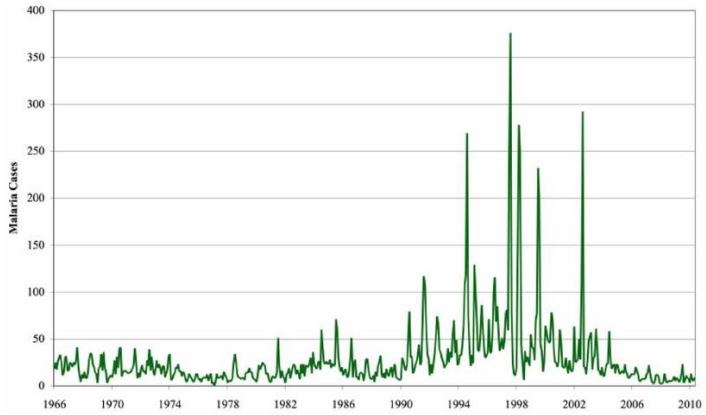
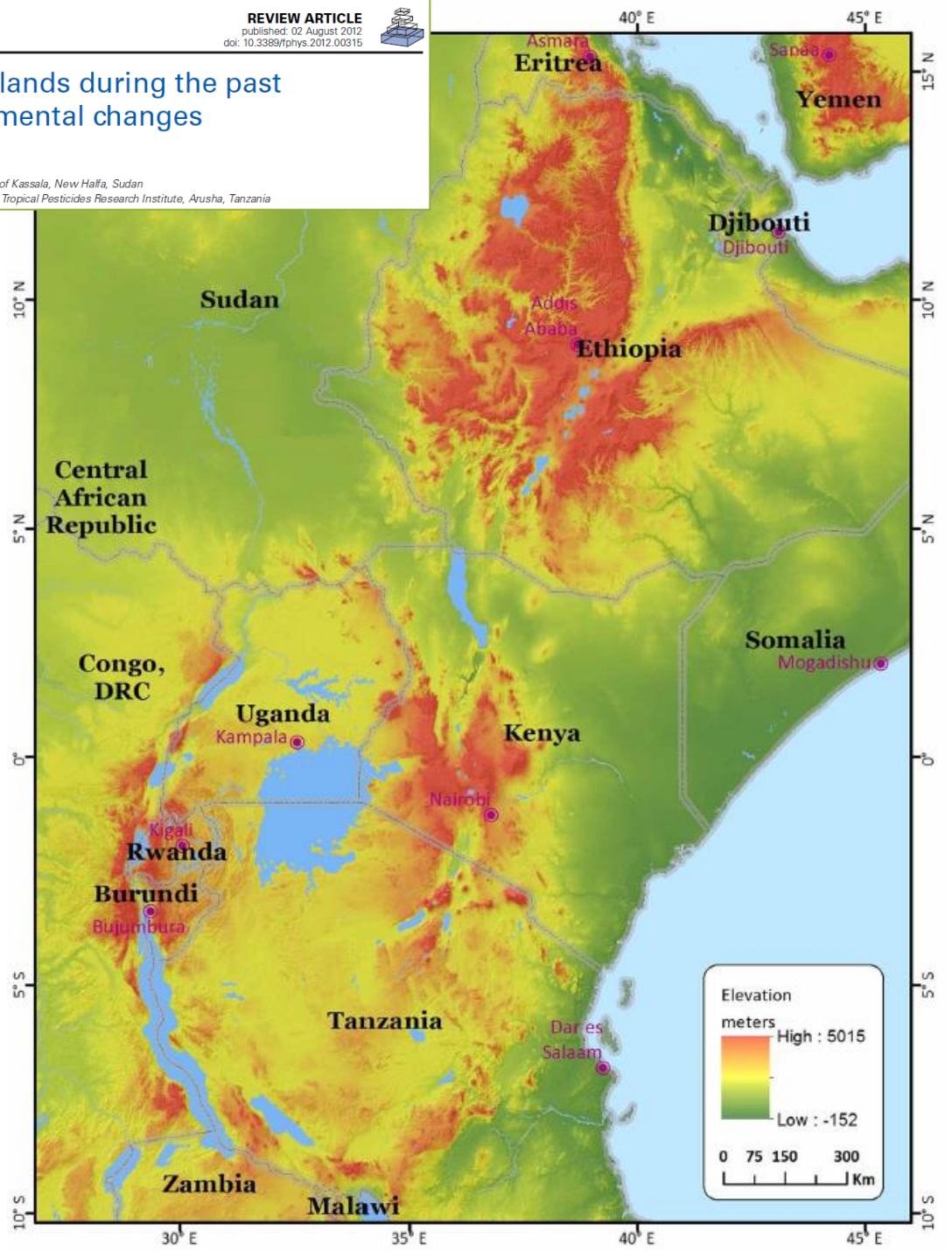


FIGURE 2 | Monthly malaria cases at Kericho Unilever Tea Kenya Ltd. Hospital. Source: Stern et al. (2011), with permission from Dr. David I. Stern, Crawford School of Economics and Government, Australian National University.



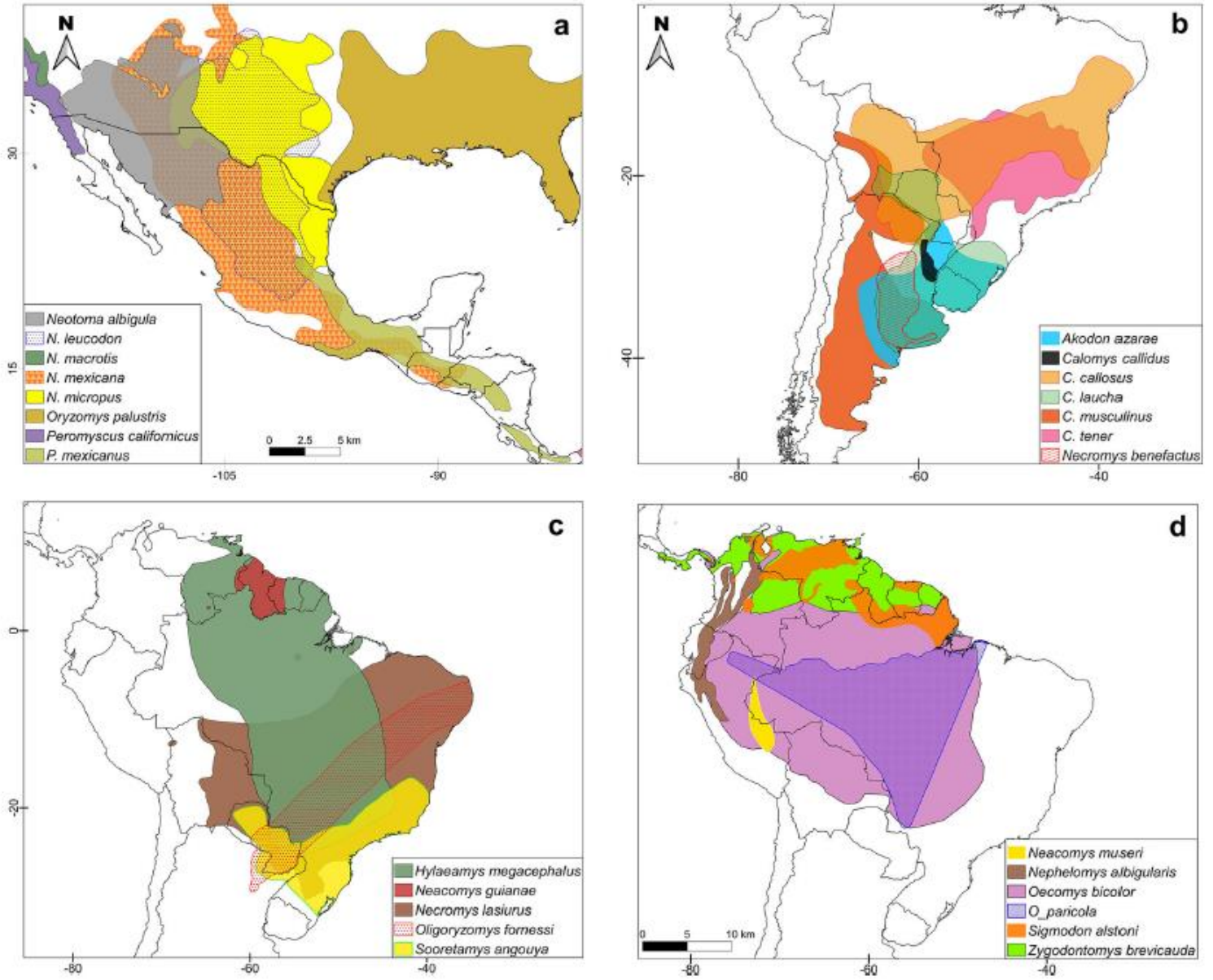


Figure 1. Geographic distributions of rodent reservoir species of mammarenaviruses in the Americas: **a** North America, **b**, **c** & **d** South America Source of data distributions: IUCN (2020).

Tapia-Ramírez G, Lorenzo C, Navarrete D, Carrillo-Reyes A, Retana Ó, Carrasco-Hernández R. A Review of Mammarenaviruses and Rodent Reservoirs in the Americas. Ecohealth. 2022 Mar;19(1):22-39. doi: 10.1007/s10393-022-01580-0. Epub 2022 Mar 5. PMID: 35247117; PMCID: PMC9090702.

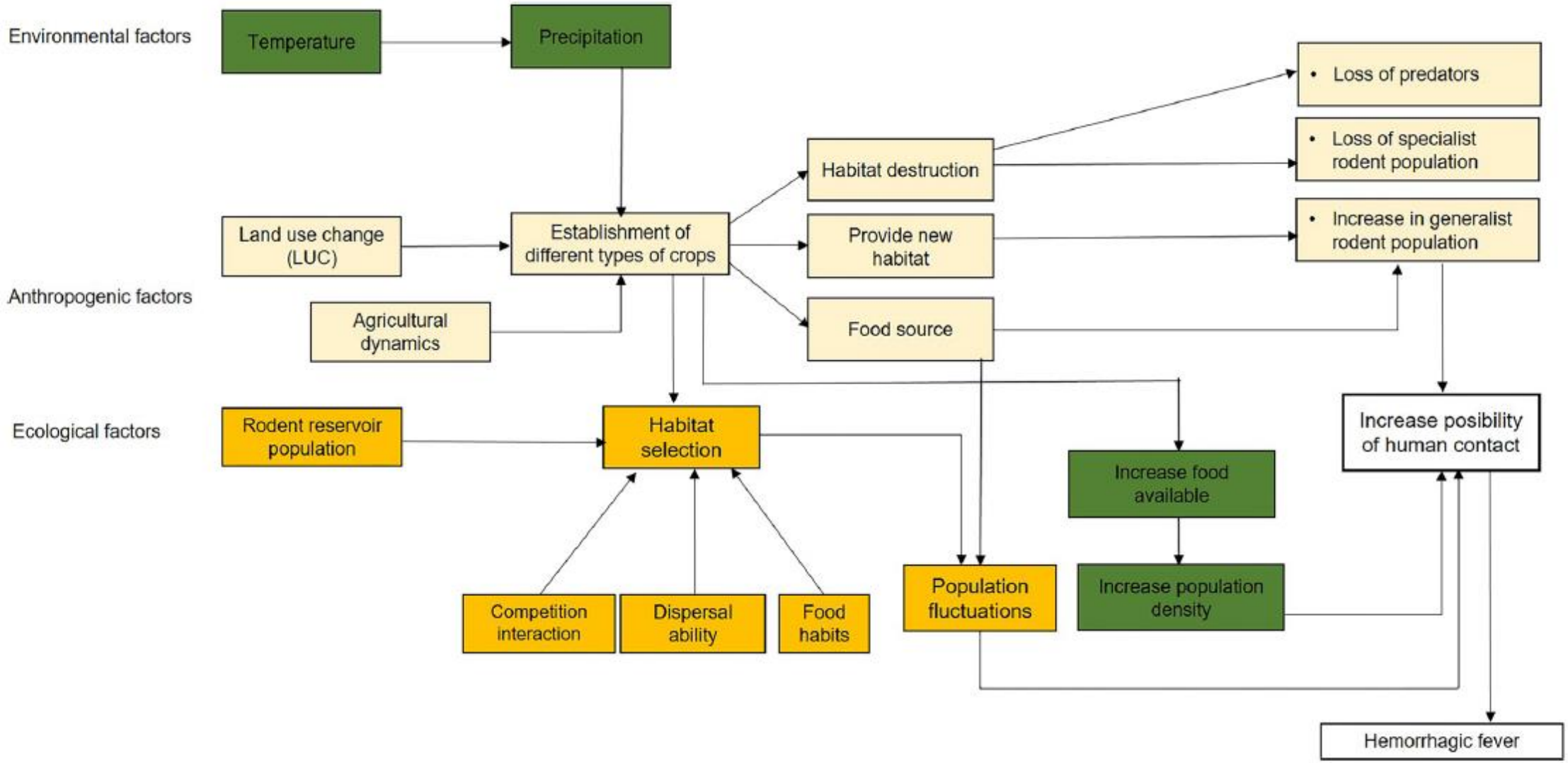
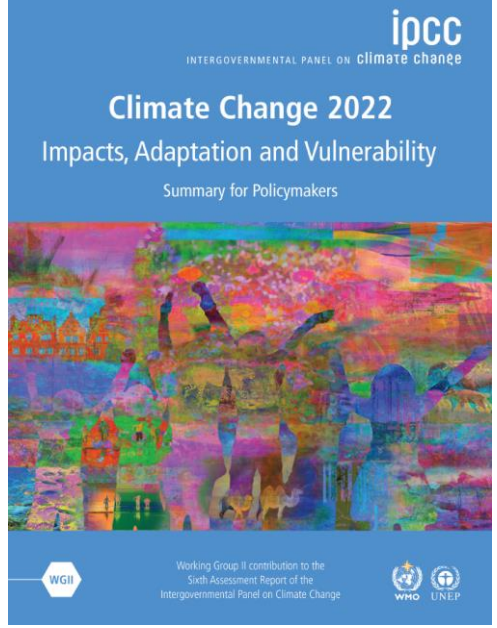


Figure 5. Conceptual model of ecology of rodent reservoirs of mammarenaviruses and their relationship with conservation of virus and transmission of it.

AIV

Contributors to the Working Group II Contribution to the IPCC Sixth Assessment Report



Annex IV

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Russian Federation

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Indian Instiute for Human Settlements
India

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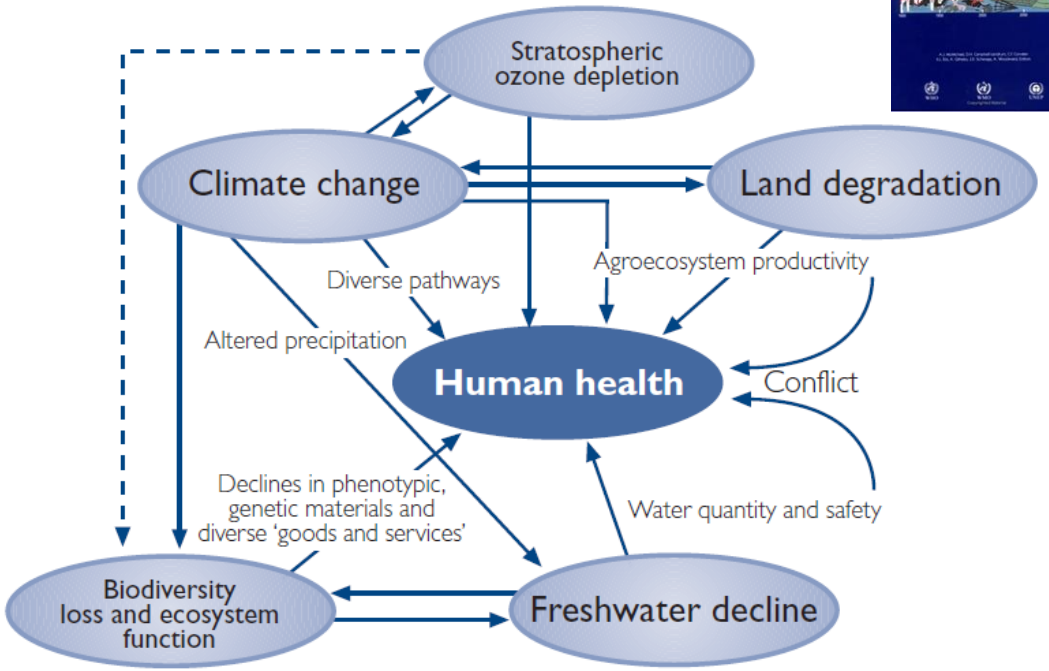
Philippines/USA

ROGELJ, Joeri
Imperial College London/International Institute for Applied Systems Analysis
UK

ROHIT, Sharma
University of Cambridge
India



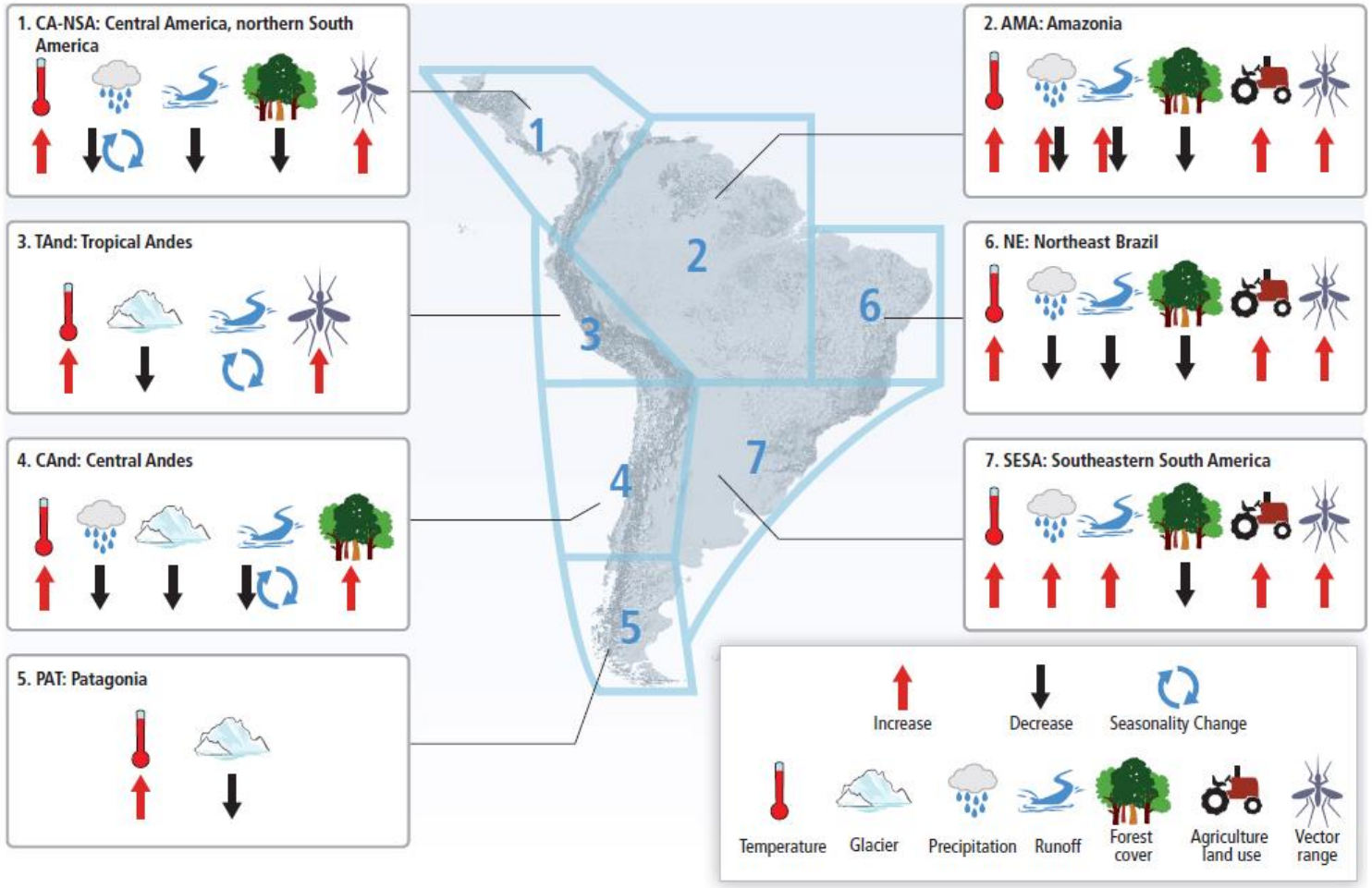


Figure 27-7 | Summary of observed changes in climate and other environmental factors in representative regions of Central and South America. The boundaries of the regions in the map are conceptual (neither geographic nor political precision). Information and references to changes provided are presented in different sections of the chapter.

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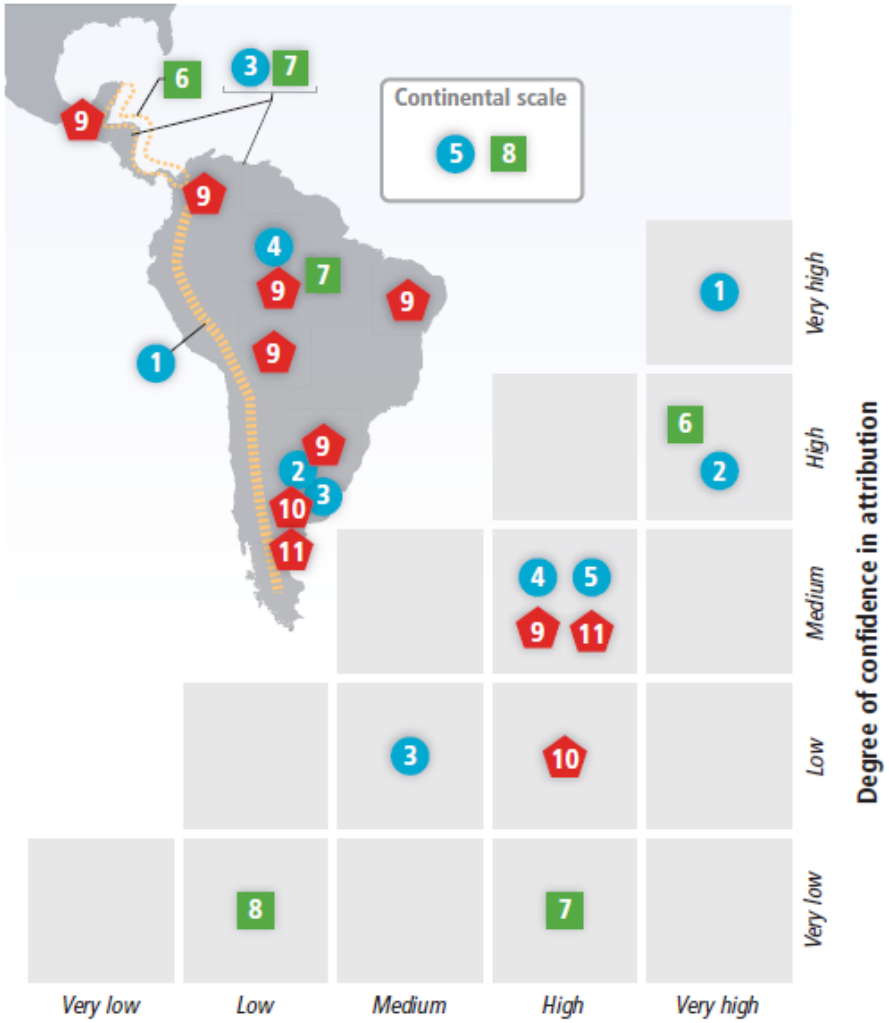

Physical systems

1. Glacier retreat in the Andes in South America (Section 27.3.1.1)
2. Streamflow increase La Plata Basin (Section 27.3.1.1)
3. Increase in heavy precipitation and in risk of land slides and flooding in southeastern South America, and in Central America and northern South America (Section 27.3.1.1)
4. Changes in extreme flows in Amazon River (Section 27.3.1.1)
5. Coastal erosion and other physical sea level impacts (Section 27.3.2.1)

Biological systems

6. Bleaching of coral reefs in western Caribbean and coast of Central America (Section 27.3.2.1)
7. Degrading and receding rainforest in Amazonia and in Central America and northern South America (Section 27.3.2.1)
8. Reduction in fisheries stock (Section 27.3.4.1)

Human and managed systems

9. Increase in frequency and extension of dengue fever and malaria (Section 27.3.7.1)
10. Increases in agricultural yield in southeastern South America (Section 27.3.4.1)
11. Shifting in agricultural zoning (Section 27.3.4.1)

Figure 27-8 | Observed impacts of climate variations and attribution of causes to climate change in Central and South America.

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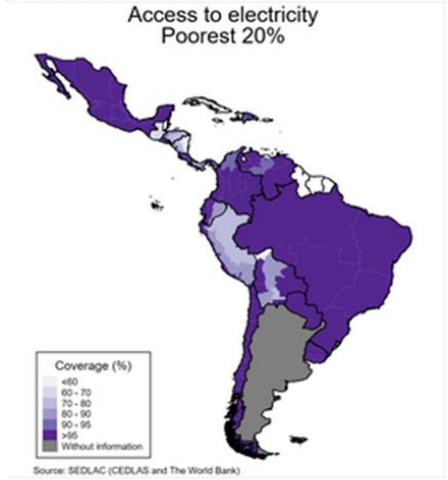
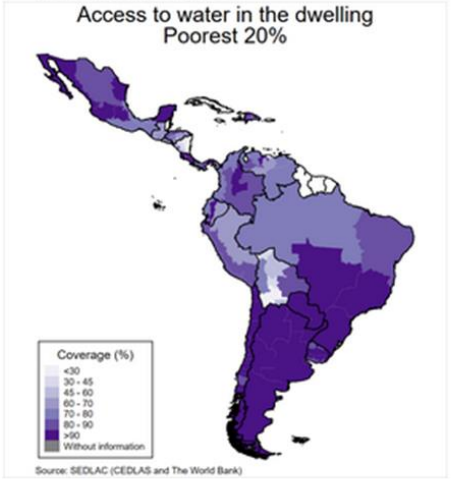
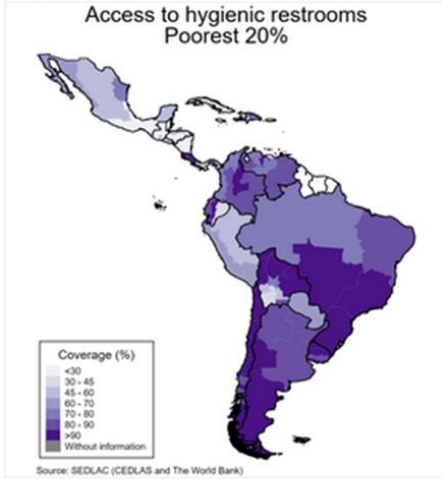
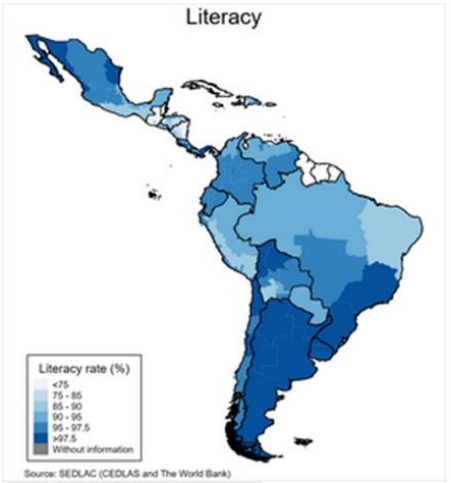
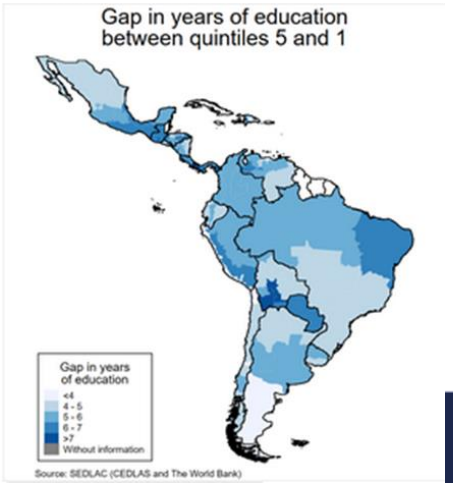
Social conditions











CEDLAS 70 AÑOS FCE FACULTAD DE CIENCIAS ECONÓMICAS UNIVERSIDAD NACIONAL DE LA PLATA

"Source: SEDLAC (CEDLAS and The World Bank)" or "Source: Socio-Economic Database for Latin America and the Caribbean (CEDLAS and The World Bank).

Latest update: December 2022

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Health and Migration Programme

The Health and Migration Programme brings together WHO's technical departments, regional and country offices, as well as partners, to secure the health rights of refugees and migrants and achieve universal health coverage.

THE LANCET
Global Health

COMMENT | VOLUME 11, ISSUE 8, E1165-E1167, AUGUST 2023 Download Full Issue

A call to action: the global failure to effectively tackle maternal mortality rates

Asma Khalil • Athina Samara • Pat O'Brien • Conrado Milani Coutinho • Silvana Maria Quintana • Shamez N Ladhani

Open Access • Published: August, 2023 • DOI: https://doi.org/10.1016/S2214-109X(23)00247-4 •
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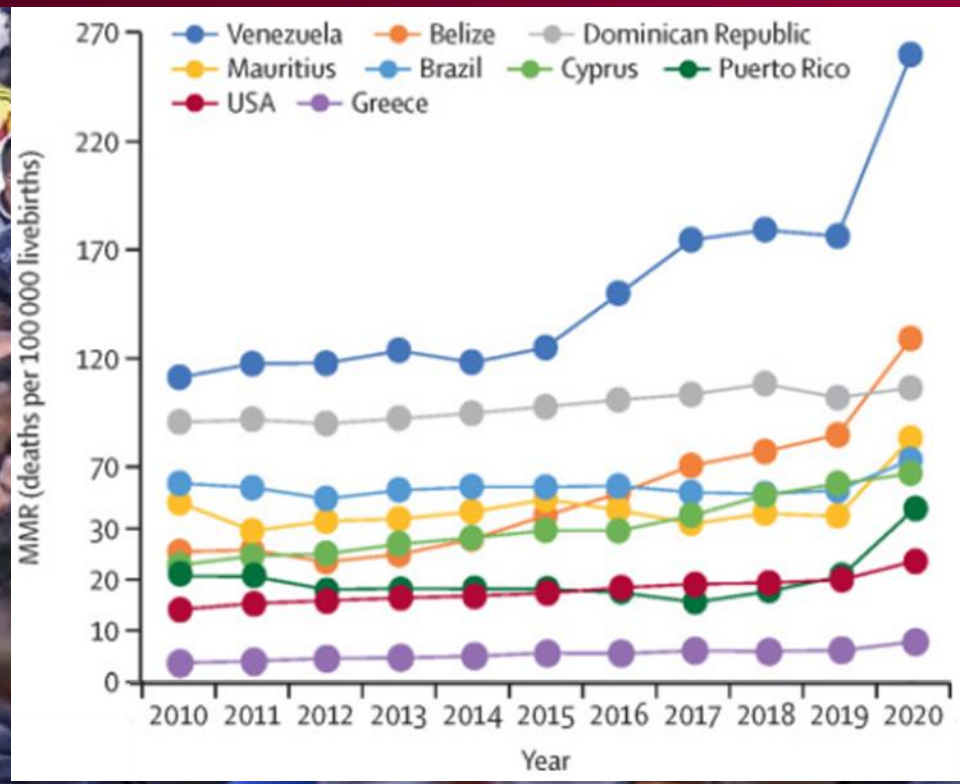
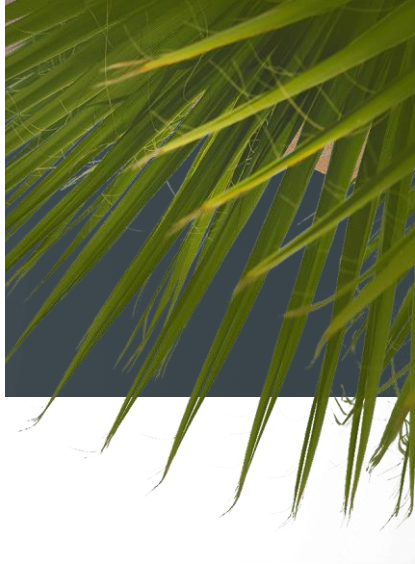


Rumichaca, border of Ecuador with Colombia. Hundreds of refugees and migrants from Venezuela queuing at the border post. ©IOM/ Cristian Méndez



Panama

Barranquilla

Paraguachón

Caracas

N

VENEZUELA, BOLIVARIAN REPUBLIC OF

Villa del Rosario

Bucaramanga

Arauca

Medellin

Bogotá

Cali

Ipiales

San Miguel

ECUADOR

PERÚ

34

RMRP Partners

in Inter-Agency Mixed Migration Flows Group (GIFMM)

Vaccine-preventable diseases

ELSEVIER

Travel Medicine and Infectious Disease

Volume 27, January–February 2019, Pages 5-8

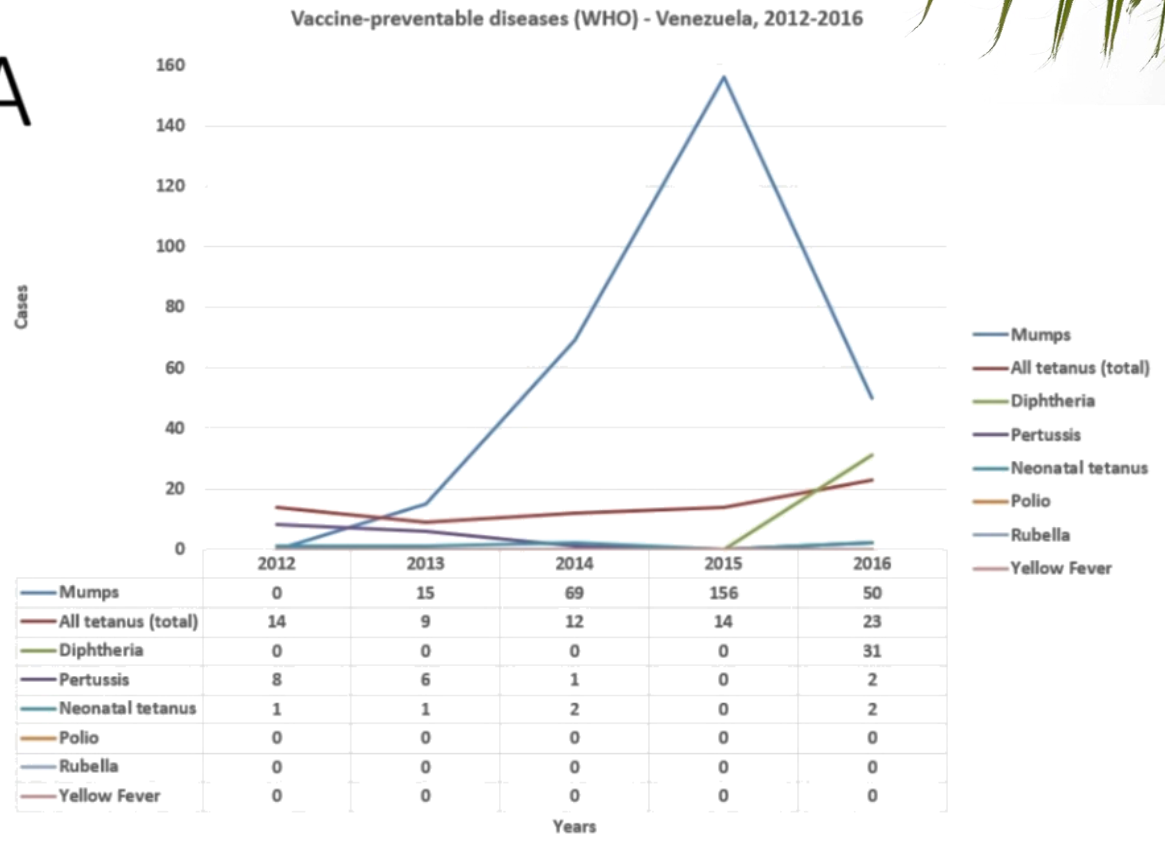
A

Editorial

The current syndemic in Venezuela: Measles, malaria and more co-infections coupled with a breakdown of social and healthcare infrastructure. *Quo vadis*?

Alfonso J. Rodríguez-Morales, José Antonio Suárez, Alejandro Risquez, Lourdes Delgado-Noguera, Alberto Paniz-Mondolfi

Received 27 September 2018, Revised 10 October 2018, Accepted 11 October 2018, Available online 14 October 2018.



	2012	2013	2014	2015	2016
Mumps	0	15	69	156	50
All tetanus (total)	14	9	12	14	23
Diphtheria	0	0	0	0	31
Pertussis	8	6	1	0	2
Neonatal tetanus	1	1	2	0	2
Polio	0	0	0	0	0
Rubella	0	0	0	0	0
Yellow Fever	0	0	0	0	0

Vaccine-preventable diseases

Measles (sarampión)

ELSEVIER

Travel Medicine and Infectious Disease

Volume 27, January–February 2019, Pages 5-8

Editorial

The current syndemic in Venezuela: Measles, malaria and more co-infections coupled with a breakdown of social and healthcare infrastructure. *Quo vadis*?

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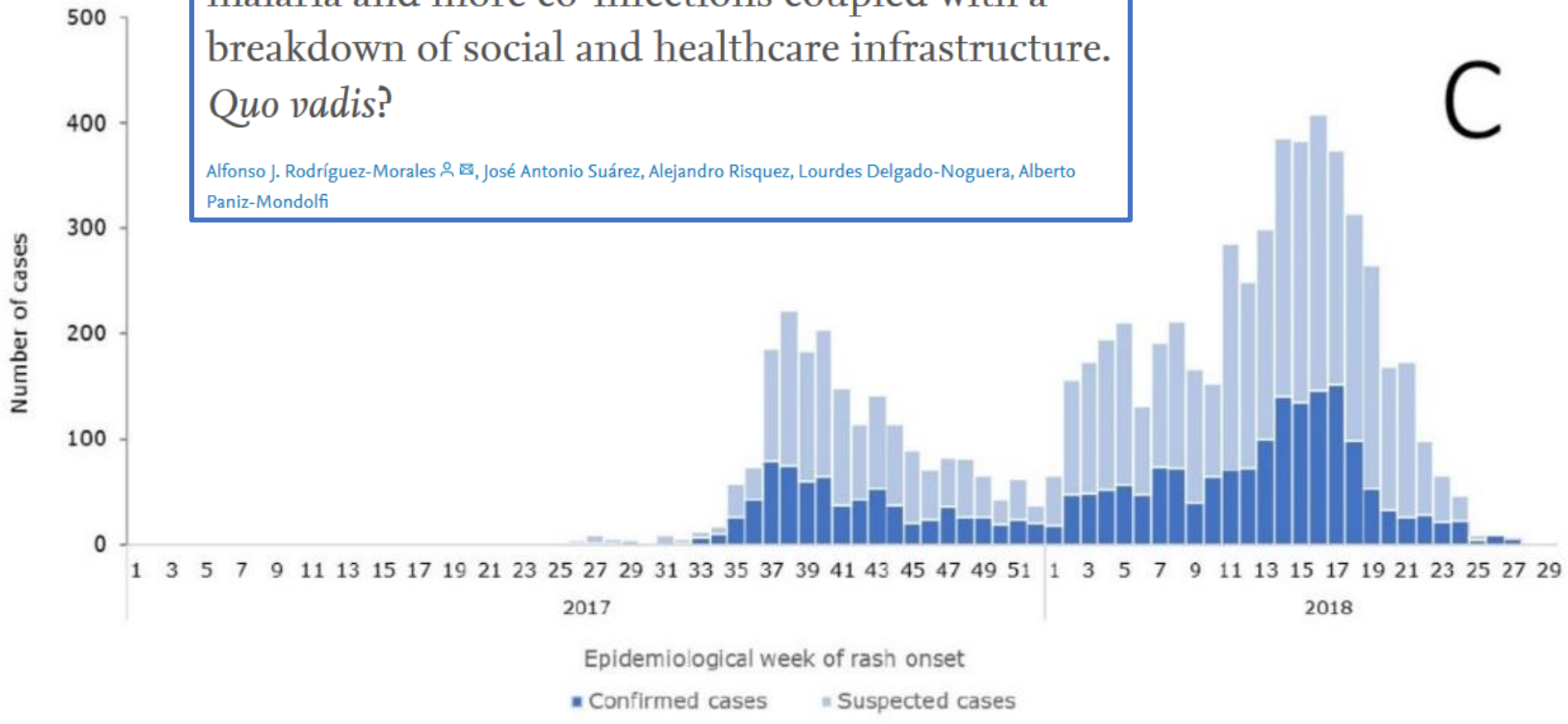
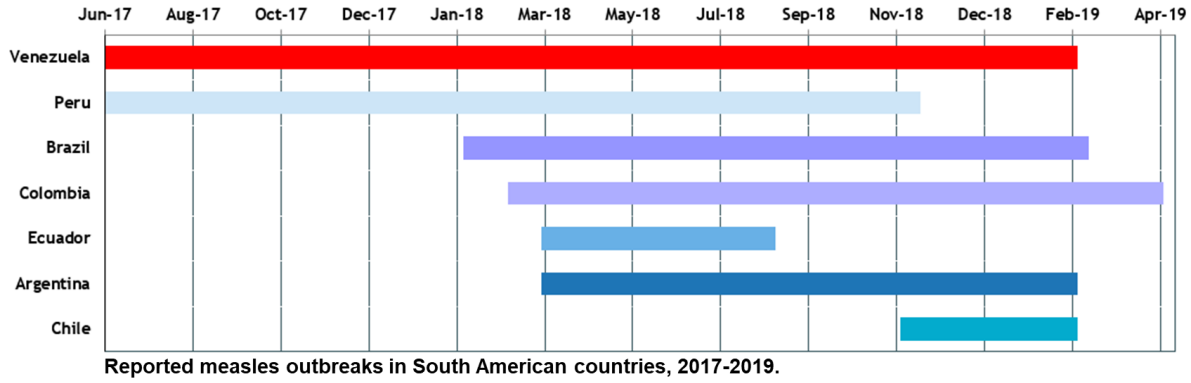


Measles

spillover

Venezuela> the origin
Confirmed by genotype D8



Reported measles outbreaks in South American countries, 2017-2019.

Rodríguez-Morales et al. 2019.

A

United States of America
555 in 2019 (up to Apr 11)
372 in 2018, 120 in 2017

Canada
33 confirmed cases
EW 1/2019-EW 13/2019
genotypes D8 and B3

Mexico
6 confirmed cases
genotype D8

Bahamas
1 confirmed case

Costa Rica
9 confirmed cases
EW 1/2019-EW 13/2019

Venezuela
6534 confirmed cases
EW 26/2017-EW 13/2019
genotype D8

Colombia
293 confirmed cases
EW 10/2018-EW 14/2019
genotype D8
26.2% imported from Venezuela and
58.2% linked to imported cases from Venezuela

Source:
Modified from WHO and PAHO.

Ecuador
19 confirmed cases
EW 13/2018-EW 33/2018
genotype D8

Brazil
10334 confirmed cases
EW 6/2018-EW 9/2019
genotype D8

Peru
38 confirmed cases
EW 26/2017-EW 46/2018
genotype D8

Uruguay
3 confirmed cases

Chile
26 confirmed cases
EW 45/2018-EW 8/2019
genotype D8

Argentina
19 confirmed cases
EW 13/2018-EW 8/2019
genotypes D8 and B3

Multisectoral Approach to the Prevention and Control of Vector-Borne Diseases

A conceptual framework

World Health Organization

TDR For research on diseases of poverty

UNICEF · UNDP · World Bank · WHO

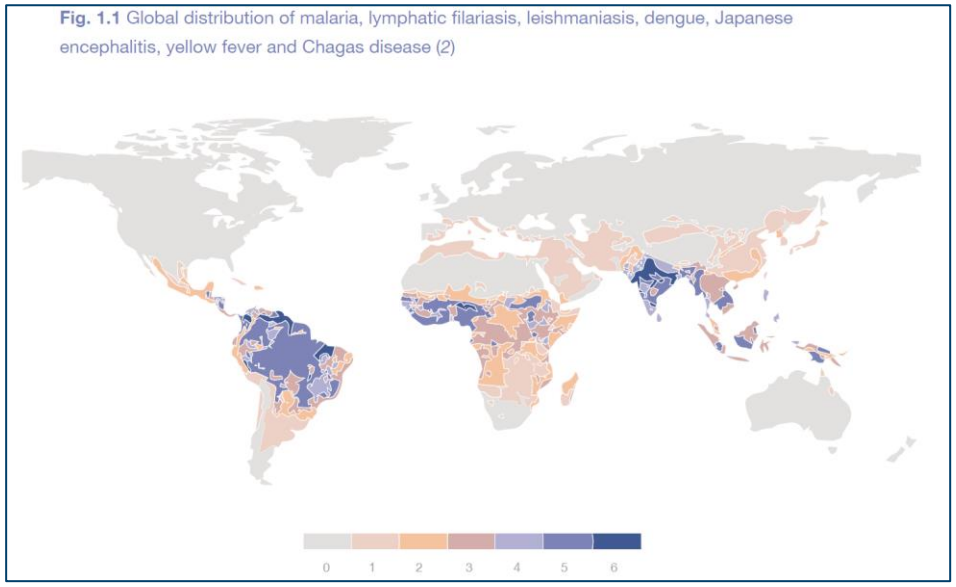


Fig. 1.1 Global distribution of malaria, lymphatic filariasis, leishmaniasis, dengue, Japanese encephalitis, yellow fever and Chagas disease (2)

We thank our Chief Scientist, Soumya Swaminathan (WHO Science Division) for constant support for TDR's work on vector-borne diseases.

This guidance document is a product of a larger collaborative undertaking of TDR, the Swiss Agency for Development and Cooperation, the Canadian International Development Research Centre and the Swiss Tropical and Public Health Institute, with support particularly from Karin Gross, Zee Leung and Konstantina Boutsika at those agencies, respectively. We acknowledge the principal investigators of the commissioned reviews and their teams for their work: Cho Naing (International Medical University, Malaysia), Robert T. Jones (London School of Hygiene and Tropical Medicine, United Kingdom), Alfonso J. Rodríguez-Morales
Asia Foundation, Indonesia), Carl Abelard
and Rashad Abdul-Ghani (Sana'a Univers
include: Annette Prüss-Üstün (Public Hea
and Lauren Carrington and Jiagang Guo

Table 1.1. Examples of VBDs by type of vectors and estimates of local or global burden

Vector	Disease	Reference	Year	Region	Disability-adjusted life years (x 1000) or cases	Deaths
Mosquitoes	Malaria	*3, 4*	2017	Global	45 015	839 518
	Dengue	*3, 4*	2017	Global	2 923	49 779
	Lymphatic filariasis	*3, 4*	2017	Global	1 364	NA
	Japanese encephalitis	*7*	2005	Global	432	9 250[a]
	Yellow fever	*3, 4*	2017	Global	314	13 761
	Chikungunya[b]	*8*	2017	Americas	61 613 (suspected no. of cases)	101
	West Nile fever[b]	*9*	2018	Europe	2 083 (reported autochthonous infections[c])	180
	Zika virus disease	*3, 4*	2017	Global	2.2	57
	Rift Valley fever[b]	*10, 11*	2006–2007 outbreak	Kenya	3.4 per 1 000 population	NA

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Contents

- Socio-environmental overview of Latin America: importance of climate change, OneHealth approach and determinants
- **Arboviruses in the region**
- We have not just mosquitoes, but many rodents involved in emerging viral infections in the region: Mammarenaviruses and Orthohantaviruses
- Cocirculation during COVID-19 pandemic, mpox, and avian influenza
- Some conclusions - mitigation

Lancet Infect Dis 2018;
18: e355–61

Published Online
June 19, 2018
http://dx.doi.org/10.1016/
S1473-3099(18)30269-X

*Contributed equally

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	Main mosquito vectors	First description of the virus (year and country)	First disease description (year and country)	Past outbreaks and ongoing circulation
Alphavirus genus				
Mayaro[8,14,39,40]	*Haemagogus* spp	1954 (Trinidad and Tobago)	1954 (Trinidad and Tobago)	Past outbreaks and ongoing circulation in South America and the Caribbean
Chikungunya[8,10,14]	*Aedes aegypti*	1952 (Tanzania)	2013 (Saint Martin in the Caribbean)	Possible outbreaks in the 18th and 19th centuries; spread in the Americas from 2013; still circulating in 2017*
Venezuelan equine encephalitis[8,41]	*Culex* spp (enzootic cycle); *Ochlerotatus; Pseudophora* spp (epizootic cycle)	1938 in horses (Venezuela)	1920s (Venezuela) and isolated in human beings in 1967 (Colombia)	Several outbreaks (in humans and horses) since 1938 in South and Central America, Mexico, and southern USA; last outbreak (75 000–100 000 human cases) in 1995 in Venezuela and Colombia
Eastern equine encephalitis[8,42]	*Culex pedroi* (enzootic cycle); *Aedes taeniorhynchus* (epizootic cycle)	1938 in humans (USA)	1972 in humans (Trinidad and Tobago)†	Sporadic equine and human encephalitis in North America, a small outbreak in Panama in 2010, and only three reported cases in Latin America (Trinidad and Tobago and Brazil)
Western equine encephalitis[43]	*Aedes* spp; *Culex* spp	1930 in horses (USA)	1941 (Canada and USA)	Widespread outbreaks of equine epizootics and encephalitis epidemics in western and North America from the 1930s to the 1950s; epizootic outbreaks in 1972–73 and 1982–83 in Argentina; and sporadic cases in South America (Uruguay in 2009)
Flavivirus genus				
Zika[16,17,44]	*Aedes aegypti*	1947 in a sentinel rhesus monkey (Uganda)	2015 (Brazil)‡	Spread in the Americas from 2015; circulation decreasing in 2017†
Yellow fever[8,45–47]	*Haemagogus* spp; *Sabethes Aedes aegypti*	1927 (Ghana)	1648 (Mexico)	13 American countries are considered endemic by WHO;§ ongoing circulation in Brazil in 2016–17
Dengue[5,48]	*Aedes aegypti; Aedes albopictus*	1944 (Japan)	1635 (Caribbean)	Most common arbovirus in Latin America (0·9–2·4 million cases annually in the past decade)*
Rocio[8,49,50]	*Psorophora ferox*	1975 (Brazil)	1975 (Brazil)	Only one outbreak in Brazil in 1973–80 (about 1000 cases)
Saint Louis encephalitis[8,49,50]	*Culex declarator; Culex coronator*	1933 (USA)	1960 in mosquitoes (Brazil)	Ongoing circulation in the Americas from Canada to Argentina
***Orthobunyavirus* genus**				
Oropuche[8,51]	*Aedes serratus; Culex quinquefasciatus; Culicoides paraensis*	1955 in humans (Trinidad and Tobago)	1955 in humans (Trinidad and Tobago)	30 major outbreaks since the first isolation of the virus in tropical America; subsequent outbreaks in Latin America (≤100 000 cases); the Oropuche virus is the second most common arbovirus in Brazil

*Pan American Health Organization website.[52] †Epizootic outbreak reported in 1973 in Latin America. ‡Outbreak of exanthematous illness reported in late 2014. §WHO website.[53]

Table 2: **Principal endemic arboviruses in tropical America.**

Personal View

THE LANCET
Infectious Diseases
November 2018

Unexpected outbreaks of arbovirus infections: lessons learned from the Pacific and tropical America

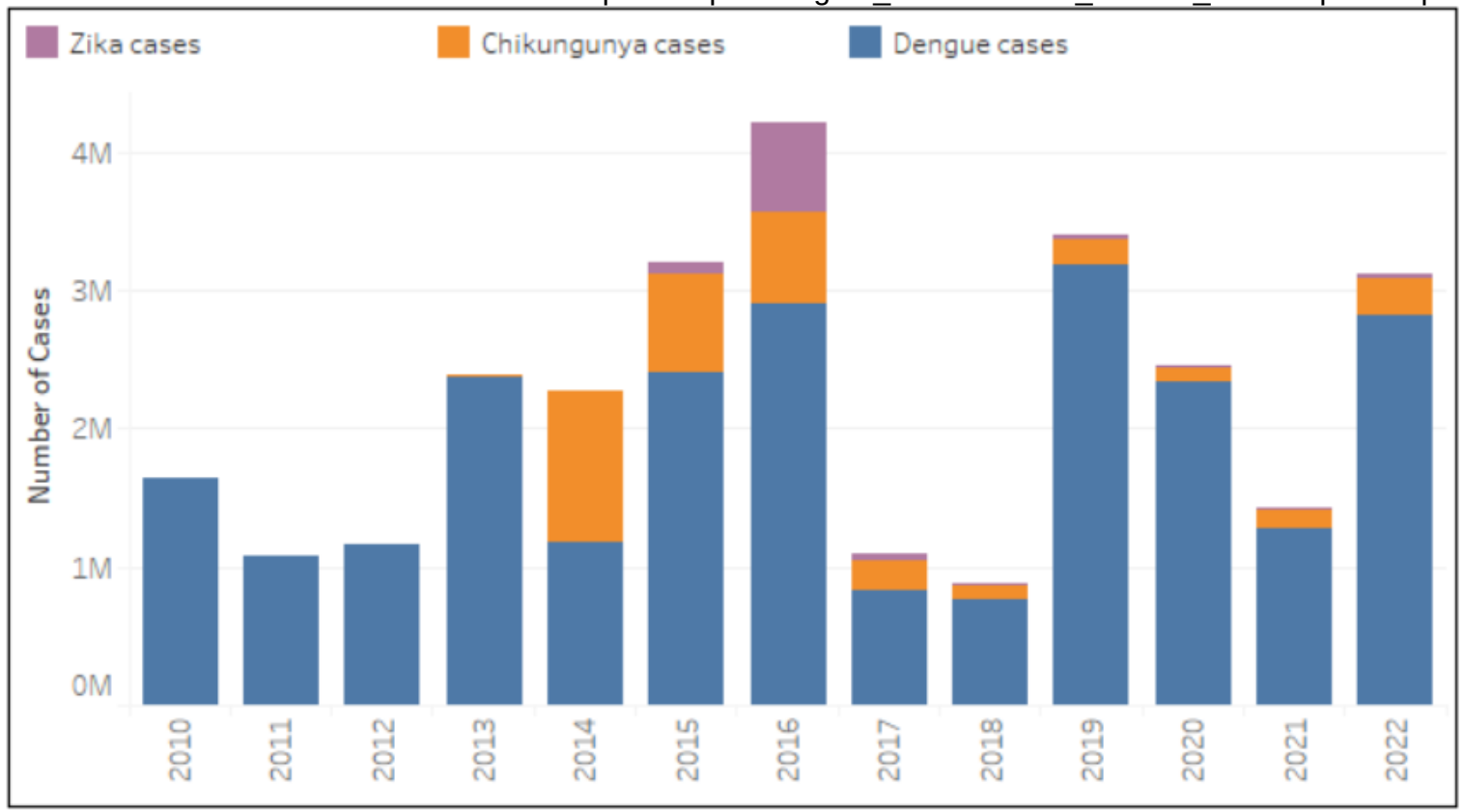
Didier Musso, Alfonso J Rodriguez-Morales, José Eduardo Levi, Van-Mai Cao-Lormeau*, Duane J Gubler**

Epidemiological Update for Dengue, Chikungunya and Zika in 2022.

PAHO
Pan American Health Organization
World Health Organization Americas

Figure 1. *Distribution of reported cases of dengue, chikungunya, and Zika by year. Region of The Americas. 2010-2022*

https://ais.paho.org/ha_viz/Arbo/Arbo_Bulletin_2022.asp?env=pri



Source: *Data entered into the Health Information Platform for The Americas (PLISA, PAHO / WHO) by the Ministries and Institutes of Health of the countries and territories of the Region. Available at: https://www.paho.org/plisa*

Updated: May 21 2023 1:00AM

Updated data as of epidemiological week 52 for Dengue, 52 for chikungunya and 52 for Zika of 2022

DENGUE
2,811,433 cases
283.39 cases x 100,000 Pop.
4,607 severe dengue (0.2%)
1,290 deaths
0.046% case fatality rate (CFR)
Nicaragua is he country with the highest cumulative incidence

CHIKUNGUNYA
273,685 cases
27.55 cases x 100,000 Pop.
87 deaths
0.032 % case fatality rate (CFR)
Belize is he country with the highest cumulative incidence

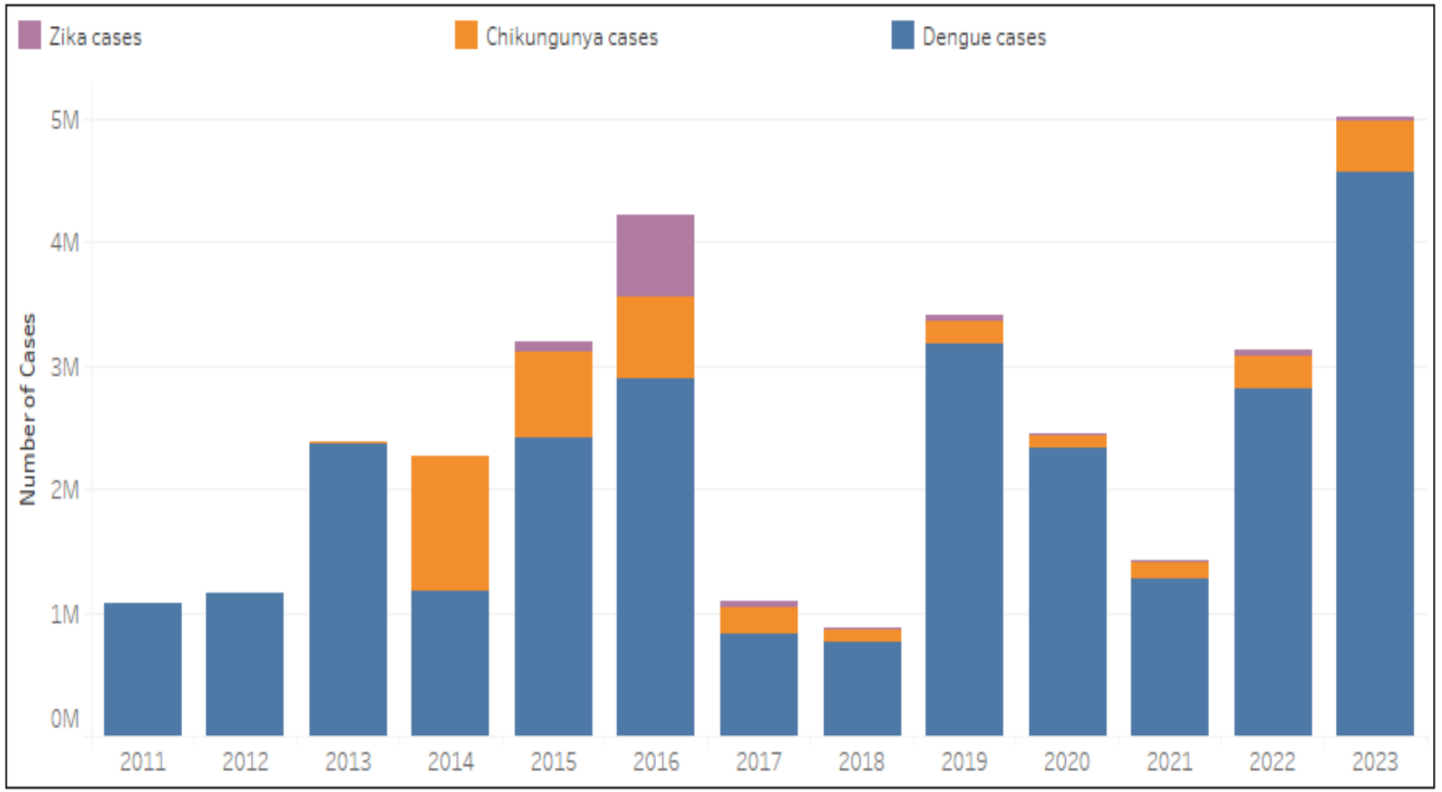
ZIKA
40,249 cases
4.05 cases x 100,000 Pop.
2 death
0.005 % case fatality rate (CFR)
Belize is he country with the highest cumulative incidence

Epidemiological Update for Dengue, Chikungunya and Zika in 2023.

Updated: Mar 5 2024 11:29AM

https://ais.paho.org/ha_viz/Arbo/Arbo_Bulletin_2023.asp?env=pri

Figure 1. *Distribution of reported cases of dengue, chikungunya, and Zika by year. Region of The Americas. 2011-2023*



Updated data as of epidemiological week 52 for Dengue, 52 for chikungunya and 52 for Zika of 2023

DENGUE

4,566,906 cases
470.25 cases x 100,000 Pop.
7,656 severe dengue (0.2%)
2,341 deaths
0.051% case fatality rate (CFR)
Saint Bartolome is he country with the highest cumulative incidence

CHIKUNGUNYA

410,017 cases
40.56 cases x 100,000 Pop.
411 deaths
0.100 % case fatality rate (CFR)
Paraguay is he country with the highest cumulative incidence

ZIKA

36,738 cases
3.70 cases x 100,000 Pop.
2 deaths
0.005 % case fatality rate (CFR)
Belize is he country with the highest cumulative incidence

revista chilena de infectología
SOCIEDAD CHILENA DE INFECTOLOGÍA

Unraveling the unparalleled 2024 epidemic of Dengue in the Americas

Desentrañando la incomparable epidemia de dengue de 2024 en Las Américas

Alfonso J. Rodriguez-Morales[1,2,3], Juan J. Montenegro-Idrogo[1,4], Juan-Carlos Celis-Salinas[5], Rodrigo Angerami[6], Wilmer E. Villamil-Gómez[7], Nicolás Sarute[8], Tomas Orduna[9], Cecilia Perret[10], Hernan D. Rodriguez-Enciso[11], Eduardo Savio-Larriera[12], Alejandro Risquez[13], David A. Forero-Peña[13,14], Rolando Ulloa-Gutierrez[15], Maritza Cabrera[16], Sergio Cimerman[17], Ranjit Sah[18,19,20], Jaime D. Acosta-España[21,22,23,24], Juan-Carlos Navarro[24,25], Nancy Sandoval[26] y Jose A. Suarez[27,28,29]

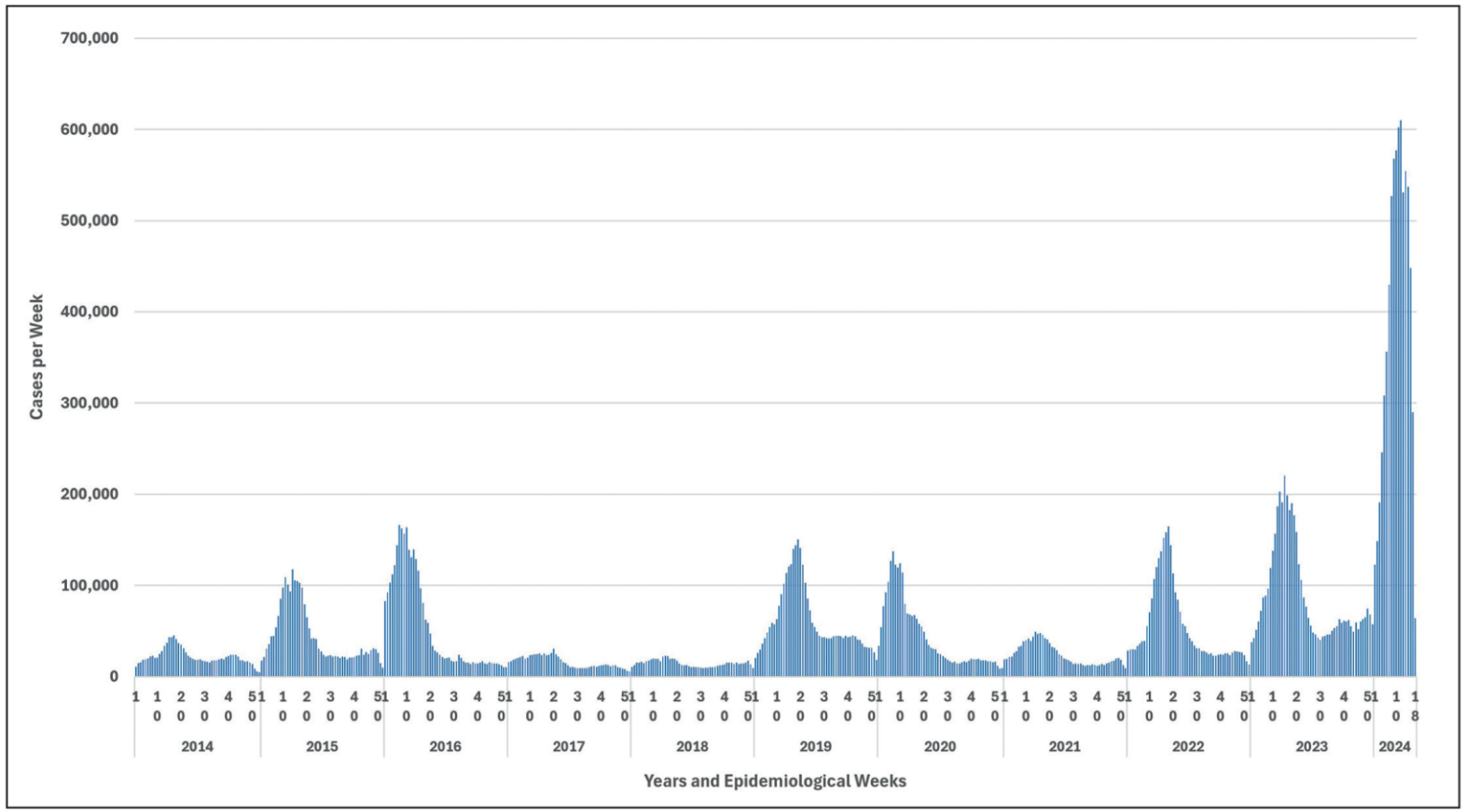


Figure 1. Dengue cases by epidemiological weeks, Americas, 2014-2024. It is modified from PAHO.

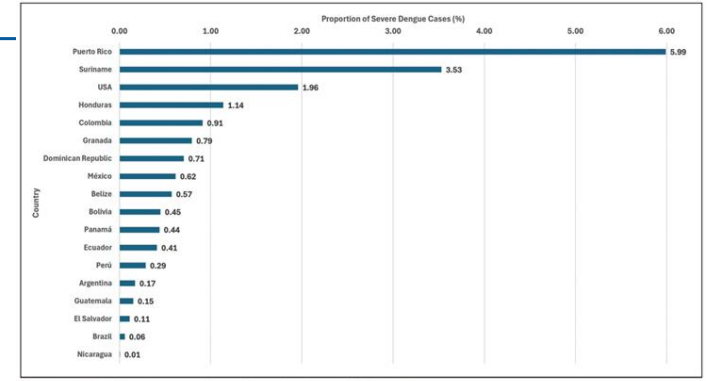


Figure 2. Proportion of Severe Dengue cases by countries, Americas, 2024. Modified from PAHO.

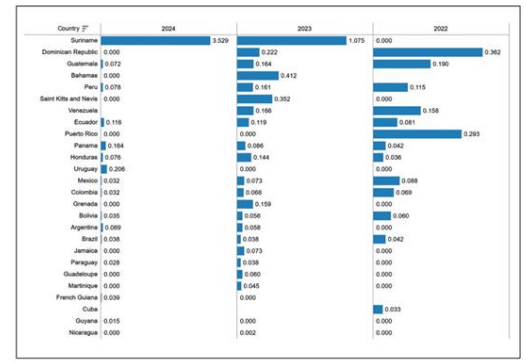


Figure 3. Case fatality rate (%CFR) associated with Dengue cases by countries, Americas, 2022-2024. From PAHO.

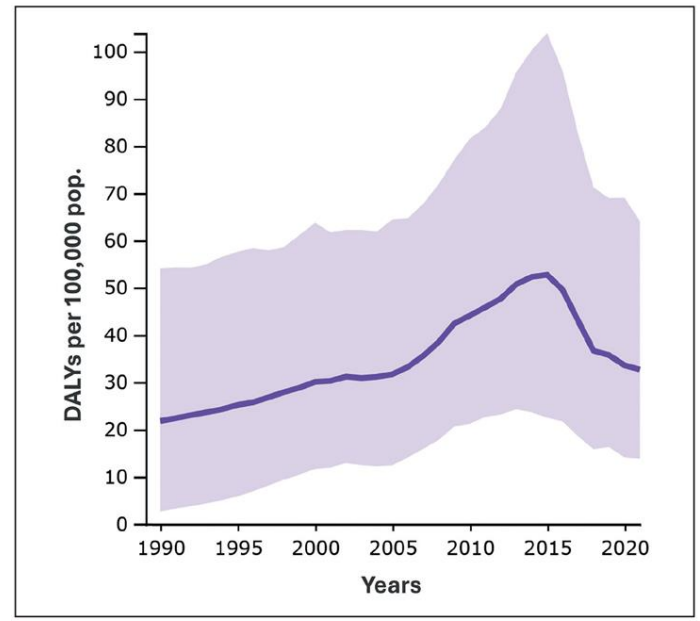


Figure 4. DALYs associated to Dengue in Latin America and the Caribbean, 1990-2021. Modified from 2021 GBS.

Kabir MA, Zilouchian H, Younas MA, Asghar W. Dengue Detection: Advances in Diagnostic Tools from Conventional Technology to Point of Care. Biosensors (Basel). 2021 Jun 23;11(7):206. doi: 10.3390/bios11070206. PMID: 34201849; PMCID: PMC8301808.

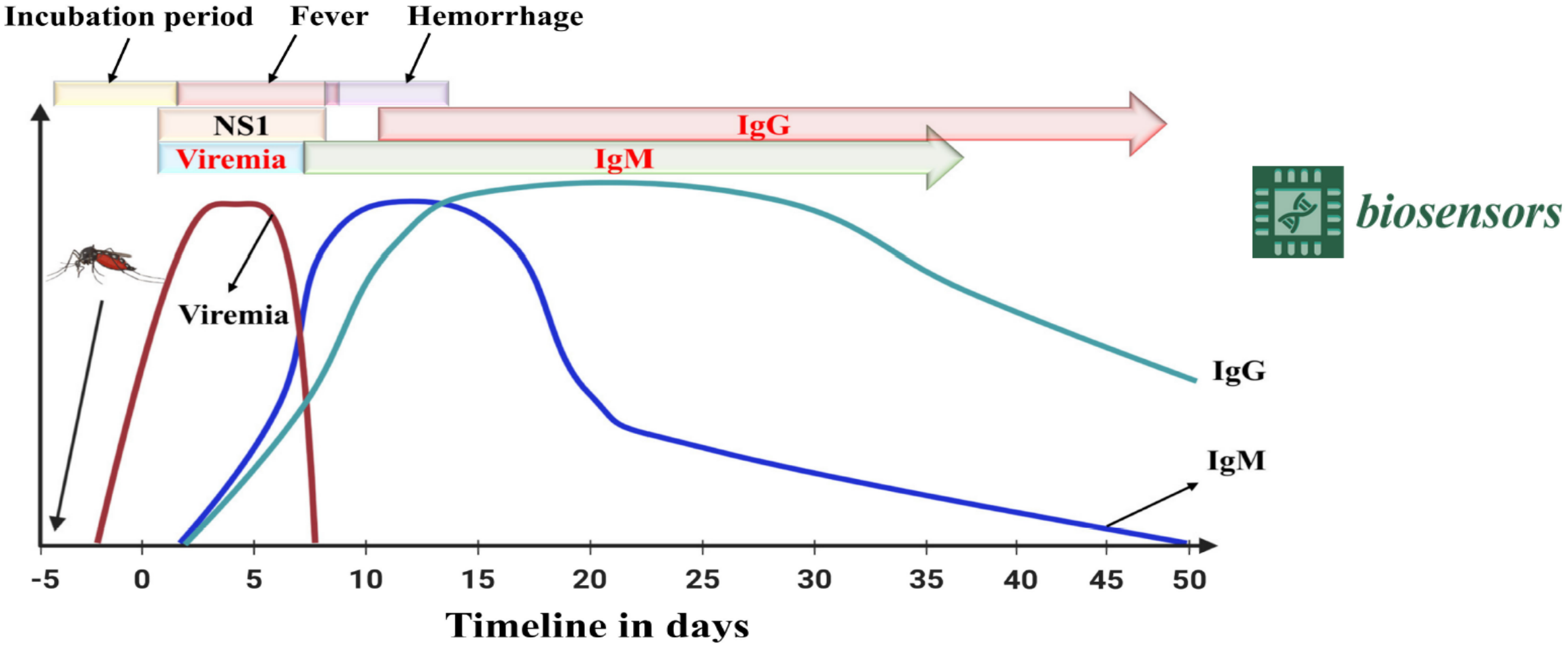
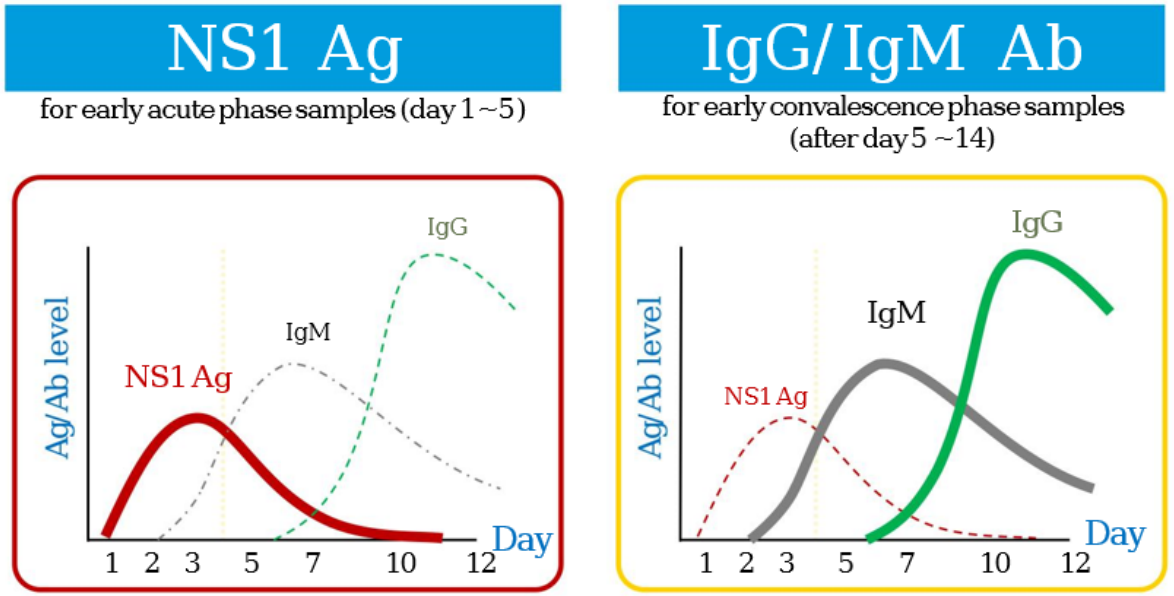


Figure 3. Immune response by the human body against the first invasion of the Dengue virus.

Deteccion dual de Ag y Ac - Dengue Duo

Detección simultánea de dengue NS1 Ag y prueba de IgG/IgM Ab juntas. Proporciona el diagnóstico óptimo de la infección por dengue desde la etapa aguda hasta la etapa convaleciente



Ejemplo: Día 3 desde el inicio de la fiebre

- Infección primaria: NS1 Ag y/o IgM POSITIVO
- Infección secundaria: IgG POSITIVA

Data adapted from: 8. J Clin Microbiol. 2010 Dec; 48(12): 4688–4689. doi: 10.1128/JCM.01668-10 Non structural Protein NS1: Givinga New Structure to Dengue Diagnosis. https://www.ncbi.nlm.nih.gov/pmc/articles/PMC3008478/

Kabir MA, Zilouchian H, Younas MA, Asghar W. Dengue Detection: Advances in Diagnostic Tools from Conventional Technology to Point of Care. Biosensors (Basel). 2021 Jun 23;11(7):206. doi: 10.3390/bios11070206. PMID: 34201849; PMCID: PMC8301808.

Table 1. Summary of conventional and POC detection methods with their advantages and limitations.

Detection Method	Advantages	Limitations	Target
Serological	Comparatively fast, easier to execute, less expensive	Expensive device required shows cross-reactivity	NS1,IgA, IgG and IgM
PCR	Accurate, early stage detection, muliplexibility, highly sensitive and specific, selective	Only suitable for high resource available settings, skilled personnel needed, prone to contamination, laborious and time consuming	RNA
Isothermal	Fast, no need of thermocycler, simpler than PCR, early stage detection	Less multiplexibility than PCR, prone to primer dimer due to high no of primers.	RNA
SPR	Real time detection, label free, low sample comsumption, early detection capability.	Lower sensitivity, susceptible to nonspecific binding	NS1, IgG and IgM
EIS	Inexpensive, label free, high throughput, sensitive, requires a low volume of samples.	Cumbersome sample preprocessing, requires cleanroom access (sometimes),	RNA, NS1
SERS	Highly specific, simple sample preparation, high throughput	Lacks robustness and reproducibility, highly expensive Raman reader	NS1, DENV Gene
LOC	Disposable, automation potential, cheaper, POC applicable, low reagent consumption, sample-in and answer-out	Manual sample loading, requires an expensive device fabrication process (sometimes),	IgM/IgG, NS1, E, and RNA
LFA	Easy, fast, no sample processing, cheaper than conventional methods.	Mishandling can be occurred, cross-reactivity, qualitative/semi-qualitative result	NS1, IgG, IgM, IgA,
LODc	Disposable, automation potential, cheaper, POC applicable, low reagent consumption	Labor intensive, requires 3D printing access, expensive equipment for device fabrication	RNA
µPAD	Disposable, automation potential, cheaper, POC applicable, low reagent consumption, smartphone integration	Manual sample loading, lower sensitivity, qualitative/semi-qualitative result	NS1, IgM
Microarray	Multiplexity, higher sensitivity, high throughput	Expensive, skilled personnel needed, lengthy time of execution, not POC applicable	Gene expression of DENV
Threads	Disposable, biocompatible, reproducible, cheaper, portable, readily available	Early stage of development, flow manipulation	Anti-DENV antibody
CRISPR	Rapid, highly sensitive, cheaper, simple	non-specific binding,	RNA

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ARTÍCULO ORIGINAL

Contribución de la prueba rápida NS1 e IgM al diagnóstico de dengue en Colombia en el periodo pre-zika

Clemen G[1], Angel J[2], Montes C[2], Tovar JR[2] Osorio L[1,*]

Cómo citar este artículo: Clemen G, *et al.* Contribución de la prueba rápida NS1 e IgM al diagnóstico de dengue en Colombia en el periodo pre-zika. Infectio 2019; 23(3): 259-265

Tabla 1. Definiciones de uso solo y combinado de diagnóstico clínico y pruebas rápidas de dengue

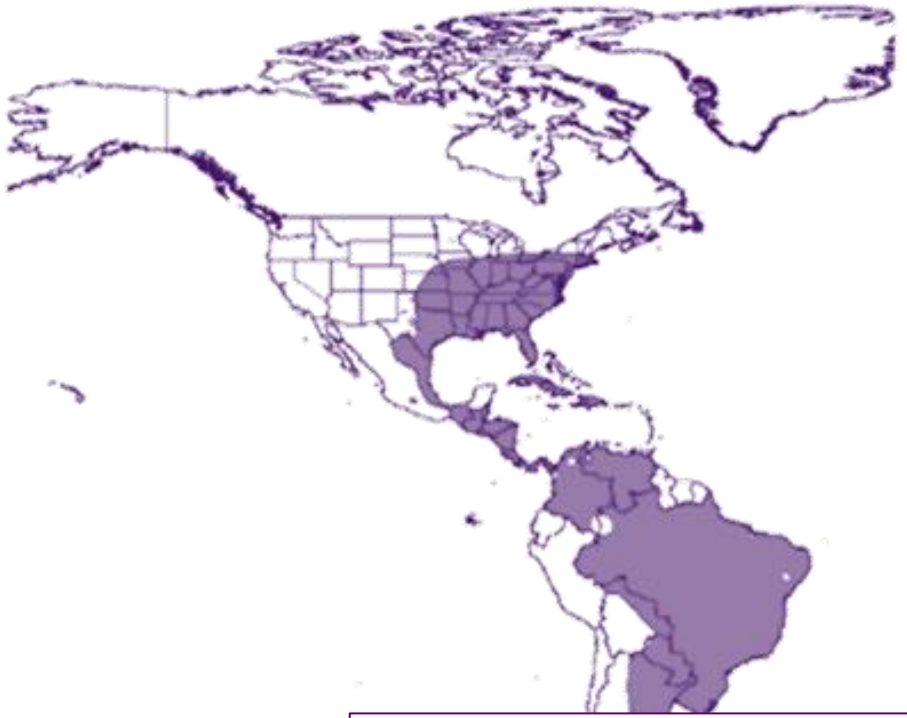
Método diagnóstico	Uso	Resultado diagnóstico clínico	Resultado prueba NS1	Resultado prueba IgM	Interpretación
NS1	Solo NS1		Positivo Negativo		Positivo Negativo
IgM	Solo IgM			Positivo Negativo	Positivo Negativo
NS1/IgM	Simultáneo NS1/IgM		Positivo Positivo Negativo Negativo	Positivo Negativo Positivo Negativo	Positivo Positivo Positivo Negativo
Clínico	Solo médico	Positivo Negativo			Positivo Negativo
Paralelo clínico/IgM	Simultáneo diagnóstico clínico e IgM	Positivo Positivo Negativo Negativo		Positivo Negativo Positivo Negativo	Positivo Positivo Positivo Negativo
Paralelo clínico /NS1/IgM	Simultáneo diagnóstico clínico, NS1 e IgM	Positivo Positivo Positivo Positivo Negativo Negativo Negativo Negativo	Positivo Positivo Negativo Negativo Positivo Positivo Negativo Negativo	Positivo Negativo Positivo Negativo Positivo Negativo Positivo Negativo	Positivo Positivo Positivo Positivo Positivo Positivo Positivo Negativo
Serie clínico positivo/IgM	IgM sólo si diagnóstico clínico positivo	Positivo Positivo Negativo		Positivo Negativo No aplica	Positivo Negativo Negativo
Serie clínico positivo/NS1/IgM	NS1 e IgM sólo si diagnóstico clínico positivo	Positivo Positivo Positivo Positivo Negativo	Positivo Positivo Negativo Negativo No aplica	Positivo Negativo Positivo Negativo No aplica	Positivo Positivo Positivo Negativo Negativo
Serie clínico negativo/ IgM	IgM sólo si diagnóstico clínico negativo	Positivo Negativo Negativo		No aplica Positivo Negativo	Positivo Positivo Negativo
Serie clínico negativo/NS1/ IgM	NS1 e IgM sólo si diagnóstico clínico negativo	Positivo Negativo Negativo Negativo Negativo	No aplica Positivo Positivo Negativo Negativo	No aplica Positivo Negativo Positivo Negativo	Positivo Positivo Positivo Positivo Negativo

Suitable entomological conditions for transmission of any *Aedes*-borne virus

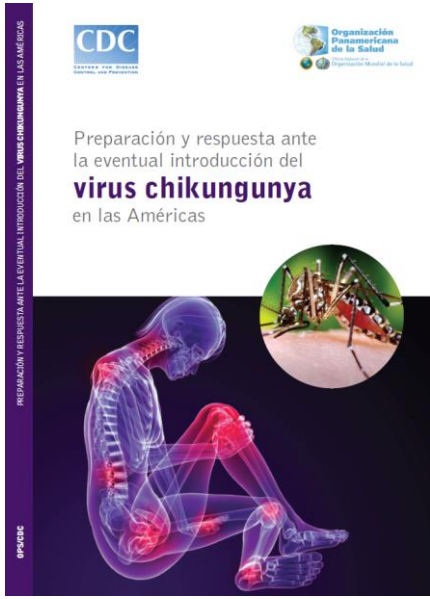
Figura 4. Distribución del *Ae. aegypti* en las Américas.[a]

[a] Adaptado de Arias, 2002.[60]

Figura 5. Distribución aproximada del *Ae. albopictus* en las Américas.[a]



[a] Adaptado de Benedict et al. 20



56 *Mem Inst Oswaldo Cruz*, Rio de Janeiro, Vol. *113*(1): 56-61, January 2018

First evidence of Zika virus venereal transmission in *Aedes aegypti* mosquitoes

Jordam William Pereira-Silva[1,2], Valdinete Alves do Nascimento[1], Heliana Christy Matos Belchior[1], Jéssica Feijó Almeida[1,2], Felipe Arley Costa Pessoa[1], Felipe Gomes Naveca[1], Claudia María Ríos-Velásquez[1]/+

State-wide survey of *Aedes aegypti* and *Aedes albopictus* (Diptera: Culicidae) in Florida

Casey Parker[1]✉, Daviela Ramirez[1], and C. Roxanne Connelly[1,2]

[1]*University of Florida, Institute of Food and Agricultural Sciences, Florida Medical Entomology Laboratory, 200 9th Street SE, Vero Beach, FL 32962, U.S.A. caseyparker@ufl.edu*

[2]*Centers for Disease Control and Prevention, Division of Vector Borne Diseases, 3156 Rampart Road, Ft. Collins, CO 80521, U.S.A.*

Received 21 January 2019; Accepted 10 April 2019

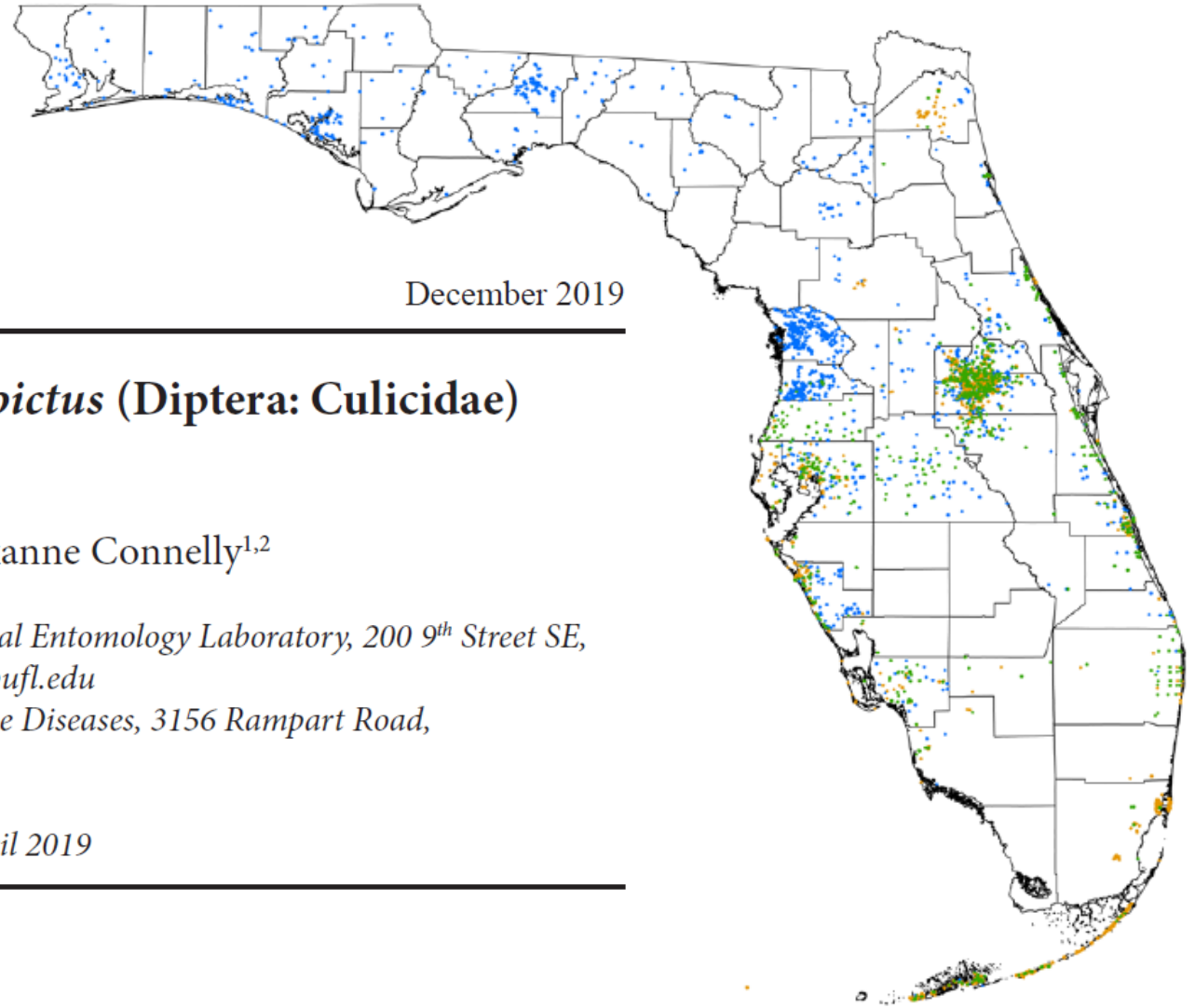


Figure 2. Estimated distribution of *Aedes aegypti* and *Aedes albopictus* in Florida based on positive collections and identifications made from 2011-2018 overlaid on the 1995 *Aedes aegypti* distribution published by Bargielowski and Lounibos (2016).

Acta Tropica
Volume 213, January 2021, 105739

Incursion and establishment of the Old World arbovirus vector *Aedes* (*Fredwardsius*) *vittatus* (Bigot, 1861) in the Americas

Benedict B. Pagac [a], Alexandra R. Spring [a], Jonathan R. Stawicki [b], Thien L. Dinh [c], Taylor Lura [d], Michael D. Kavanaugh [e], David B. Pecor [f g], Silvia A. Justi [f g], Yvonne-Marie Linton [f g h]

JOURNAL ARTICLE

The First Record of *Aedes vittatus* (Diptera: Culicidae) in the Dominican Republic: Public Health Implications of a Potential Invasive Mosquito Species in the Americas

P M Alarcón-Elbal, M A Rodríguez-Sosa, B C Newman, W B Sutton

Journal of Medical Entomology, Volume 57, Issue 6, November 2020, Pages 2016–2021, https://doi.org/10.1093/jme/tjaa128
Published: 11 August 2020 **Article history**

Transboundary and Emerging Diseases

ORIGINAL ARTICLE

Global potential distribution of three underappreciated arboviruses vectors (*Aedes japonicus*, *Aedes vexans* and *Aedes vittatus*) under current and future climate conditions

Abdelkrim Outammassine, Said Zouhair, Souad Loqman

First published: 25 November 2021 | https://doi.org/10.1111/tbed.14404

Acta Tropica
Volume 220, August 2021, 105959

Mosquitoes (Diptera: Culicidae) on the islands of Puerto Rico and Vieques, U.S.A.

Donald A. Yee [a], Limarie J. Reyes-Torres [a], Catherine Dean [a], Nicole A. Scavo [a], Thomas J. Zavortink [b]

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DISPATCHES

Autochthonous Dengue Outbreak, Paris Region, France, September–October 2023

Marta Zatta,[1] Ségolène Brichler, William Vindrios, Giovanna Melica, Sébastien Gallien[1]

Table. Clinical and laboratory findings in an outbreak of autochthonous dengue, Paris Region, France, September–October 2023*

Clinical, epidemiologic and laboratory parameters	Case-patient 1			Case-patient 2	Case-patient 3
Date of symptom onset	Sep 13			Sep 11	Sep 14
Symptoms	Fever, malaise, frontal headache, nausea and vomiting			Fever, malaise, frontal headache, and maculopapular rash	Fever, chills, frontal headache, myalgia, papular rash, and trunk and upper limbs itching
Date of symptom resolution	Sep 21			Sep 14	Sep 21
Epidemiologic link	Index case			Household contact of index case	Household contact of index case
Sample collection dates	Sep 19	Sep 22	Oct 7	Oct 13	Oct 13
Delay between sample collection and symptom onset, d	7	10	25	33	30
DENV RNA in blood	DENV-2†	Not tested	Not tested	Not tested	Not tested
DENV NS1 antigen	Positive‡	Not tested	Not tested	Not tested	Not tested
DENV IgM	Not tested	Positive.§ r = 72	Positive.§ r = 70	Positive,¶ r = 30	Positive,¶ r = 28
DENV IgG	Not tested	Negative.§ r<5	Positive.§ r = 12	Positive,¶ r = 15	Positive,¶ r = 17

*DENV, dengue virus; NS1, nonstructural protein 1; r, ratio; RT-PCR, reverse transcription PCR.
†DENV RNA was amplified, after purifying total nucleic acids from plasma, by real-time RT-PCR by using Realstar Dengue RT-PCR kit 3.0 and RealStar Dengue Type RT-PCR Kit 1.0 (Altona Diagnostics, https://www.altona-diagnostics.com).
‡DENV NS1 antigen was detected in plasma by using Dengue NS1 Ag Strips (Biosynex SA, https://www.biosynex.com) immunochromatographic assay.
§DENV IgM and IgG were detected by using Virclia Dengue IgM/IgG (Orgentec, https://www.orgentec.com/en) chemiluminescence immunoassay; results are positive if r>11.
¶DENV IgM and IgG were detected by Vircell Dengue IgM/IgG (Orgentec) ELISA immunoassay; results are positive if r>11.

PAHO

Pan American Health Organization

World Health Organization
REGIONAL OFFICE FOR THE Americas

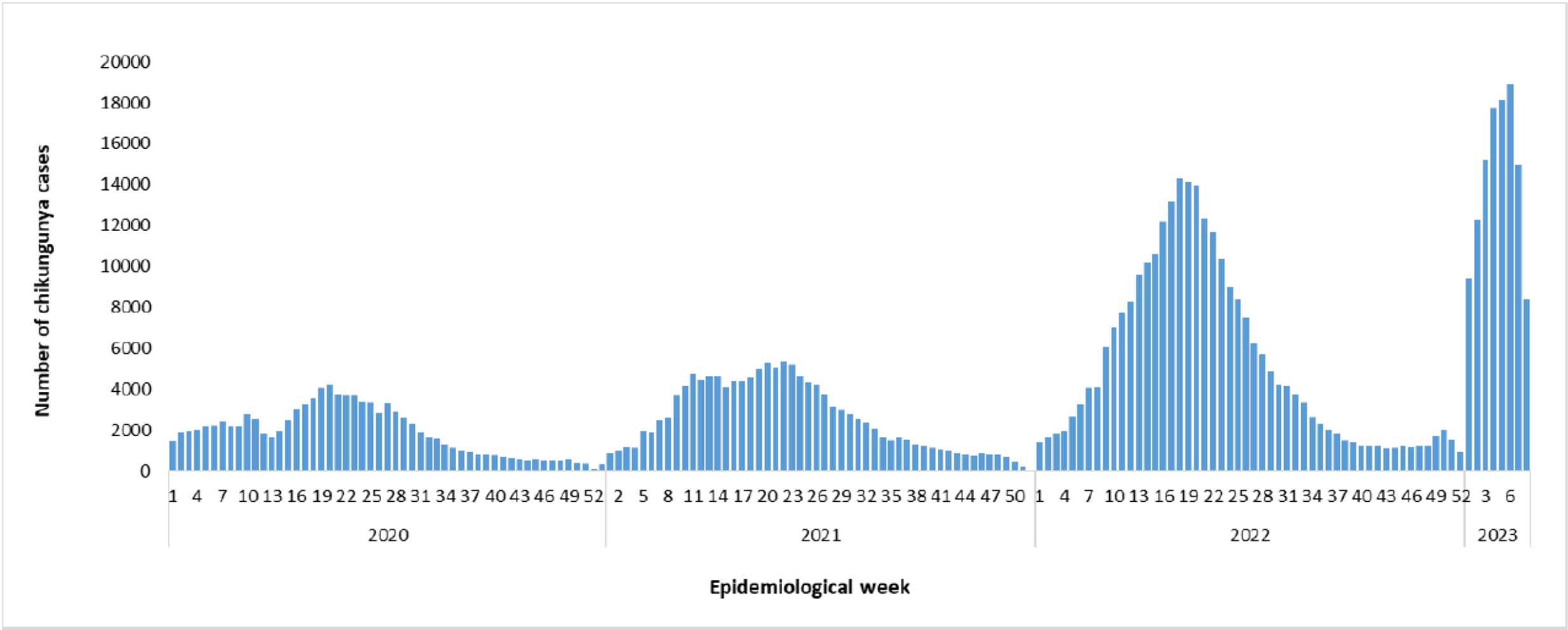
Epidemiological Alert
Increase in cases and deaths from chikungunya in the Region of the Americas

8 March 2023

In 2022, the Region of the Americas registered an increase in the number of cases and deaths from chikungunya above the numbers reported in previous years. Moreover, in the current season, an expansion of the disease occurrence has been observed beyond the historical areas of transmission reported since 2014.

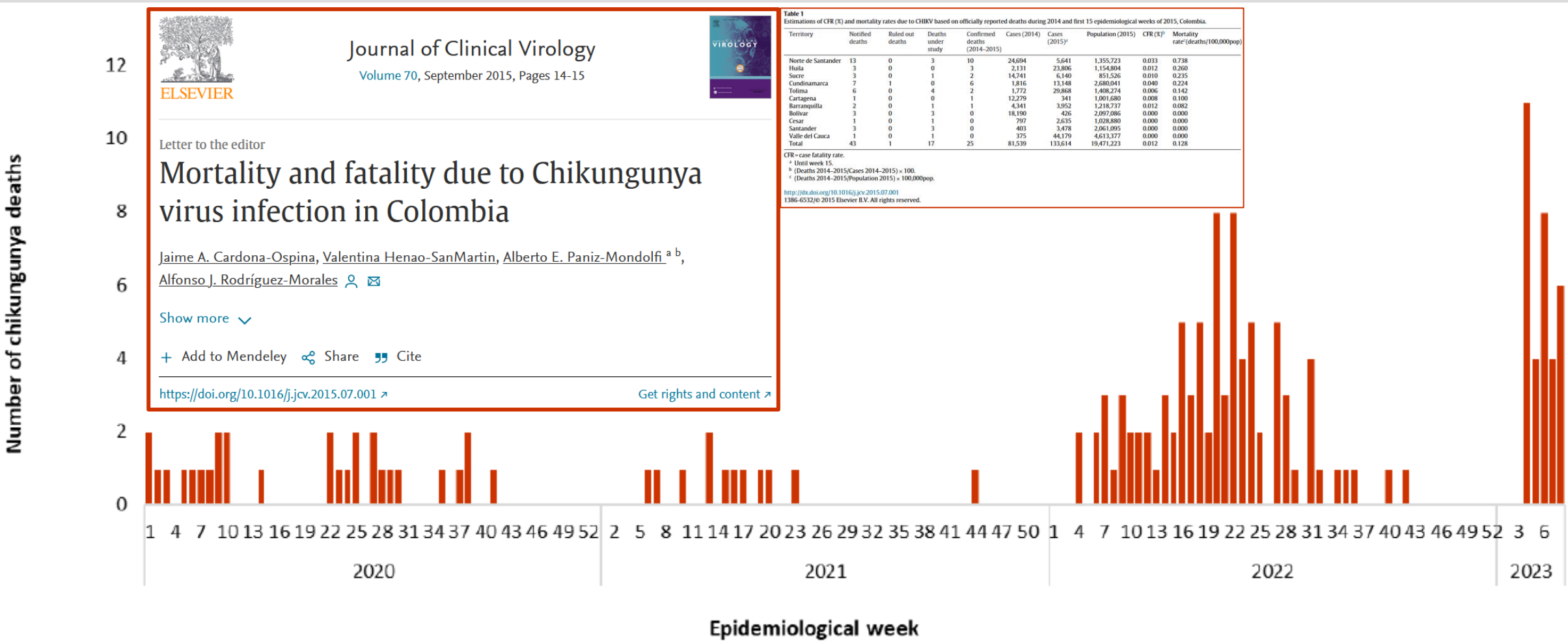
This trend has continued during the first weeks of 2023, in which this increase in cases and deaths has become even more evident representing an unusual behavior. Given this situation, the Pan American Health Organization / World Health Organization (PAHO/WHO) reiterates that Member States intensify actions to prepare health care services, including the diagnosis and proper management of cases; and to strengthen prevention and vector control measures to reduce the impact of this and other arboviral diseases.

Figure 1. Chikungunya cases by epidemiological week (EW) of report. Region of the Americas, 2020-2023 (until EW 8 of 2023).



Source: PAHO/WHO Health Information Platform for the Americas (PLISA per its acronym in Spanish) as provided by Ministries and Institutes of Health of the countries and territories of the Region of the Americas. Washington DC: PAHO. Accessed 8 March 2023. Available from: https://bit.ly/3F5JFEg

Figure 2. Chikungunya deaths by EW of report. Region of the Americas, 2020-2023 (until EW 8 of 2023).



ELSEVIER

Journal of Clinical Virology

Volume 70, September 2015, Pages 14-15

Letter to the editor

Mortality and fatality due to Chikungunya virus infection in Colombia

Jaime A. Cardona-Ospina, Valentina Henao-SanMartin, Alberto E. Paniz-Mondolfi [a b], Alfonso J. Rodríguez-Morales

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Table 1
Estimations of CFR (%) and mortality rates due to CHIKV based on officially reported deaths during 2014 and first 15 epidemiological weeks of 2015, Colombia.

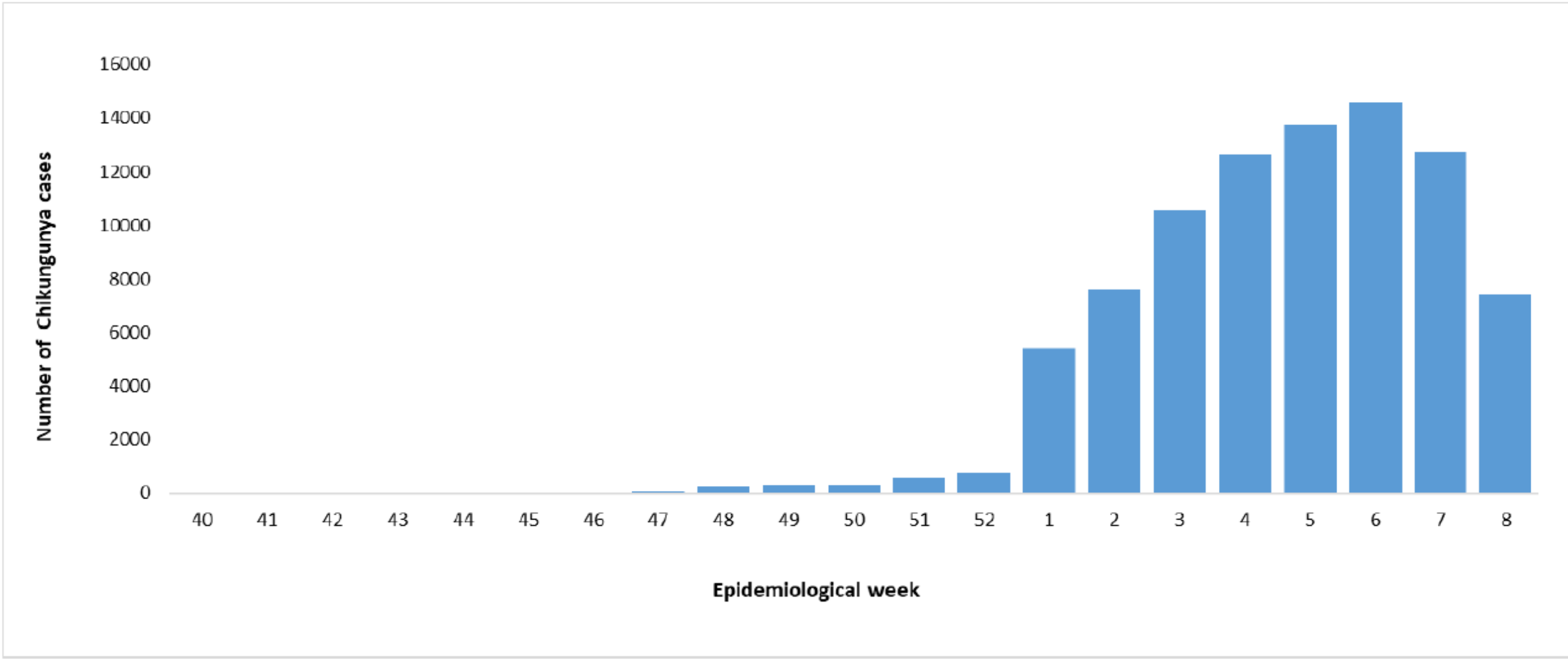
Territory	Notified deaths	Ruled out deaths	Deaths under study	Confirmed deaths (2014–2015)	Cases (2014)	Cases (2015)[a]	Population (2015)	CFR (%)[b]	Mortality rate[c] (deaths/100,000pop)
Norte de Santander	13	0	3	10	24,694	5,641	1,355,723	0.033	0.738
Huila	3	0	0	3	2,131	23,806	1,154,804	0.012	0.260
Sucre	3	0	1	2	14,741	6,140	851,526	0.010	0.235
Cundinamarca	7	1	0	6	1,816	13,148	2,680,041	0.040	0.224
Tolima	6	0	4	2	1,772	29,868	1,408,274	0.006	0.142
Cartagena	1	0	0	1	12,279	341	1,001,680	0.008	0.100
Barranquilla	2	0	1	1	4,341	3,952	1,218,737	0.012	0.082
Bolívar	3	0	3	0	18,190	426	2,097,086	0.000	0.000
Cesar	1	0	1	0	797	2,635	1,028,880	0.000	0.000
Santander	3	0	3	0	403	3,478	2,061,095	0.000	0.000
Valle del Cauca	1	0	1	0	375	44,179	4,613,377	0.000	0.000
Total	43	1	17	25	81,539	133,614	19,471,223	0.012	0.128

CFR = case fatality rate.
[a] Until week 15.
[b] (Deaths 2014–2015/Cases 2014–2015) × 100.
[c] (Deaths 2014–2015/Population 2015) × 100,000pop.

http://dx.doi.org/10.1016/j.jcv.2015.07.001
1386-6532/

Sources: PAHO/WHO Health Information Platform for the Americas (PLISA per its acronym in Spanish) as provided by Ministries and Institutes of Health of the countries and territories of the Region of the Americas. Washington DC: PAHO. Accessed 8 March 2023. Available from: https://bit.ly/3F5JFEg

Figure 3. Chikungunya cases by EW of report. Paraguay 2022-2023 (up to EW 8, 2023)



Source: National Programme on Vector Diseases - DIVET - DGVS. Ministry of Public Health of Paraguay

Affected Countries 2023 - CHIKV

- In the first four months of 2023, an increase in the circulation of chikungunya was detected in the region, with more than **214,000** reported cases.
- The most affected country is **Paraguay**, which registers the worst epidemic in its history, with **138,730** cases.
- **Argentina and Uruguay** also reported local transmission for the first time in 2023, and **Bolivia** recorded high levels of chikungunya transmission (1,150 cases).

- Recent report of cases in Uruguay
- At Paysandú and Montevideo
- Patients with no history of recent travel

Ministerio de Salud Pública

Comunicado

Montevideo, 21 de abril de 2023

Aedes aegipti y chikungunya

Se informa a la población que en las últimas horas se confirmaron casos de infección por virus Chikungunya en personas sin antecedentes de viaje residentes en la ciudad de Paysandú. A la fecha el total de casos es de 7. Todas ellas han cursado la enfermedad en forma ambulatoria con buena evolución.

Ante este hallazgo, se debe considerar que existe por primera vez en Uruguay evidencia de circulación viral en la ciudad de Paysandú, constituyendo un brote de enfermedad por virus Chikungunya.

Ministerio de Salud Pública

Montevideo, 13 de mayo de 2023

Enfermedad por virus Chikungunya en Montevideo

Se informa a la población que en las últimas horas se confirmó un caso de enfermedad por virus Chikungunya en una persona sin antecedentes de viaje residente en Montevideo, que cursó la enfermedad en forma ambulatoria y con buena evolución. En respuesta a este hallazgo, se han intensificado las acciones de vigilancia y control según protocolo.

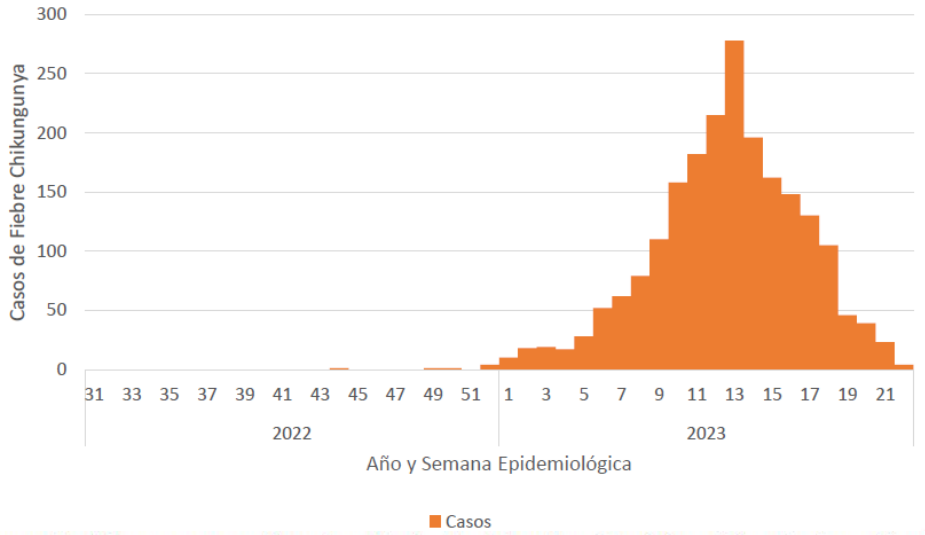
Tal como se ha comunicado, Uruguay registró en los últimos años un número variable de casos importados de esta enfermedad, habiéndose identificado casos autóctonos en el departamento de Paysandú en el pasado mes de abril.

Argentina

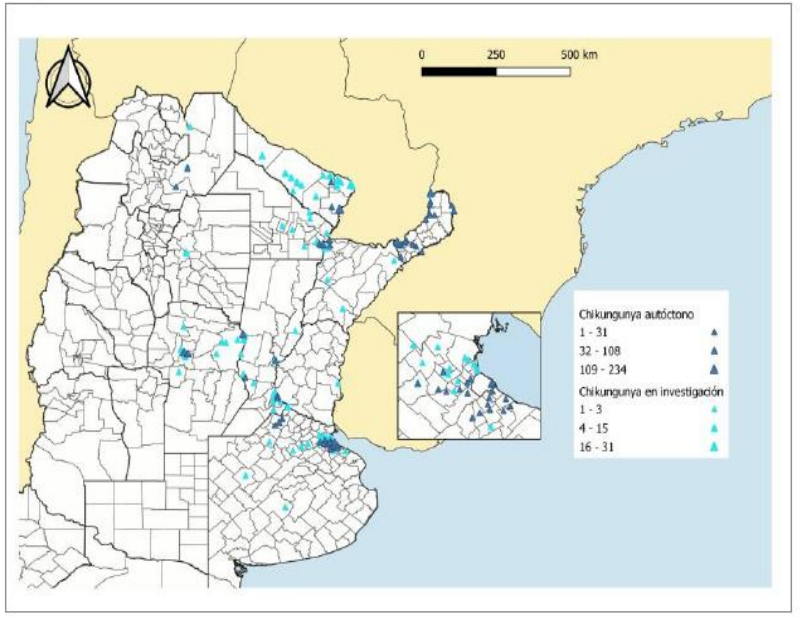
Tabla 3. Casos de fiebre chikungunya por provincia según antecedente de viaje. SE 31/2022 a 22/2023.

Provincia	Autóctonos*	En investigación*	Importados*	Total casos de Chikungunya	Investigados
Buenos Aires	468	67	121	656	4.140
CABA	97	2	68	167	614
Córdoba	169	17	9	195	2.252
Entre Ríos	0	1	0	1	31
Santa Fe	113	23	6	142	1.473
Centro	**847**	**110**	**204**	**1.161**	**8.510**
Mendoza	0	1	2	3	14
San Juan	0	0	0	0	1
San Luis	0	0	1	1	21
Cuyo	**0**	**1**	**3**	**4**	**36**
Chaco	31	13	8	52	457
Corrientes	100	10	12	122	224
Formosa	238	112	53	403	1.743
Misiones	220	64	39	323	642
NEA	**589**	**199**	**112**	**900**	**3.066**
Catamarca	0	0	0	0	4
Jujuy	0	1	0	1	258
La Rioja	0	0	0	0	28
Salta	16	2	0	18	159
Santiago del Estero	0	2	0	2	13
Tucumán	0	0	0	0	42
NOA	**16**	**5**	**0**	**21**	**504**
Chubut	0	0	0	0	2
La Pampa	0	0	0	0	4
Neuquén	0	0	1	1	3
Río Negro	0	0	0	0	1
Santa Cruz	0	0	1	1	7
Tierra del Fuego	0	0	0	0	2
Sur	**0**	**0**	**2**	**2**	**19**
Total PAIS	**1.452**	**315**	**321**	**2.088**	**12.135**

Gráfico 11. Casos de Chikungunya por SE epidemiológica. SE 31/2022 a SE 22/2023, Argentina.



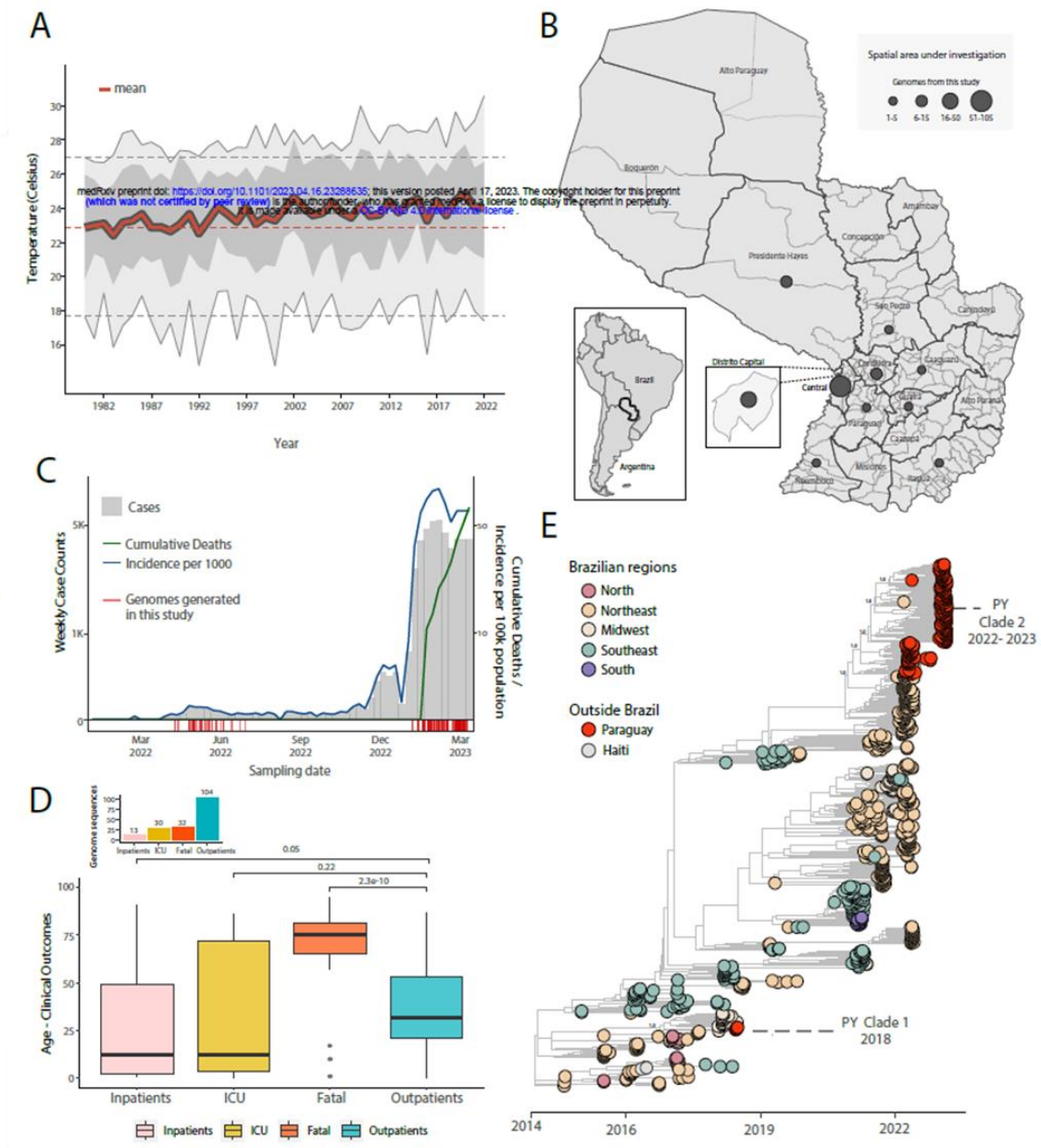
Mapa 3. Casos de chikungunya según antecedente de viaje y localidad de residencia. Argentina. SE 31/2022 a SE 21/2023.



Rapid epidemic expansion of chikungunya virus-ECSA lineage in Paraguay

Marta Giovanetti, Cynthia Vazquez, Mauricio Lima, Emerson Castro, Analia Rojas, Andrea Gomez de la Fuente, Carolina Aquino, Cesar Cantero, Fatima Fleitas, Juan Torales, Julio Barrios, Maria Jose Ortega, Maria Liz Gamarra, Shirley Villalba, Tania Alfonzo, Joilson Xavier, Talita Adelino, Hegger Fritsch, Felipe C. M. Iani, Glauco Carvalho Pereira, Carla de Oliveira, Gabriel Schuab, Evandra Strazza Rodrigues, Simone Kashima, Juliana Leite, Lionel Gresh, Leticia Franco, Houriiyah Tegally, Wesley C. Van Voorhis, Richard Lessels, Ana Maria Bispo de Filippis, Andrea Ojeda, Guillermo Sequera, Romeo Montoya, Edward C. Holmes, Tulio de Oliveira, Jairo Mendez Rico, José Lourenço, Vagner Fonseca, Luiz Carlos Junior Alcantara

doi: https://doi.org/10.1101/2023.04.16.23288635



CDC Centers for Disease Control and Prevention
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EMERGING INFECTIOUS DISEASES®

Rapid Epidemic Expansion of Chikungunya Virus East/Central/South African Lineage, Paraguay

Marta Giovanetti,[1] Cynthia Vazquez,[1] Mauricio Lima,[1] Emerson Castro,[1] Analia Rojas, Andrea Gomez de la Fuente, Carolina Aquino, Cesar Cantero, Fatima Fleitas, Juan Torales, Julio Barrios, Maria J. Ortega, Maria L. Gamarra, Shirley Villalba, Tania Alfonzo, Joilson Xavier, Talita Adelino, Hegger Fritsch, Felipe C.M. Iani, Glauco C. Pereira, Carla de Oliveira, Gabriel Schuab, Evandra S. Rodrigues, Simone Kashima, Juliana Leite, Lionel Gresh, Leticia Franco, Houriiyah Tegally, Wesley C. Van Voorhis, Richard Lessels, Ana Maria Bispo de Filippis, Andrea Ojeda, Guillermo Sequera, Romeo Montoya, Edward C. Holmes, Tulio de Oliveira, Jairo M. Rico, José Lourenço, Vagner Fonseca, Luiz C.J. Alcantara

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Chikungunya virus vaccine: a decade of progress solving epidemiological dilemma, emerging concepts, and immunological interventions

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[1]Y. B. Chavan College of Pharmacy, Aurangabad, Maharashtra, India, [2]School of Pharmacy, Al – Karim University, Katihar, India, [3]Centre for Global Health Research, Saveetha Institute of Medical and

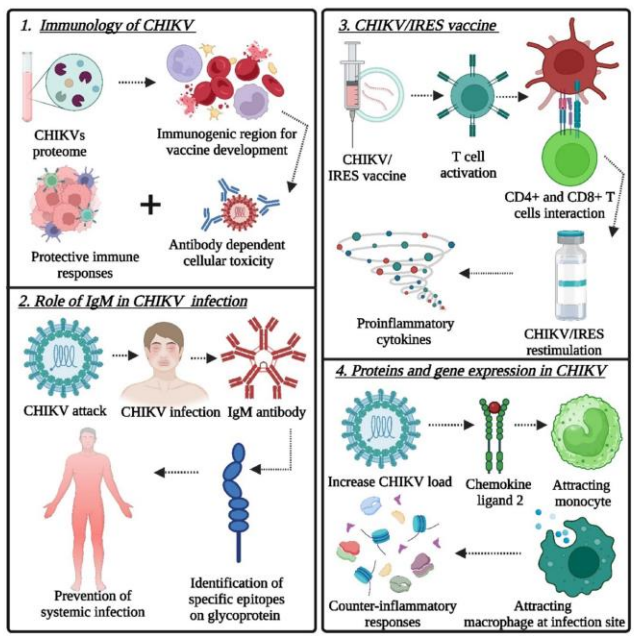

FIGURE 2
Target points of the immune system for the design and development of novel immunotherapeutics (vaccine technology): (1) role of protective immune responses, (2) role of IgM in CHIKV infection, (3) CHIKV/IRES vaccine for the induction of proinflammatory cytokines after CHIKV/IRES re-stimulation, and (4) proteins and gene expression in CHIKV (Created by using Biorender.com).

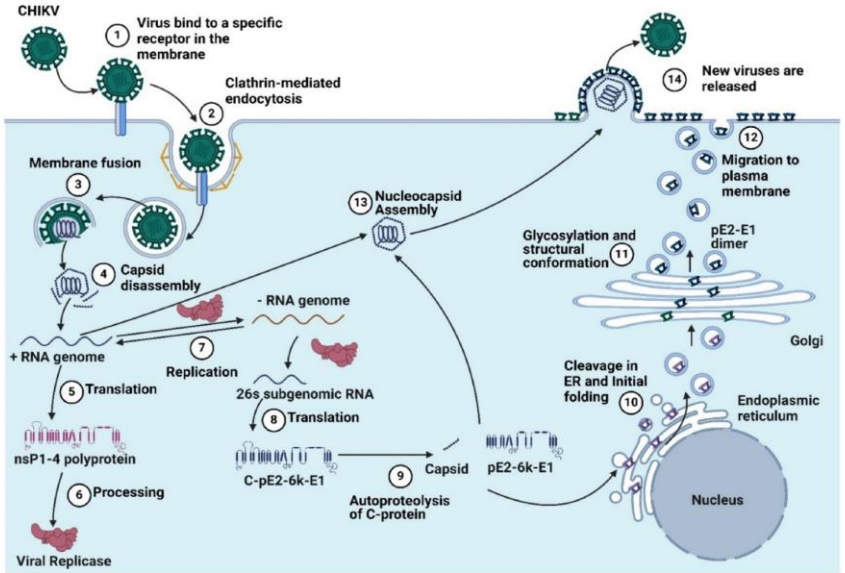

FIGURE 1
The chikungunya virus replication cycle includes (1) virus binding to a specific receptor in the membrane, (2) clathrin-mediated endocytosis, (3) membrane fusion, (4) capsid disassembly, (5) translation, (6) processing, (7) replication, (8) 26's subgenomic RNA translation, (9) autoproteolysis, (10) cleavage in the endoplastic reticulum and initial folding, and (11). Glycosylation and structural conformation, (12) migration to the plasma membrane, (13) nucleocapsid assembly, and (14) the release of new viruses (Created by using Biorender.com).

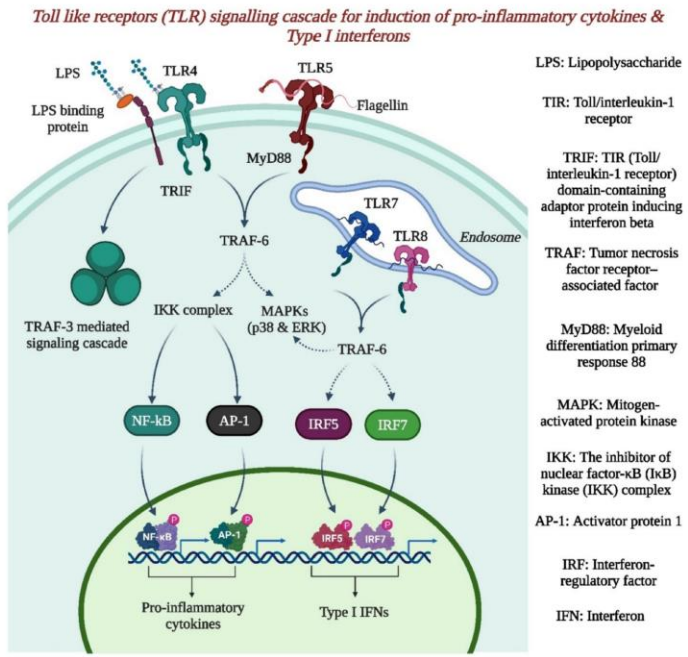

FIGURE 3
The toll like receptor signaling cascade for induction of proinflammatory cytokines & type 1 interferons (Created by using Biorender.com).

TABLE 1 CHIKV vaccine clinical trials are registered on the following websites: https://www.clinicaltrials.gov and https://www.anzctr.org.au.

Vaccine candidate	Clinical trial status	Intervention (Biological – B, Drug – D)	Sponsored by	Collaborator	Clinical trial registration no.	Study Status	Sex	Age	Phase	Enrollment	Study design Allocation: na intervention model	Study type	References
Pxvx0317	Completed	Biological – Chikv Vlp, Adjuvanted	Bavarian Nordic	Emergent Biosolutions	Nct05065983	Completed	All	Adult	2	25	Single – Group Masking – None (Primary Purpose – Prevention)	Interventional	https://clinicaltrials.gov/study/NCT05065983?intr=Nct05065983&rank=1
Pxvx031	Recruiting	Biological – Pxvx0317 Vaccine Booster & Placebo Booster	Bavarian Nordic		Nct06007183	Recruiting	All	Child, Adult, Older Adult	3	800	Parallel – Masking: Triple (Participant, Care Provider, Investigator) (Primary Purpose – Prevention)	Interventional	https://clinicaltrials.gov/study/NCT06007183?intr=PXVX0317%20vaccine%20booster&rank=1
Live-Attenuated Chikungunya Virus Vaccine	Completed	Biological – Vla1553 & Placebo	Valneva Austria Gmbh		Nct04546724	Completed	All	Adult, Older Adult	3 3	4,128	Parallel – Masking: Double (Participant, Investigator) (Primary Purpose – Prevention)	Interventional	https://clinicaltrials.gov/study/NCT04546724?intr=Nct04546724&rank=1
Vla1553	Not Yet Recruiting	Biological – Vla1553	Valneva Austria		Nct06028841	Not Yet Recruiting	All	Adult, Older Adult	3	75	Single – Group Masking – None (Primary Purpose – Prevention)	Interventional	https://clinicaltrials.gov/study/NCT06028841?intr=Nct06028841&rank=1
Chikungunya Vaccine	Active Not Recruiting	Drug – Bbv87 Chikungunya Vaccine & Normal Saline	International Vaccine Institute		Nct04566484	Active Not Recruiting	All	Child, Adult, Older Adult	2	3,210	Sequential – Masking Double (Participant, Investigator) (Primary Purpose – Prevention)	Interventional	https://clinicaltrials.gov/study/NCT04566484?intr=Nct04566484&rank=1
Live-Attenuated Chikungunya Virus Vaccine	Completed	Biological – Biological Vaccine Vla1553	Valneva Austria Gmbh		Nct04786444	Completed	All	Adult	3	409	Parallel – Masking: Double (Participant, Investigator) (Primary Purpose –Prevention)	Interventional	https://clinicaltrials.gov/study/NCT04786444?intr=Nct04786444&rank=1

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Infectious Diseases
Volume 20, Issue 6, June 2020, Pages e129-e137

Review

Prevention of yellow fever in travellers: an update

Elaine Reno MD [a], Nicolas G Quan BS [b], Carlos Franco-Paredes MD [b, c], Daniel B Chastain PharmD [d], Lakshmi Chauhan MD [b], Alfonso J Rodriguez-Morales MD [e, f] ✉, Andrés F Henao-Martínez MD [b]

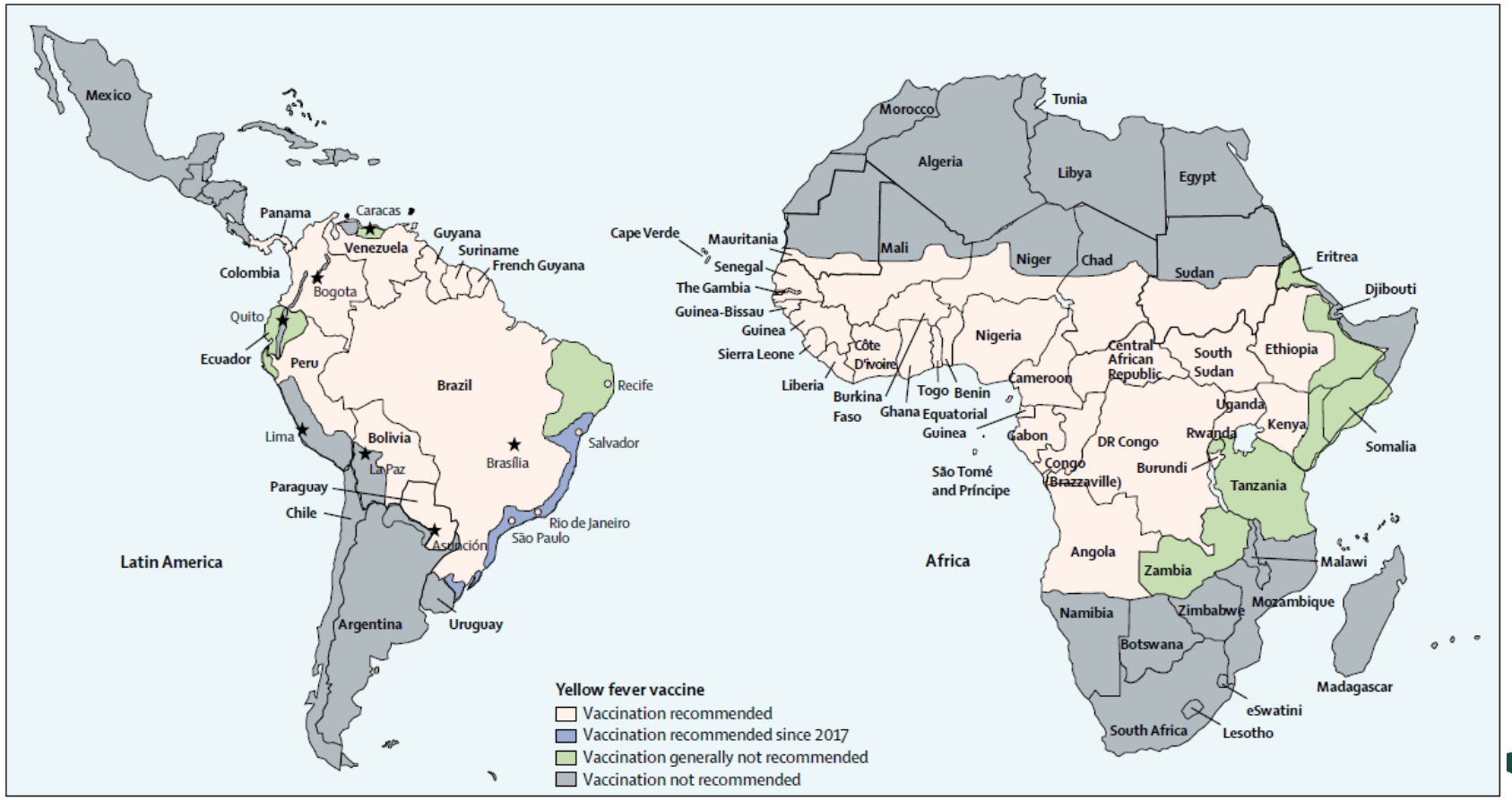
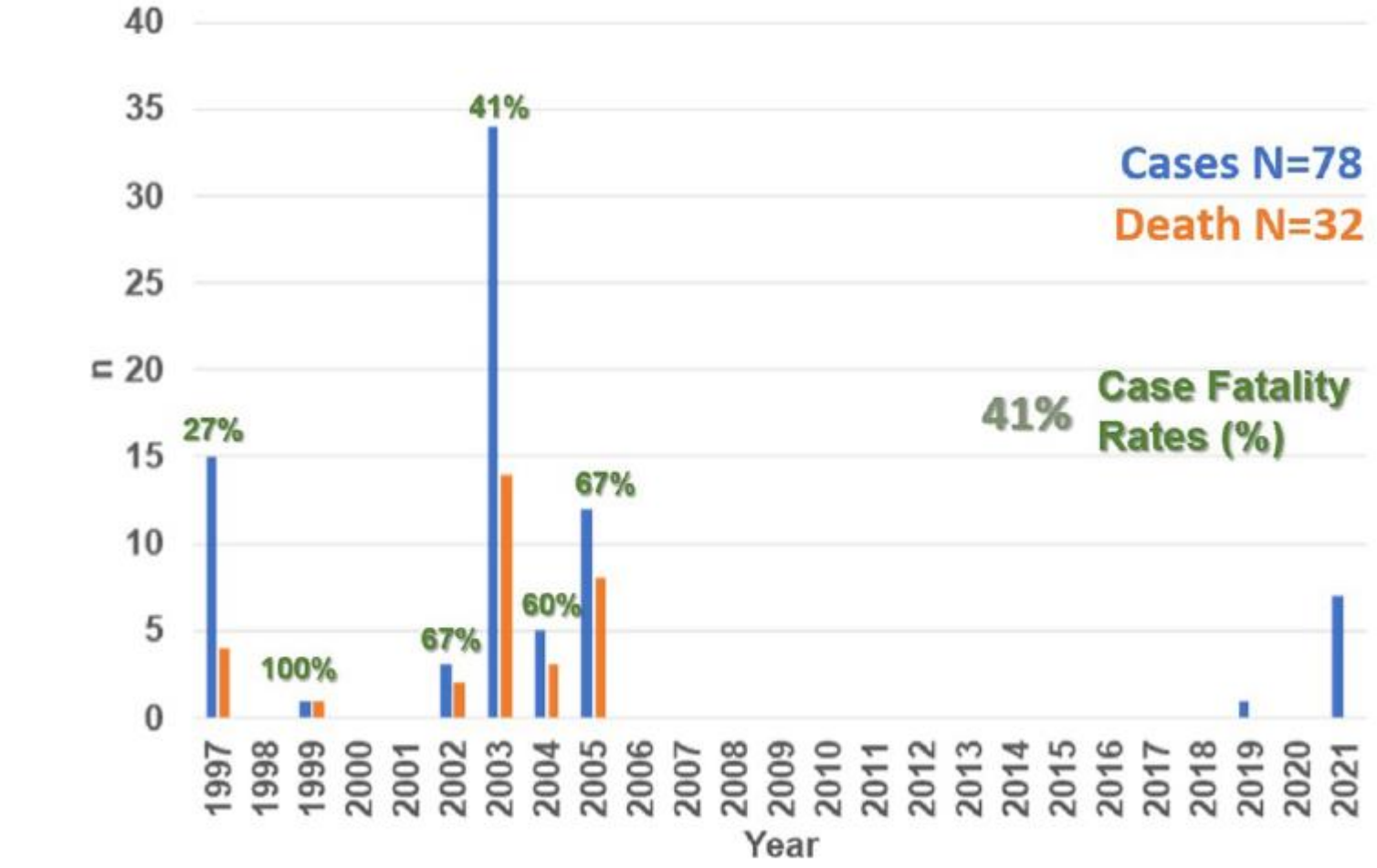


Figure 1: Geographical areas with risk of yellow fever virus transmission in Latin America and Africa

Travel Medicine and Infectious Disease
Volume 44, November–December 2021, 102192

Yellow fever reemergence in Venezuela – Implications for international travelers and Latin American countries during the COVID-19 pandemic

Alfonso J. Rodríguez-Morales [a, b, c, d, e, f, bf, bg], D. Katterine Bonilla-Aldana [b, c, d, bg], José Antonio Suárez [e, g], Carlos Franco-Paredes [e, h, i], David A. Forero-Peña [j], Salim Mattar [b, k], Wilmer E. Villamil-Gómez [b, e, l, m], Julián Ruíz-Sáenz [b, n], Jaime A. Cardona-Ospina [a, b, d, e, o, bf], Manuel E. Figuera [p], Leandro Luis Sierra-Carrero [q], Alejandro Risquez [e, r], Sergio Cimerman [s], Nereida Valero-Cedeño [t], Maritza Cabrera [u], Andrea J. Robaina-Barrios [v], Luis López-Díaz [w], Rosa Barbella [x], Rosa M. Navas [y], Fredi Díaz-Quijano [z], Yenddy Carrero [aa], Anishmenia Pineda [ab], Maximo O. Brito [ac], Eduardo Savio-Larriera [ad], Marlen Martinez-Gutierrez [ae], Julio Maquera-Afaray [af, ag], Marco A. Solarte-Portilla [ah], Sebastián Hernández-Botero [ai, aj], Krisell Contreras [ak, al], Maria Graciela López [am, an], Andrés F. Henao-Martinez [h], Yeimer Ortiz-Martinez [ao], Tânia do Socorro Souza Chaves [ap, aq], Tomas Orduna [ar], Alejandro Lepetic [as], Alejandra Macchi [at], Sergio Verbanaz [au], Cecilia Perret [av], Sofía Echazarreta [ar], Susana Cristina Lloveras [ar, aw], Viviana Gallego [ax], Juan-Carlos Navarro [ay, az], Alberto Paniz-Mondolfi [e, ba, bb, bc, bd, be]



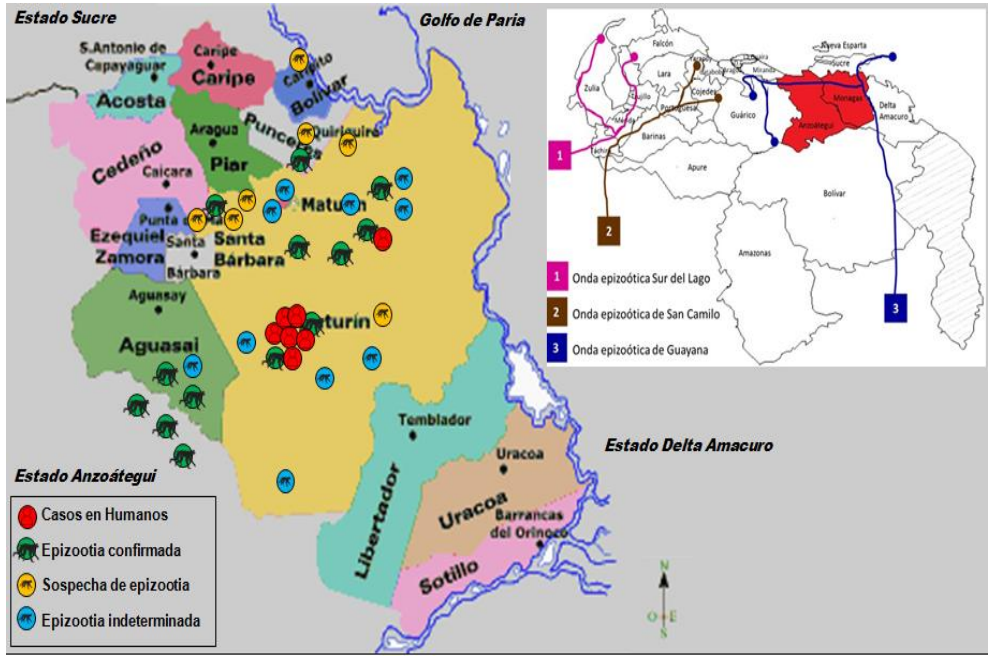
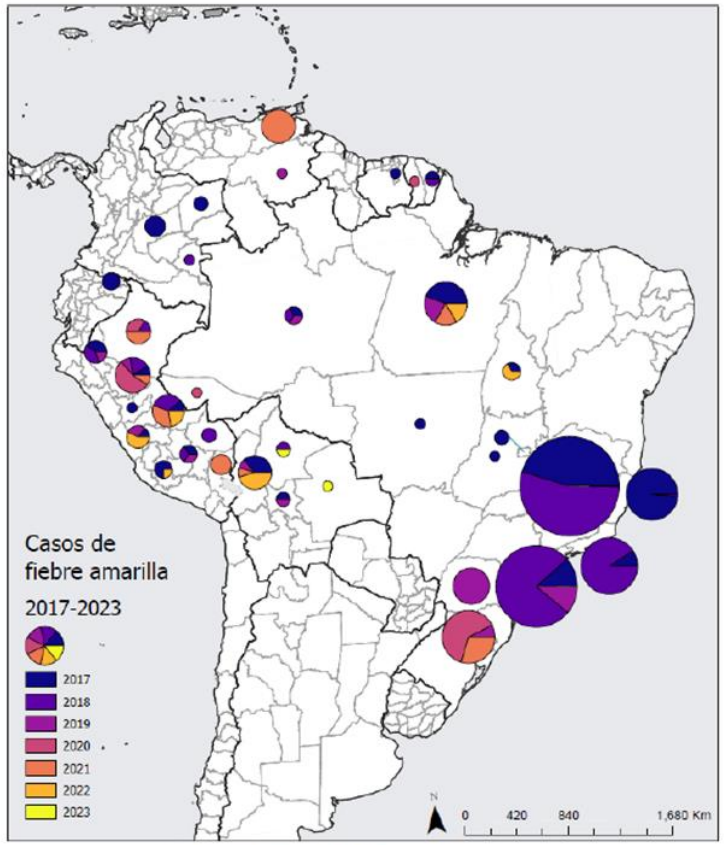


Fig. 1. Trends in the number of cases and deaths of YF in Venezuela, 1997–2021.

Rodríguez-Morales AJ, Bonilla-Aldana DK, Suárez JA, Franco-Paredes C, Forero-Peña DA, Mattar S, Villamil-Gómez WE, Ruíz-Sáenz J, Cardona-Ospina JA, Figuera ME, Sierra-Carrero LL, Risquez A, Cimerman S, Valero-Cedeño N, Cabrera M, Robaina-Barrios AJ, López-Díaz L, Barbella R, Navas RM, Díaz-Quijano F, Carrero Y, Pineda A, Brito MO, Savio-Larriera E, Martinez-Gutierrez M, Maquera-Afaray J, Solarte-Portilla MA, Hernández-Botero S, Contreras K, López MG, Henao-Martinez AF, Ortiz-Martinez Y, Chaves TDSS, Orduna T, Lepetic A, Macchi A, Verbanaz S, Perret C, Echazarreta S, Lloveras SC, Gallego V, Navarro JC, Paniz-Mondolfi A. ***Travel Med Infect Dis***. 2021 Oct 29;44:102192.

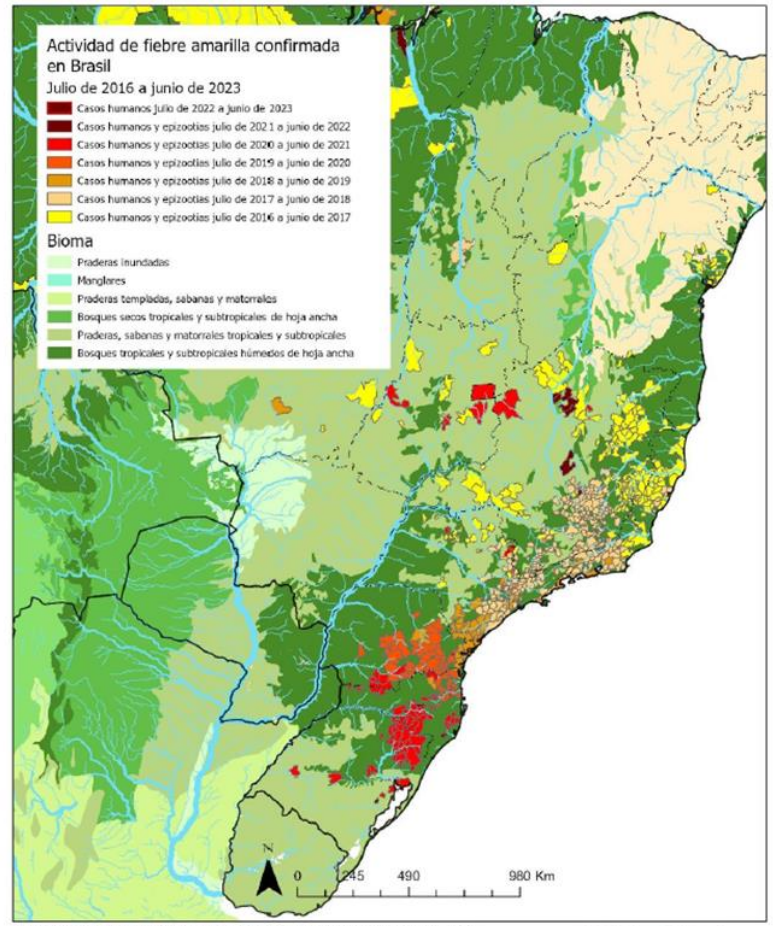
Figura 1. Distribución geográfica de casos de fiebre amarilla en humanos en la Región de las Américas, de enero 2017 a abril 2023.



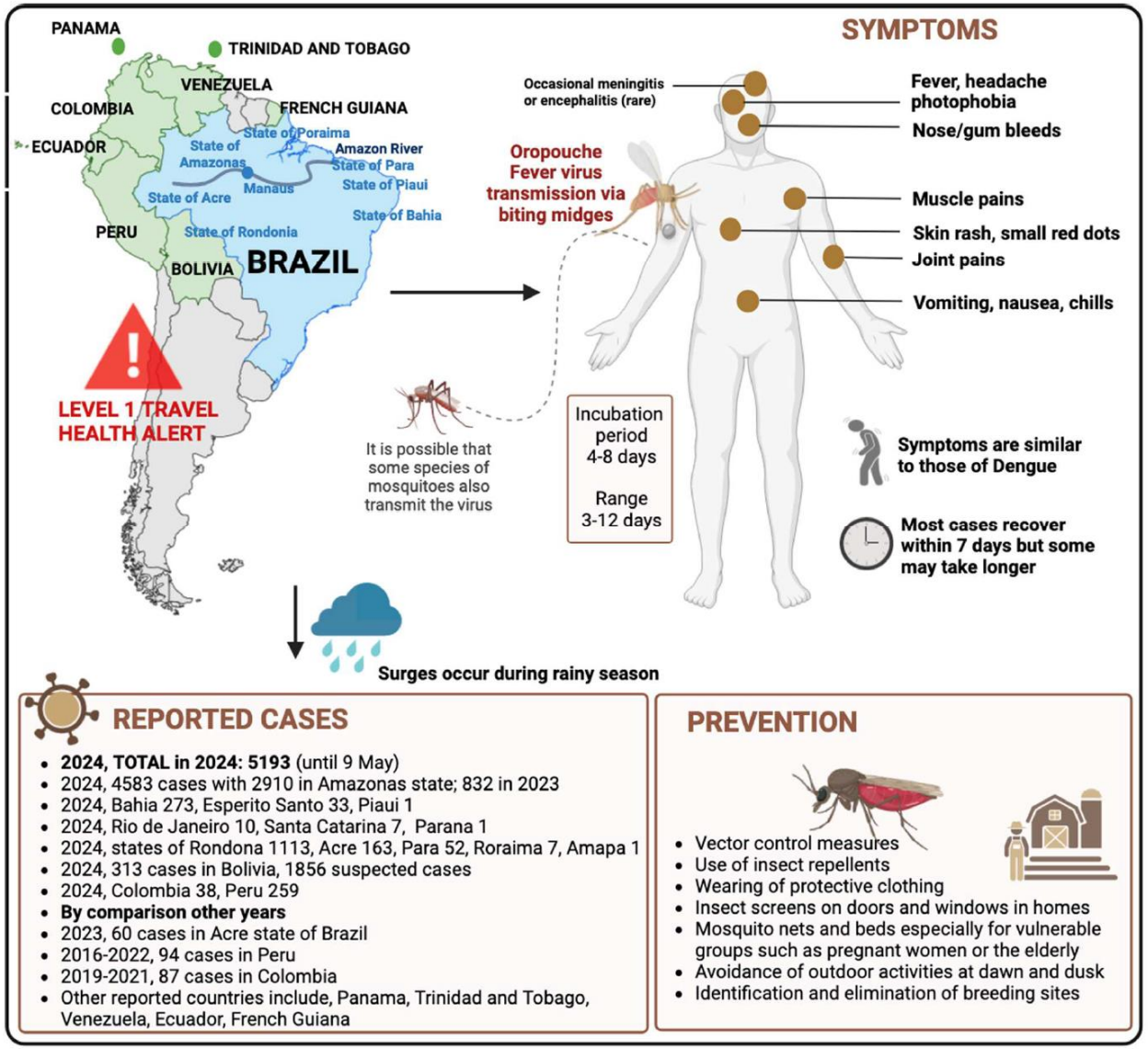
En lo que va del 2023, se registraron casos humanos en Bolivia (dos) y Brasil (tres).

Fuente: Datos aportados por los países o publicados por los Ministerio de Salud y reproducidos por la OPS/OMS

Figura 2. Distribución geográfica de casos de fiebre amarilla en humanos y epizootias. Brasil, enero 2017 a abril 2023.



Fuente: Datos publicados por el Ministerio de Salud del Brasil y reproducidos por la OPS/OMS



Oropouche fever outbreak in Brazil: an emerging concern in Latin America

*Ranjit Sah, *Shriyansh Srivastava, Sachin Kumar, Pougang Golmei, SK Abdul Rahaman, Rachana Mehta, Carolina Ferraz, Vasso Apostolopoulos, Alfonso J Rodriguez-Morales

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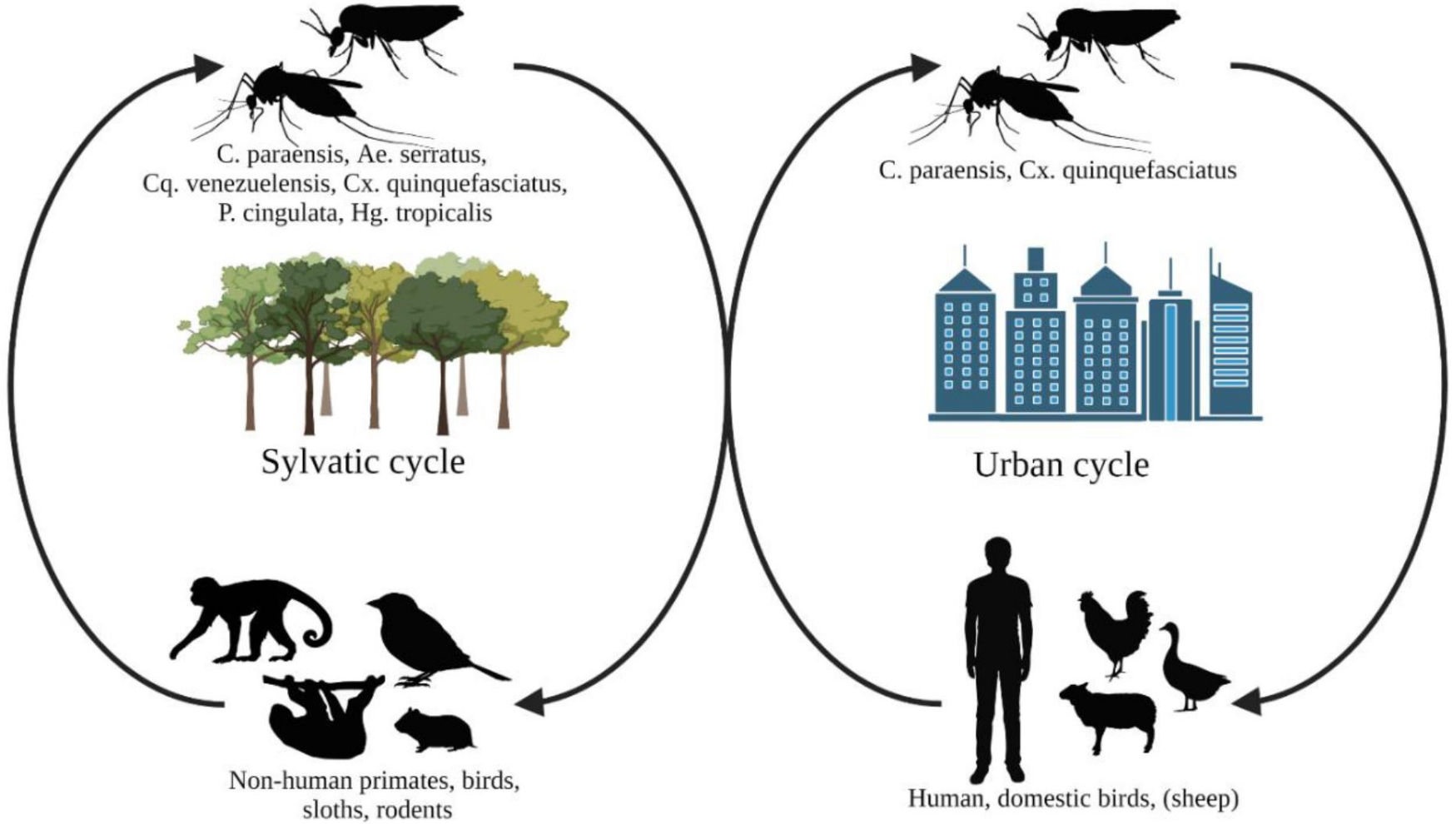


Figure S1. Representation of the sylvatic and urban transmission cycles of Oropouche virus. Created with BioRender.com.

Wesselmann KM, Postigo-Hidalgo I, Pezzi L, et al. Emergence of Oropouche fever in Latin America: a narrative review. *Lancet Infect Dis* 2024; published online Jan 25. https://doi.org/10.1016/S1473-3099(23)00740-5.

PAHO

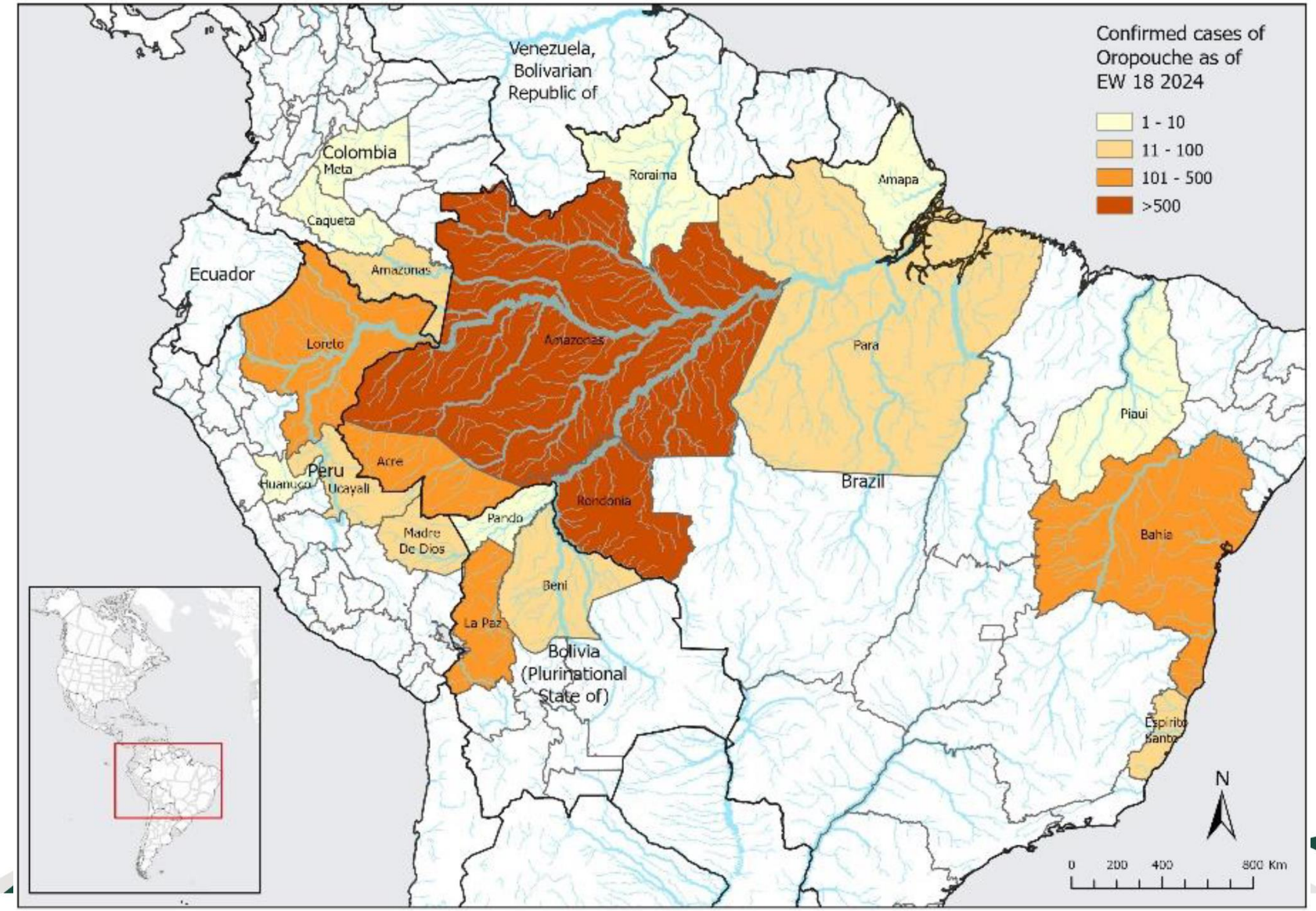
Pan American Health Organization

World Health Organization Americas

Epidemiological Alert Oropouche in the Region of the Americas

9 May 2024

In 2024, 5,193 confirmed cases of Oropouche have been reported in four countries in the Region of the Americas: the Plurinational State of Bolivia, Brazil, Colombia, and Peru.



THREAT ASSESSMENT BRIEF

Oropouche virus disease cases imported into the European Union

9 August 2024

Summary

Epidemiological situation

In June and July 2024, 19 imported cases of Oropouche virus disease were reported for the first time in EU countries: Spain (12), Italy (5), and Germany (2). Eighteen of the cases had a travel history to Cuba and one to Brazil. Oropouche virus disease is a zoonotic disease caused by the Oropouche virus (OROV). To date, outbreaks of OROV disease have been reported in several countries across South America, Central America and the Caribbean. During 2024, outbreaks have been reported in Brazil, Bolivia, Colombia, Peru, and more recently in Cuba. Oropouche virus is mainly transmitted to humans as a result of being bitten by infected midges, however some mosquitoes species can also spread the virus. The principal vector (*Culicoides paraensis* midge) is widely distributed across the Americas, but absent in Europe. To date, there has been a lack of evidence as to whether European midges or mosquitoes could transmit the virus. Oropouche virus disease can manifest as an acute febrile illness with headache, nausea, vomiting, muscle and joint pains, and occasionally more severe symptoms. The prognosis for recovery is good and fatal outcomes are extremely rare. There are no vaccines to prevent or specific medication to treat OROV disease. Direct, horizontal, human-to-human transmission of the virus has not been documented so far. Recently, the Brazilian Ministry of Health reported six possible cases of OROV disease being passed from mother-to-child during pregnancy. The potential risk during pregnancy and fetopathic effects of OROV infection are still under investigation and have not been confirmed.

Risk assessment

The likelihood of infection for EU/EEA citizens travelling to, or residing in epidemic areas in South and Central America is currently assessed as moderate. The likelihood of infection increases if travellers visit the more-affected municipalities of the northern states of Brazil and/or the Amazon region, and/or if personal protection measures are not taken. Given the good prognosis for recovery, the impact is assessed as low. The risk of infection for EU/EEA citizens travelling to OROV-epidemic countries in the Americas is therefore assessed as moderate.

Recent data indicate that OROV infection in pregnant women may lead to miscarriage, abortion and/or developmental problems, and deformities of the foetus. The impact of OROV infection for pregnant women, foetuses and newborns could therefore be higher than for the general population, although this is still under investigation.

The likelihood of human exposure to OROV in the EU/EEA is considered very low, despite the possible importation of further OROV disease cases, as the competent vectors commonly described in the Americas are absent from continental Europe, and to date, no secondary transmission has ever been reported. Therefore, the risk of locally-acquired OROV disease in the EU/EEA is low.

Suggested citation: European Centre for Disease Prevention and Control. Oropouche virus disease cases imported into the European Union – 9 August 2024. Stockholm; ECDC: 2024.

Stockholm, August 2024

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Catalogue number: TQ-05-24-660-EN-N

The Lancet Regional Health - Americas

Volume 38, October 2024, 100896

Comment

Oropouche fever fatalities and vertical transmission in South America: implications of a potential new mode of transmission

Ranjit Sah [a b c], Shriyansh Srivastava [d e], Rachana Mehta [f g h], Sharib Raza Khan [i], Sachin Kumar [d], Prakashini Satpathy [j], Aroop Mohanty [k], Carolina Ferraz [l], Jack Feehan [m], Vasso Apostolopoulos [m q], Camila Luna [n], Alfonso J. Rodriguez-Morales [n o p q]

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Oropouche fever fatalities and vertical transmission in South America: implications of a potential new mode of transmission

Ranjit Sah [a b c], Shriyansh Srivastava [d e], Rachana Mehta [f g h], Sharib Raza Khan [i], Sachin Kumar [d], Prakashini Satpathy [j], Aroop Mohanty [k], Carolina Ferraz [l], Jack Feehan [m], Vasso Apostolopoulos [m q], Camila Luna [n], Alfonso J. Rodriguez-Morales [n o p q]

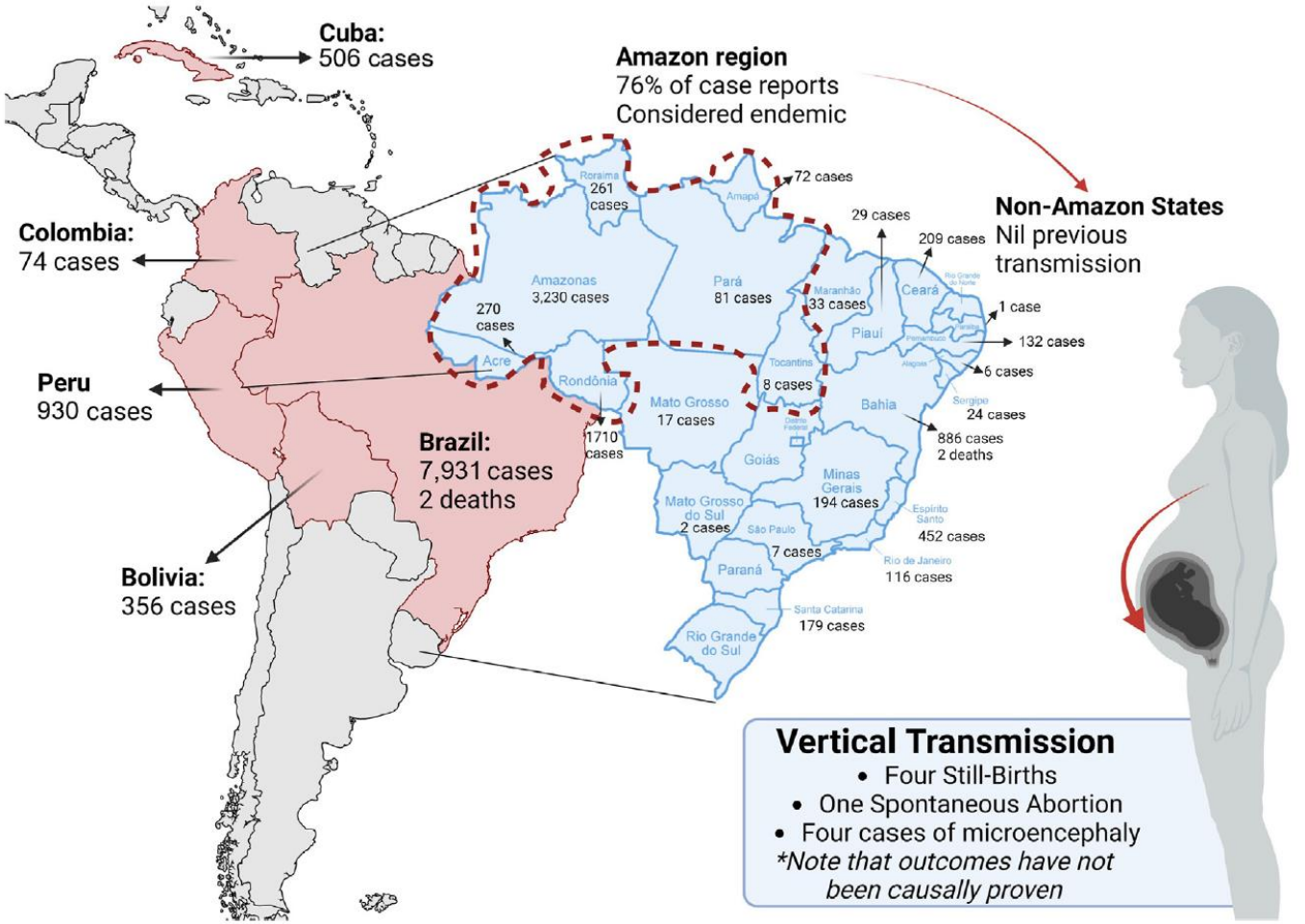

Fig. 1: Oropouche virus in Latin America has led to reported cases, including two deaths in Brazil. Vertical transmission has been observed, with one fetal death, one miscarriage, and four instances of microcephaly in newborns, although no causal link has been confirmed. This remains to be confirmed. Additionally, there are three more fetal deaths in Pernambuco state, with two cases still under investigation. These instances of vertical transmission complicate the understanding of new infection routes, potentially contributing to emerging epidemic patterns, and suggest further research into their implications for maternal and neonatal health.

First diagnoses of Oropouche virus in Europe: how can we strengthen communication and preparedness globally?

Lancet Infect Dis 2024

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A

B

Traveller 1

	2 days from symptom onset (diagnosis)			5 days from symptom onset			19 days from symptom onset			32 days from symptom onset		
	Whole blood (Ct)	Serum (Ct)	Urine (Ct)	Whole blood (Ct)	Serum (Ct)	Urine (Ct)	Whole blood (Ct)	Serum (Ct)	Urine (Ct)	Whole blood (Ct)	Serum (Ct)	Urine (Ct)
Oropouche virus (RT-PCR)	+ (24·51)	+ (22·60)	– (>45)	+ (34·99)	+ (32·93)	– (>45)	+ (37·28)	– (>45)	+ (39·13)	– (>45)	– (>45)	NA

Traveller 2

	7 days from symptom onset (diagnosis)			14 days from symptom onset			30 days from symptom onset		
	Whole blood (Ct)	Serum (Ct)	Urine (Ct)	Whole blood (Ct)	Serum (Ct)	Urine (Ct)	Whole blood (Ct)	Serum (Ct)	Urine (Ct)
Oropouche virus (RT-PCR)	+ (37·89)	– (>45)	+ (38·50)	+ (40·67)	– (>45)	– (>45)	– (>45)	– (>45)	– (>45)

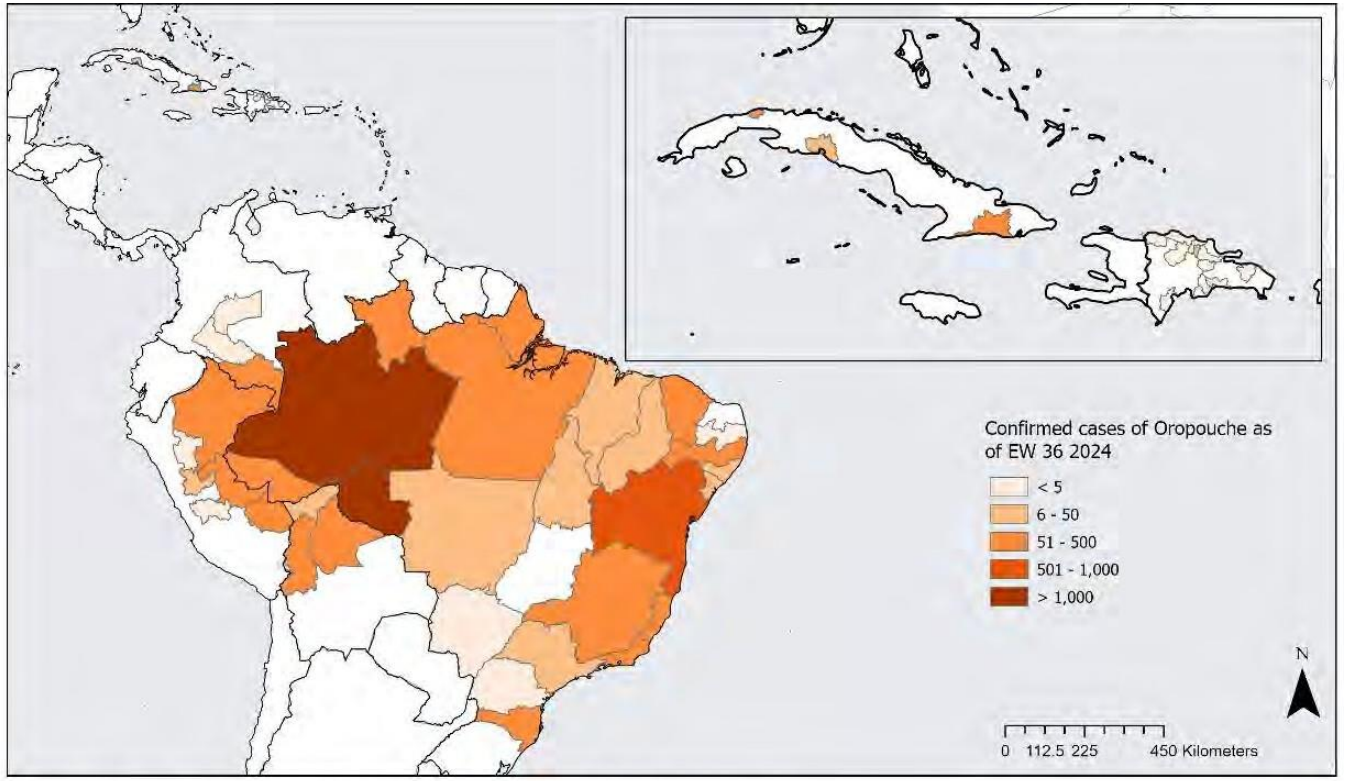
Figure: **Oropouche virus in Cuba and Italy**
(A) Map of Cuba in which the presence of the Oropouche virus in nine provinces and 23 municipalities was confirmed by the national reference laboratory of the Pedro Kourí Institute of Tropical Medicine. (B) Virological findings in two people with Oropouche fever during 1-month follow-up. Oropouche virus-specific molecular tests were done as previously described.[6,7] Both assays were done with Reliance One-Step Multiplex Supermix 4X (Biorad, Hercules, CA, USA). Ct=cycle threshold. NA=not available.

Sept 2024 – Further spread, > 9800 cases

Country	Confirmed
Bolivia	356
Brazil	7931
Canada*	1
Cuba	506
Colombia	74
Dom. Rep.	33
Europe*	30
Peru	930
USA*	21
Total	9852

*imported cases only

Source: PAHO Bulletin (06/08/2024)



PAHO
Pan American Health Organization
World Health Organization Americas

Map production: PAHO Health Emergencies Department, Health Emergency Information and Risk Assessment Unit, GIS Team.

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Review | Open Access | Published: 19 May 2020

Venezuelan equine encephalitis virus: the problem is not over for tropical America

Camilo Guzmán-Terán, Alfonso Calderón-Rangel, Alfonso Rodriguez-Morales & Salim Mattar

Annals of Clinical Microbiology and Antimicrobials **19**, Article number: 19 (2020) | Cite this article

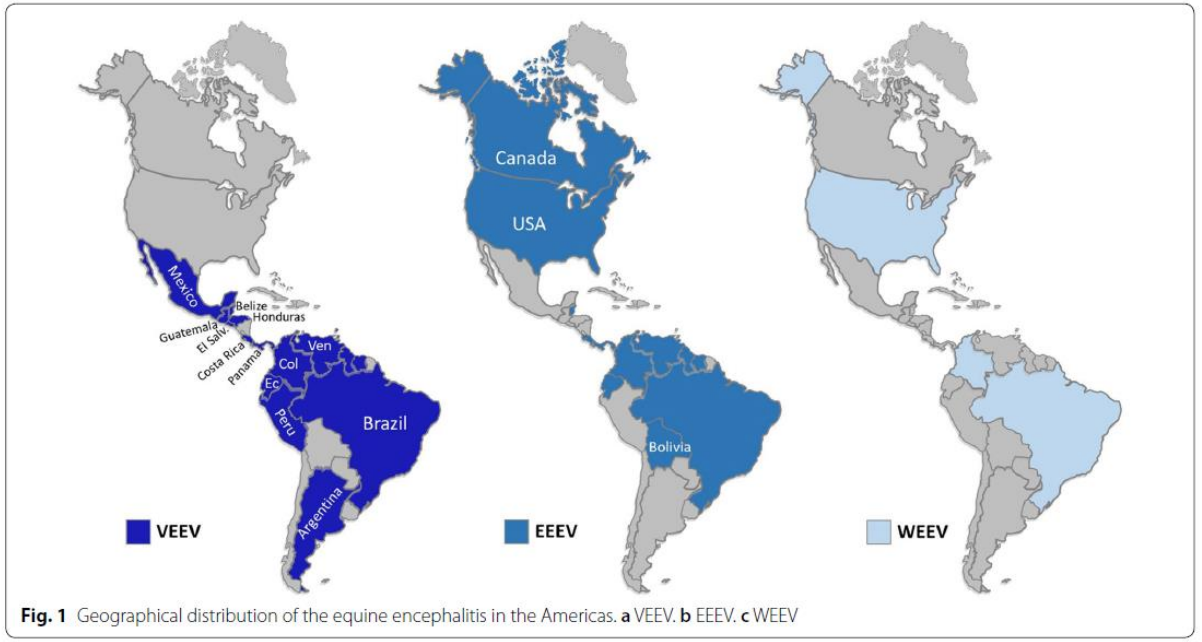

Fig. 1 Geographical distribution of the equine encephalitis in the Americas. **a** VEEV. **b** EEEV. **c** WEEV

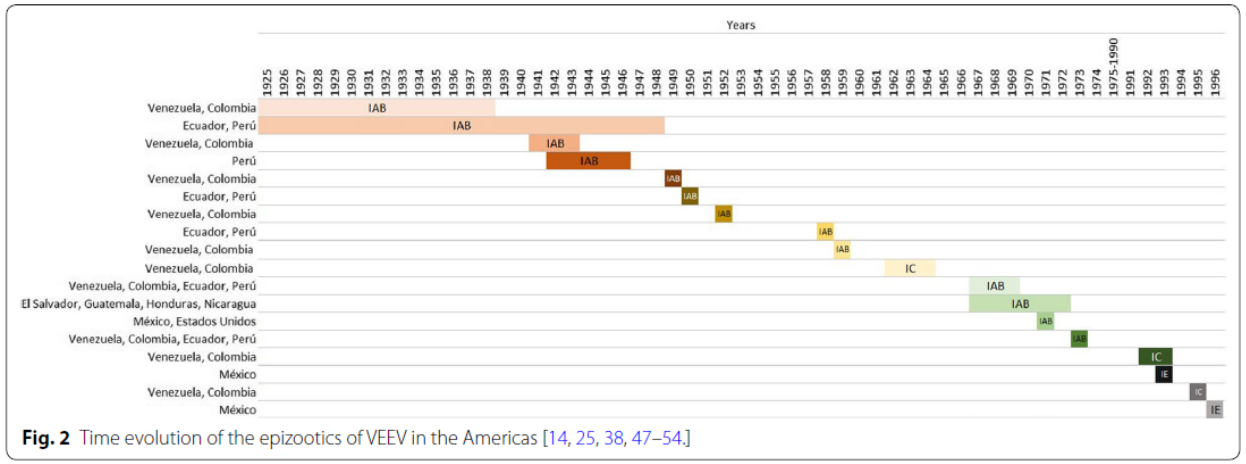

Fig. 2 Time evolution of the epizootics of VEEV in the Americas [14, 25, 38, 47–54.]

Table 1 Subtypes and serotypes of the VEEV complex

Subtypes	Species	Serotypes	Transmission cycles
I	VEE virus	AB	Epizootic
	VEE virus	C	
	VEE virus	D	Enzootic
	VEE virus	E	
	Mosso das Pedras virus	F	
II	Everglades virus		
III	Mucambo virus	A	
	Tonate virus	B	
	Mucambo virus	C	
	Mucambo virus	D	
IV	Pixuna		
V	Cabassou virus		
VI	Rio Negro virus		

viruses

MDPI

Article

Mapping Eastern (EEE) and Venezuelan Equine Encephalitides (VEE) among Equines Using Geographical Information Systems, Colombia, 2008–2019

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Abstract: Introduction: Eastern equine encephalitis virus (EEEV) and Venezuelan equine encephalitis virus (VEEV) viruses are zoonotic pathogens affecting humans, particularly equines. These neuroarboviruses compromise the central nervous system and can be fatal in different hosts. Both have significantly influenced Colombia; however, few studies analyse its behaviour, and none develop maps using geographic information systems to characterise it. Objective: To describe the temporal-spatial distribution of those viruses in Colombia between 2008 and 2019. Methods: Retrospective cross-sectional descriptive study, based on weekly reports by municipalities of the ICA, of the surveillance of both arboviruses in equines, in Colombia, from 2008 to 2019. The data were converted into databases in Microsoft Access 365®, and multiple epidemiological maps were generated with the Kosmo RC1®3.0 software coupled to shape files of all municipalities in the country. Results: In the study period, 96 cases of EEE and 70 of VEE were reported, with 58% of EEE cases occurring in 2016 and 20% of EEV cases in 2013. The most affected municipalities for EEE corresponded to the department of Casanare: Yopal (20), Aguazul (16), and Tauramena (10). In total, 40 municipalities in the country reported ≥1 case of EEE. Conclusions: The maps allow a quick appreciation of groups of neighbouring municipalities in different departments (1° political division) and regions of the country affected by those viruses, which helps consider the expansion of the disease associated with mobility and transport of equines between other municipalities, also including international borders, such as is the case with Venezuela. In that country, especially for EEV, municipalities in the department of Cesar are bordering and at risk for that arboviral infection. there is a high risk of equine encephalitis outbreaks, especially for VEE. This poses a risk also, for municipalities in the department of Cesar, bordering with Venezuela.

Keywords: eastern equine encephalitis virus (EEEV); infection; Venezuelan equine encephalitis (VEEV); GIS; geographic information systems; equines; epidemiology

check for updates

Citation: Bonilla-Aldana, D.K.; Bonilla Carvajal, C.D.; Moreno-Ramos, E.; Barboza, J.J.; Rodriguez-Morales, A.J. Mapping Eastern (EEE) and Venezuelan Equine Encephalitides (VEE) among Equines Using Geographical Information Systems, Colombia, 2008–2019. *Viruses* **2023**, *15*, 707. https://doi.org/10.3390/v15030707

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1. Introduction

Vector-borne diseases remain a significant public health problem in tropical and subtropical regions, especially those of viral aetiology. Beyond dengue, chikungunya, and Zika, other particularly zoonotic arboviruses, such as the case of equine encephalitides,

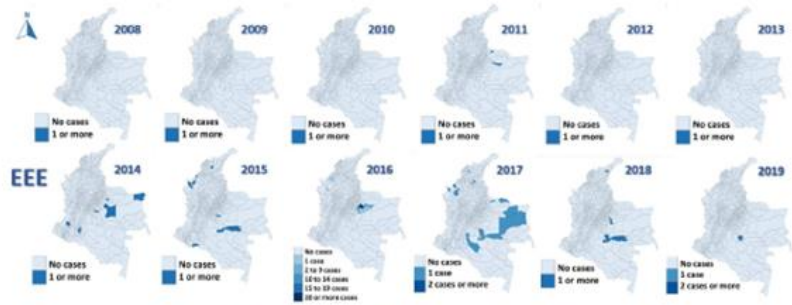


Figure 3. Distribution maps of EEE among equines, Colombia, 2008–2019.

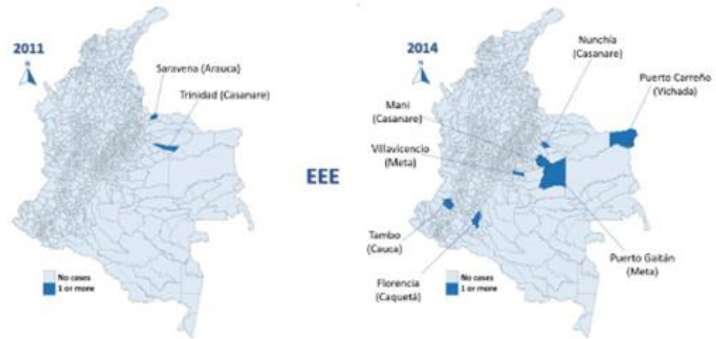


Figure 4. EEE among equines in affected municipalities of Colombia, 2011 and 2014.

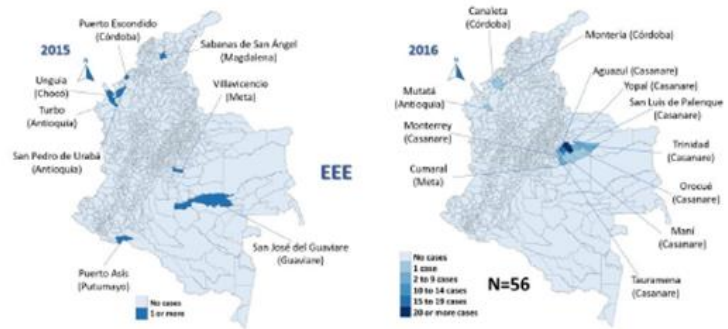


Figure 5. EEE among equines in affected municipalities of Colombia, 2015 and 2016.

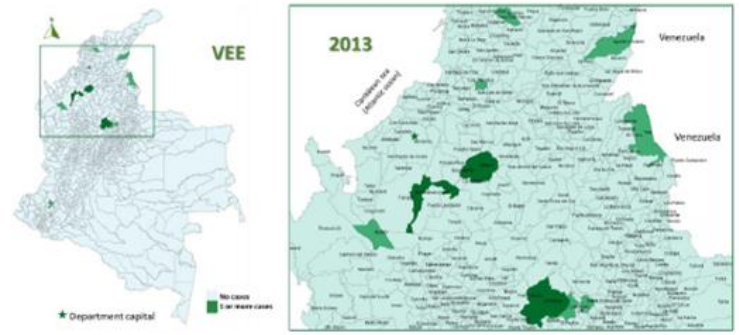


Figure 9. VEE among equines in affected municipalities of Colombia, 2013.

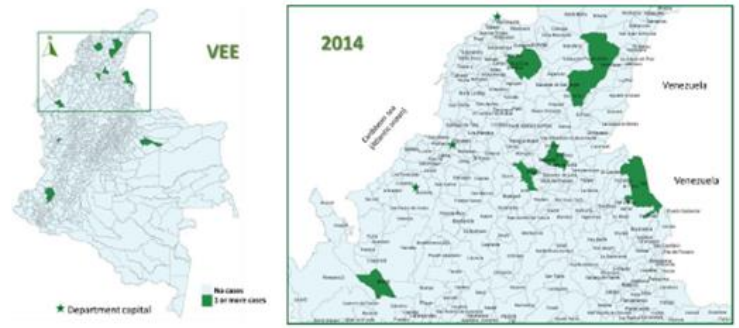
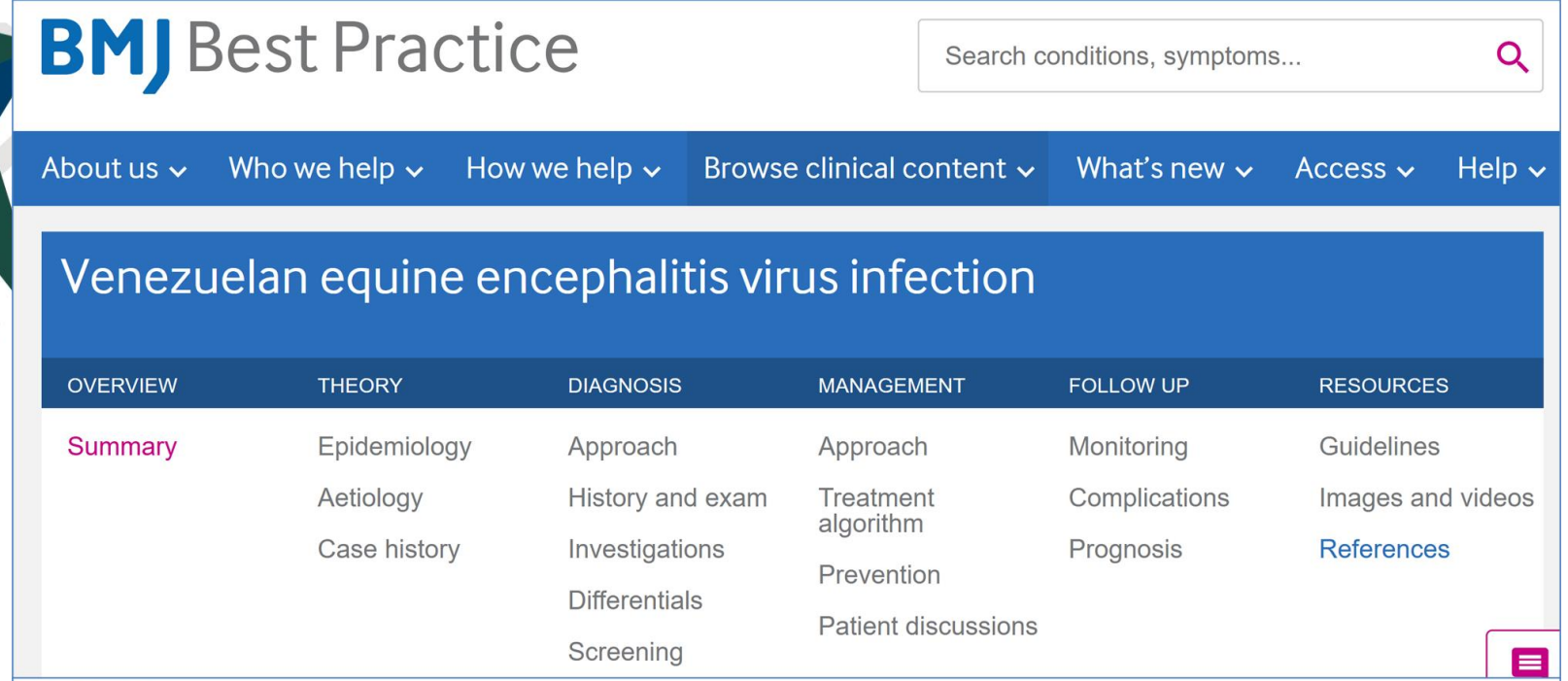


Figure 10. VEE among equines in affected municipalities of Colombia, 2014.

Figure 11. VEE among equines in affected municipalities of Colombia, 2016.



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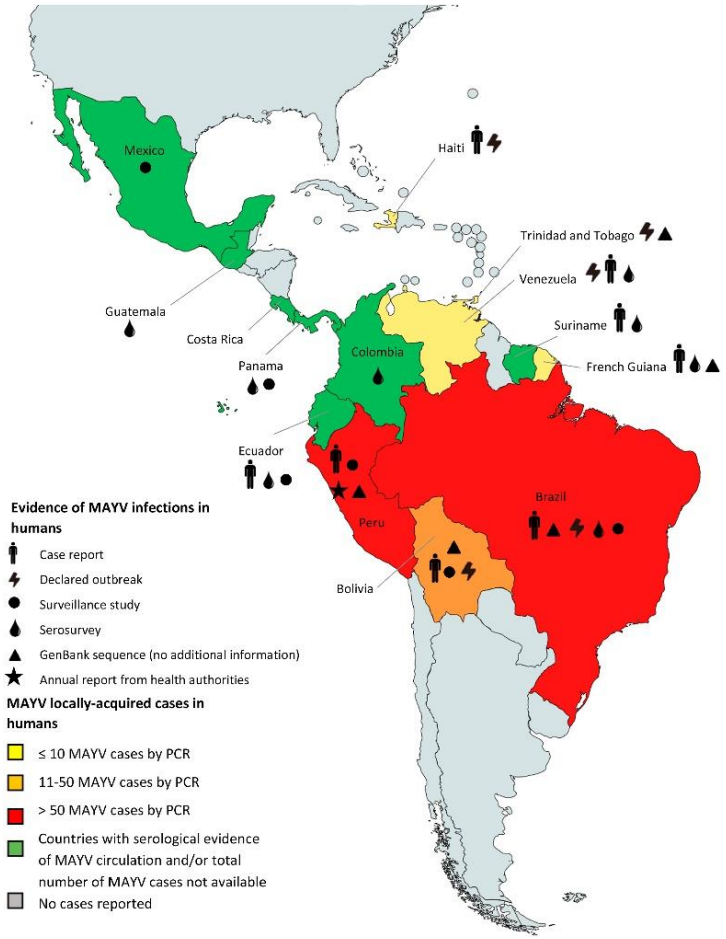
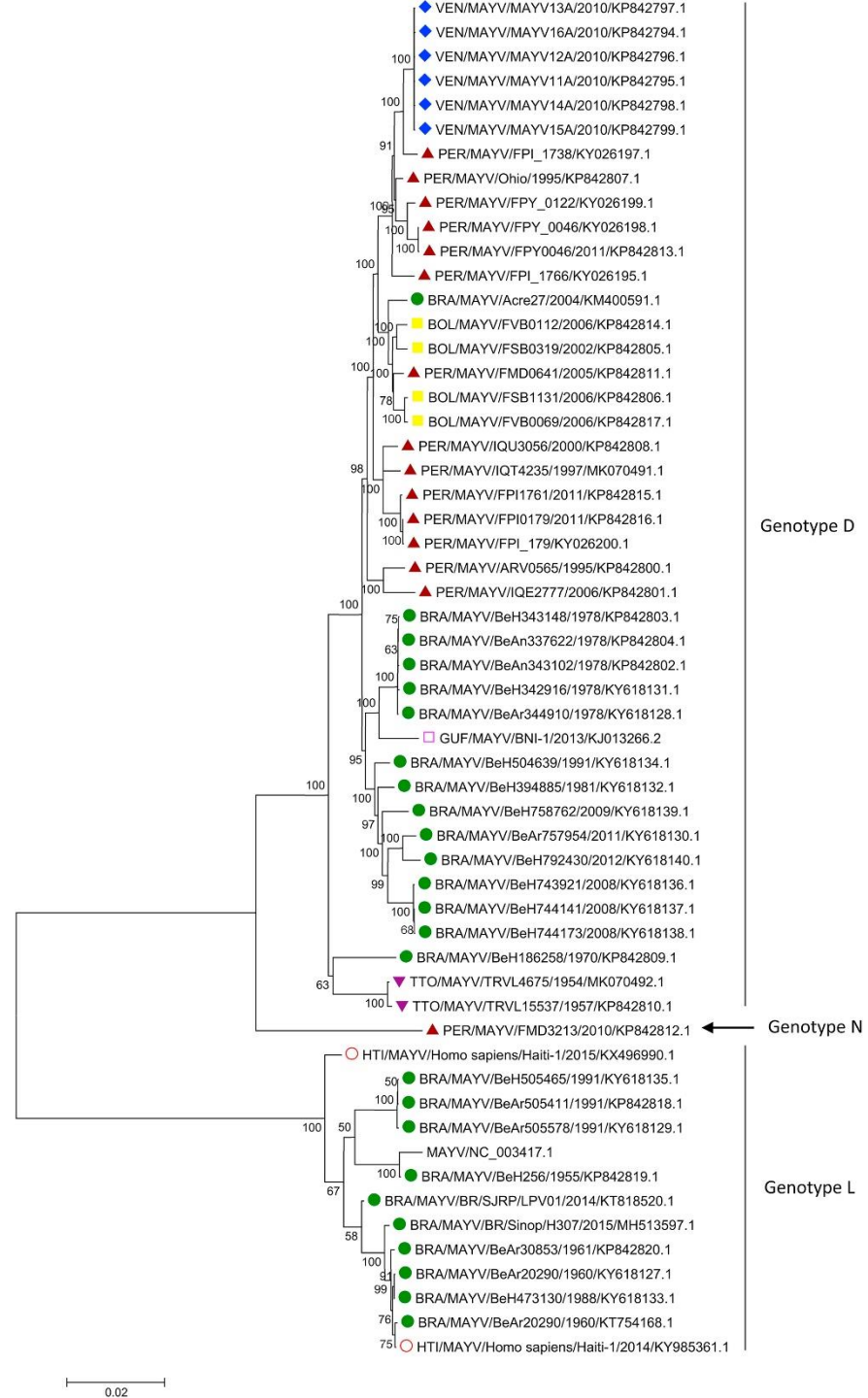
Antiviral Research
Volume 172, December 2019, 104610

GloPID-R report on chikungunya, o'nyong-nyong and Mayaro virus, part 3: Epidemiological distribution of Mayaro virus

L. Pezzi [a, b], A.J. Rodriguez-Morales [c], C.B. Reusken [d, e], G.S. Ribeiro [f], A.D. LaBeaud [g], R. Lourenço-de-Oliveira [h], P. Brasil [i], M. Lecuit [j], A.B. Failloux [k], P. Gallian [l], T. Jaenisch [m], F. Simon [n], A.M. Siqueira [i], M.G. Rosa-Freitas [h], A. Vega Rua [o], S.C. Weaver [p], J.F. Drexler [q, r], N. Vasilakis [s] ... G. Simmons [ae, af]





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Published online: 27 November 2023

REVIEW

Clinical, Epidemiological, and Laboratory Features of Mayaro Virus Infection: a Systematic Review

Carlos Ramiro Silva-Ramos[1] · Julián A. Mejorano-Fonseca[1] · Marylin Hidalgo[1] · Alfonso J. Rodríguez-Morales[2,3] · Álvaro A. Faccini-Martínez[4,5,6]

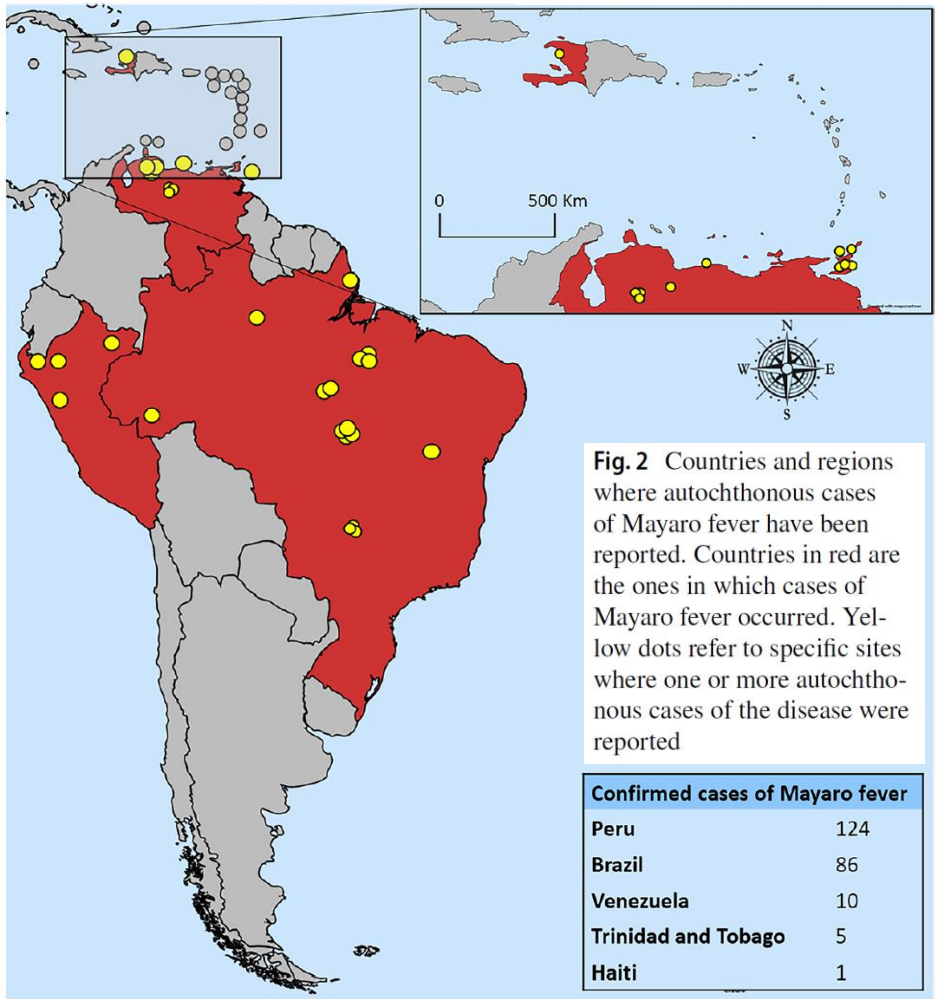

Fig. 2 Countries and regions where autochthonous cases of Mayaro fever have been reported. Countries in red are the ones in which cases of Mayaro fever occurred. Yellow dots refer to specific sites where one or more autochthonous cases of the disease were reported

Confirmed cases of Mayaro fever	
Peru	124
Brazil	86
Venezuela	10
Trinidad and Tobago	5
Haiti	1

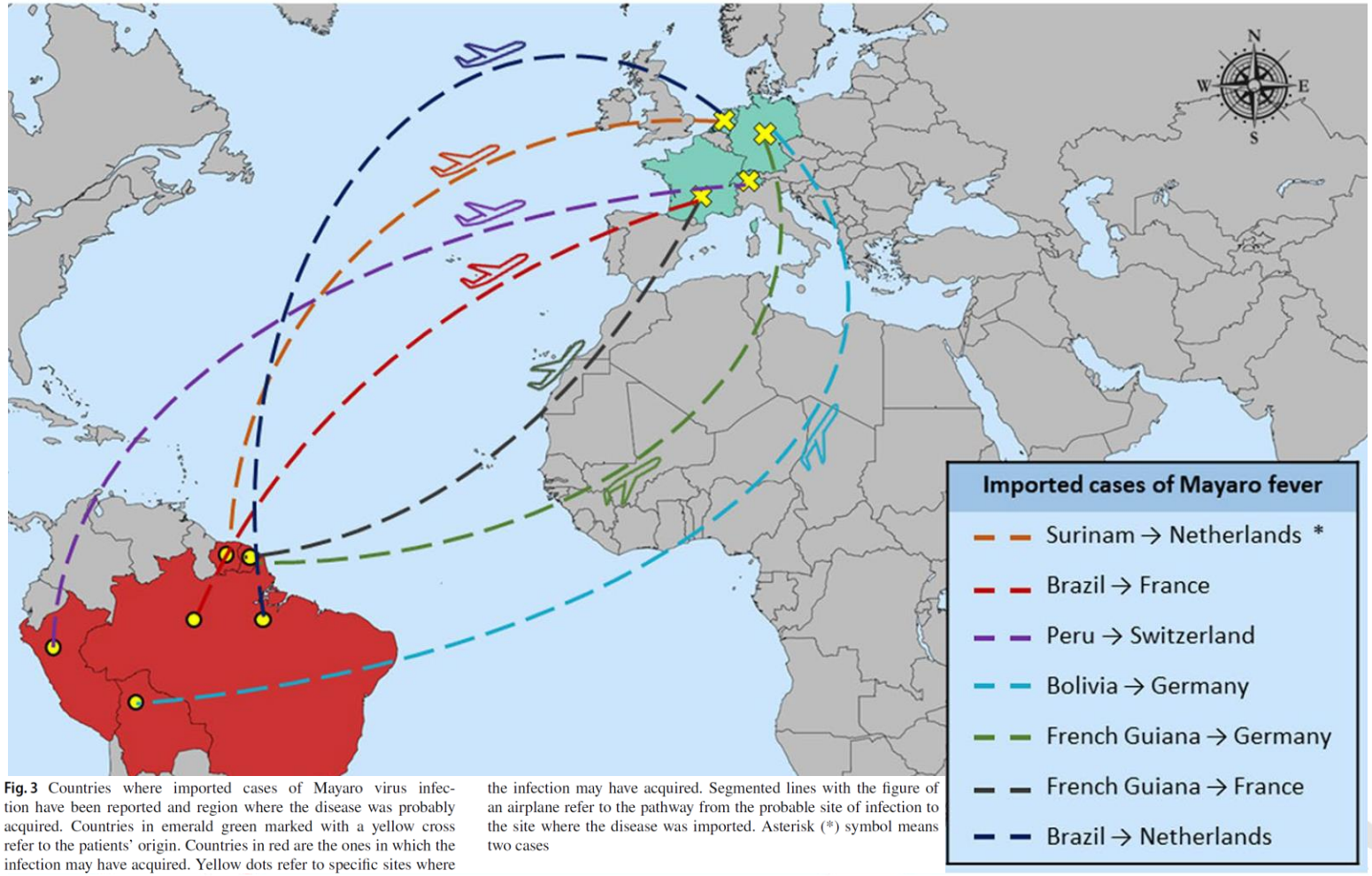

Fig. 3 Countries where imported cases of Mayaro virus infection have been reported and region where the disease was probably acquired. Countries in emerald green marked with a yellow cross refer to the patients' origin. Countries in red are the ones in which the infection may have acquired. Yellow dots refer to specific sites where the infection may have acquired. Segmented lines with the figure of an airplane refer to the pathway from the probable site of infection to the site where the disease was imported. Asterisk (*) symbol means two cases

Journal of Infection and Public Health 17 (2024) 102510

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journal homepage: www.elsevier.com/locate/jiph

Original article

Unexpected arboviruses found in an epidemiological surveillance of acute tropical febrile syndrome in the department of Meta, Eastern Colombia

Liliana Sánchez-Lerma [a], Andres Rojas-Gulloso [a], Jorge Miranda [b], Vanesa Tique [b], Luz Helena Patiño [c], Derly Rodriguez [d], Verónica Contreras [b], Alberto Paniz-Mondolfi [e], Norma Pavas [a], Juan David Ramírez [c,e], Salim Mattar [b,*]

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[e] Molecular Microbiology Laboratory, Department of Pathology, Molecular and Cell-based Medicine, Icahn School of Medicine at Mount Sinai, NY, USA

Usutu in Colombia

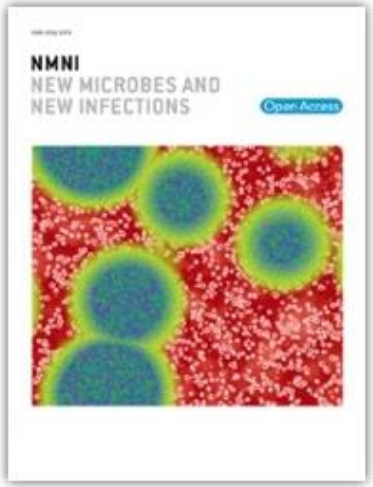
Table 2
Serological information of arboviruses in patients with positive RT-PCR for USUV.

Patient	Usutu (IgG)*				Chikungunya (IgG)**	Mayaro (IgG)**	Dengue (IgM) ***
	Acute serum	Convalescent serum	Seroconversion	CtRT-qPCR	Convalescent serum	Convalescent serum	Acute serum
4	Neg	Pos	Yes	32.4	Posit (3,8 > 5,8) ♦	Posit (0,6 > 5,2) ♦	Neg
37	Neg	Neg	No	30.3	Neg	Pos	Neg
72	Neg	Neg	No	26.8	Neg	Neg	Neg
75	Neg	Pos	Yes	32.0	Neg	Neg	Neg
82	Neg	Neg	No	31.0	Neg	Neg	Neg
84	Pos	Pos	Yes	34.3	Pos	Neg	Pos
94	Neg	Neg	No	33.1	Neg	Neg	Neg
97	Neg	Neg	No	32.4	Neg	Pos	Neg
100	Pos	ND	ND	29.8	Neg	ND	Neg

Neg: negative
Pos: Positive
ND: Not done
*All patients were RT-qPCR positive for USUV.
**PCR Neg, except for patient 4, serology was only done on convalescent serum.
***PCR Neg, was not determined in convalescent serum.
♦patients with high seroconversion (acute serum < convalescent serum).

Contents

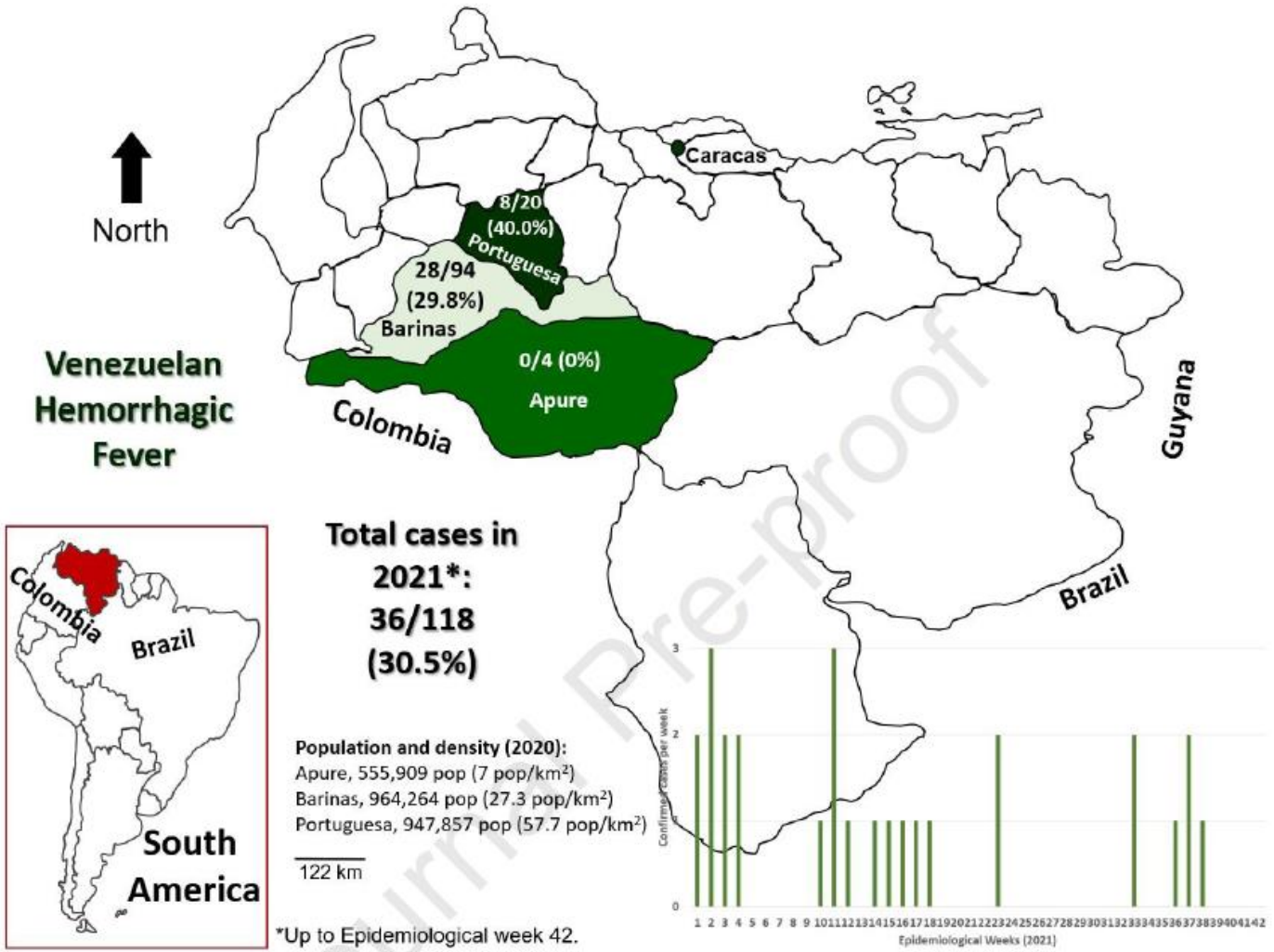
- Socio-environmental overview of Latin America: importance of climate change, OneHealth approach and determinants
- Arboviruses in the region
- **We have not just mosquitoes, but many rodents involved in emerging viral infections in the region: Mammarenaviruses and Orthohantaviruses**
- Cocirculation during COVID-19 pandemic, mpox, and avian influenza
- Some conclusions - mitigation



ISSN 2052-2975

Rodriguez-Morales AJ, Bonilla-Aldana DK, Risquez A, Paniz-Mondolfi A, Suárez JA. **Should we be concerned about Venezuelan Hemorrhagic Fever? – A reflection on its current situation in Venezuela and potential impact in Latin America amid the migration crisis**. *New Microbes New Infect* 2021 Epub Ahead Nov 11; https://www.sciencedirect.com/science/article/pii/S2052297521001098

Figure 1. Geographic distribution of Venezuelan Hemorrhagic Fever cases in Venezuela, 2021 (up to the Epidemiological Week 42); cases were confirmed by RT-PCR at Virology Reference Laboratory in Caracas. Apure, Barinas and Portuguesa are endemic for *Zygodontomys brevicauda*, *Sigmodon alstoni* and *S. hispidus*, who serve as natural reservoirs of the virus. Source: Dirección de Vigilancia Epidemiológica, Ministerio del Poder Popular para la Salud (Ministry of Health of Venezuela).

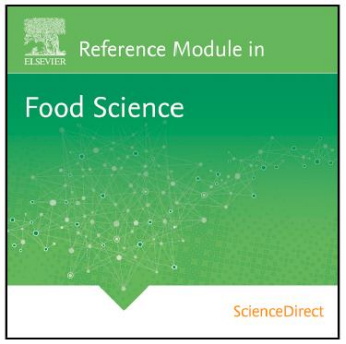


*Up to Epidemiological week 42.

https://colombia.inaturalist.org/taxa/44879-Zygodontomys-brevicauda

http://repository.humboldt.org.co/handle/20.500.11761/33864

https://www.naturalista.mx/taxa/44902-Sigmodon-hispidus



Rodriguez-Morales AJ, et al. **Organisms of Concern But Not Foodborne or Confirmed Foodborne: Bolivian Hemorrhagic Fever Virus (Machupo Virus).** En: Smithers GW, Glibetic M, Robertson G, Varelis P, Day L, Knoerzer K, Schasteen C, Ferranti P, Lee A, Smith N, Fischer A, McSweeney P, Tanner D**. Reference Module in Food Science.** ISBN 978-0-08-100596-5. Elsevier, San Diego, CA, EUA, Jan 2019. Pag:1-5. doi: 10.1016/B978-0-08-100596-5.22639-5.

Figure 1 Map of Latin America showing Bolivia (in yellow), the Beni department (in red) with its provinces (box) and indicating the countries with borders to this country.

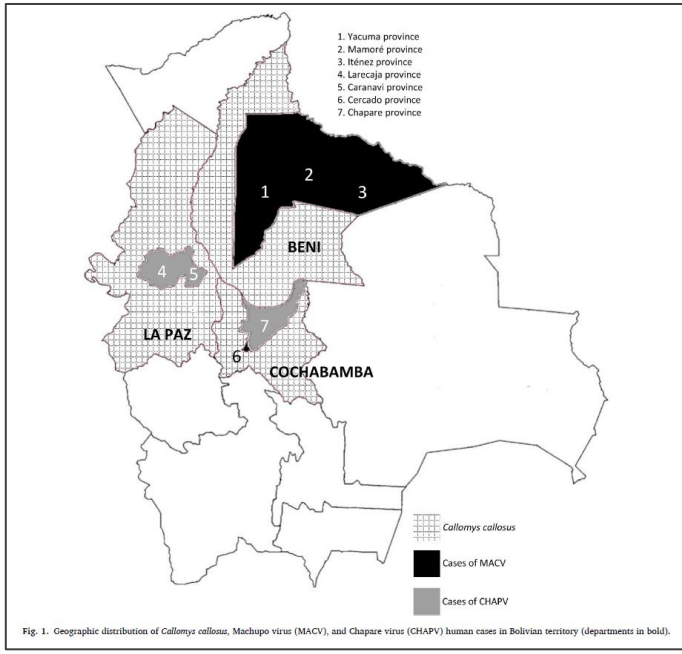


Fig. 1. Geographic distribution of *Callomys callosus*, Machupo virus (MACV), and Chapare virus (CHAPV) human cases in Bolivian territory (departments in bold).

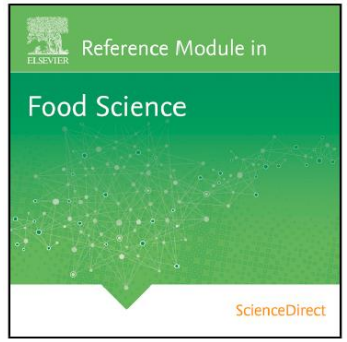
Silva-Ramos CR, Faccini-Martínez ÁA, Calixto OJ, Hidalgo M. Bolivian hemorrhagic fever: A narrative review. Travel Med Infect Dis. 2021 Mar-Apr;40:102001. doi: 10.1016/j.tmaid.2021.102001. Epub 2021 Feb 25. PMID: 33640478.

Table 2 Cases reported through ProMEDmail (http://www.promedmail.org), 1959–2017 historical records and surveillance of the Bolivian Ministry of Health (http://www.sns.gob.bo/), 1959–2012 and the national system of information in health (http://estadisticas.minsalud.gob.bo/), 2013–17

Year	*Number of cases*	*Fatal cases*	*%CFR*[a]	*Location*
1959–63	1100	260	23.6	Mamoré and Iténez provinces, Beni
1963–64	650	122	18.8	San Joaquin, Mamoré province, Beni
1963	2	–	–	Panama (imported from Beni)
1968	6	6	100.0	Magdalena, Iténez province, Beni
1969	9	–	–	Magdalena, Iténez province, Beni
1971	6	5	83.3	Cochabamba department (southern border of Beni), nosocomial, index case came from Beni, one case was health care occupational
1971	4	–	–	Yacuma province, Beni
1974–75	4	2	50.0	El Recuerdo, Mamoré province, Beni
1976–92	–	–	–	Apparently, no cases reported
1993	1	1	100.0	San Ramon, Mamoré province, Beni
1994	10	7	70.0	Magdalena, Iténez province, Beni
1996	3	–	–	Beni deparment
1999	5	–	–	Santa Cruz department (southeast border of Beni)
1999	3	–	–	Tarija department (without borders with Beni, border with Argentina)
2004	2	2	100.0	Huacaraje and Magdalena, Iténez province, Beni
2007	20	3	15.0	Magdalena, Iténez province, Beni
2010	1	1	100.0	Beni deparment
2011	3	1	33.3	Beni deparment
2012	1	1	100.0	Beni deparment
2012	1	1	100.0	San Ramón, Mamoré province, Beni
2012	1	1	100.0	Penas Verdes, Mamoré province, Beni
2012	9	4	44.4	Beni department
2012	1	0	0.0	Beni department
2013	9	2	22.2	Nirumo, Guayanamerín, Beni; Tarija; Santa Cruz
2014–17	–	–	–	Twenty-one suspected cases in 2014, none in 2015. One suspected case in Beni in 2016, another in Beni in 2017.
2018	–	–	–	One suspected case in Santa Cruz.
Total	1851	419	22.6	

[a]%CFR: case fatality rate.

Rodriguez-Morales AJ, et al. **Organisms of Concern But Not Foodborne or Confirmed Foodborne: Bolivian Hemorrhagic Fever Virus (Machupo Virus).** En: Smithers GW, Glibetic M, Robertson G, Varelis P, Day L, Knoerzer K, Schasteen C, Ferranti P, Lee A, Smith N, Fischer A, McSweeney P, Tanner D**. Reference Module in Food Science.** ISBN 978-0-08-100596-5. Elsevier, San Diego, CA, EUA, Jan 2019. Pag:1-5. doi: 10.1016/B978-0-08-100596-5.22639-5.



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PLoS PATHOGENS

Chapare Virus, a Newly Discovered Arenavirus Isolated from a Fatal Hemorrhagic Fever Case in Bolivia

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Abstract

A small focus of hemorrhagic fever (HF) cases occurred near Cochabamba, Bolivia, in December 2003 and January 2004. Specimens were available from only one fatal case, which had a clinical course that included fever, headache, arthralgia, myalgia, and vomiting with subsequent deterioration and multiple hemorrhagic signs. A non-cytopathic virus was isolated from two of the patient serum samples, and identified as an arenavirus by IFA staining with a rabbit polyvalent antiserum raised against South American arenaviruses known to be associated with HF (Guanarito, Machupo, and Sabiá). RT-PCR analysis and subsequent analysis of the complete virus S and L RNA segment sequences identified the virus as a member of the New World Clade B arenaviruses, which includes all the pathogenic South American arenaviruses. The virus was shown to be most closely related to Sabiá virus, but with 26% and 30% nucleotide difference in the S and L segments, and 26%, 28%, 15% and 22% amino acid differences for the L, Z, N, and GP proteins, respectively, indicating the virus represents a newly discovered arenavirus, for which we propose the name Chapare virus. In conclusion, two different arenaviruses, Machupo and Chapare, can be associated with severe HF cases in Bolivia.

Citation: Delgado S, Erickson BR, Agudo R, Blair PJ, Vallejo E, et al. (2008) Chapare Virus, a Newly Discovered Arenavirus Isolated from a Fatal Hemorrhagic Fever Case in Bolivia. PLoS Pathog 4(4): e1000047. doi:10.1371/journal.ppat.1000047

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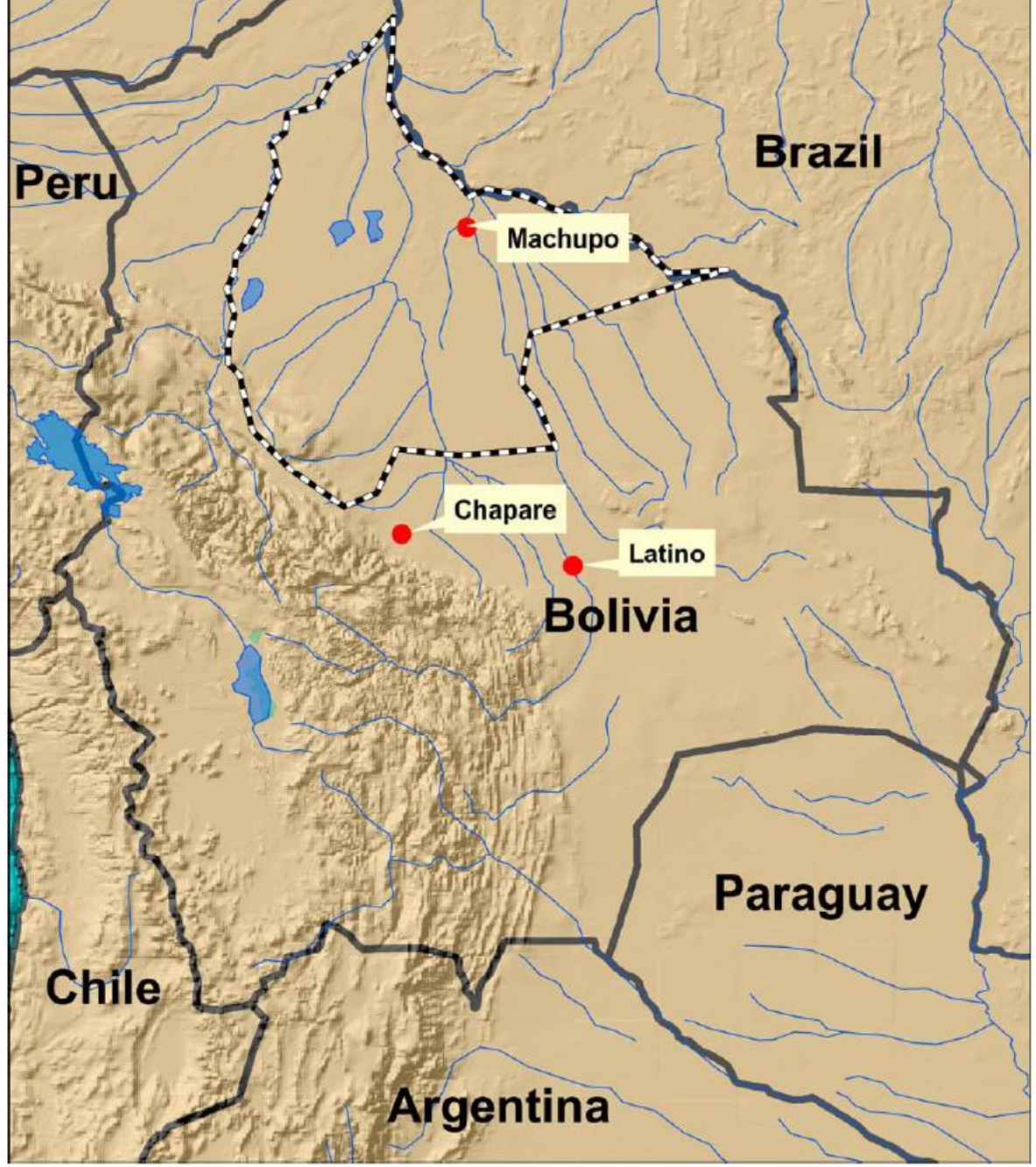

Figure 1. Map of Bolivia showing location of the Chapare virus-associated HF case relative to the Beni region where Machupo virus-associated HF cases originate. The Beni Department boundary is depicted by the checkered line. Multiple Machupo isolates have been recorded from the Beni Department. The single Latino and Chapare virus locations are labeled and represented as dots.
doi:10.1371/journal.ppat.1000047.g001

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Clinical features of fatal cases of Chapare virus hemorrhagic fever originating from rural La Paz, Bolivia, 2019: A cluster analysis

Juan Pablo Escalera-Antezana[a], Omar J. Rodriguez-Villena[b], Ariel Weimar Arancibia-Alba[c], Lucia Elena Alvarado-Arnez[a], D. Katterine Bonilla-Aldana[d,e], Alfonso J. Rodríguez-Morales[a,e,f,*]

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[f] Grupo de Investigación Biomedicina, Faculty of Medicine, Fundación Universitaria Autónoma de las Américas, Pereira, Risaralda, Colombia

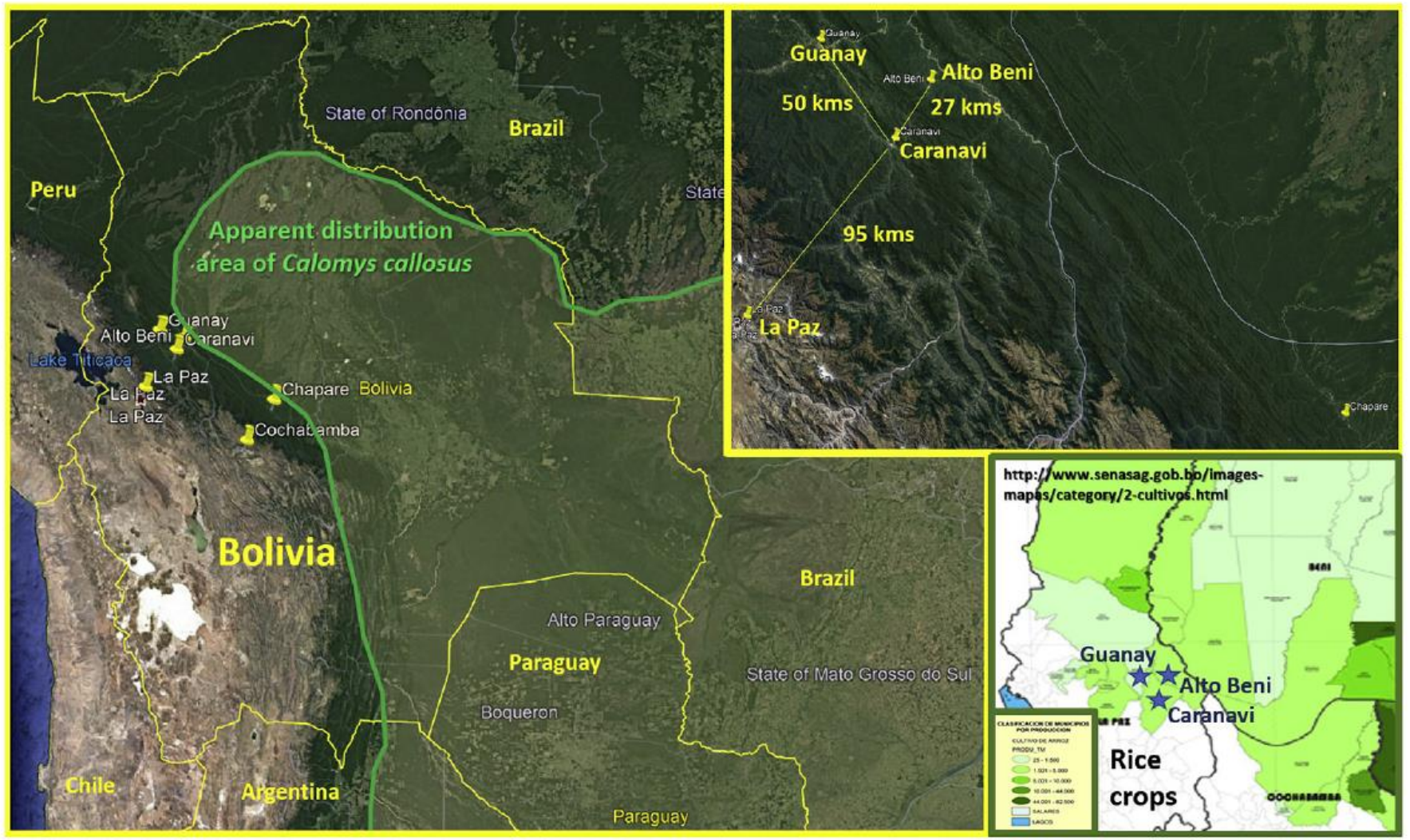


Fig. 1. Location of Bolivia, and towns of precedence of patients with CHAPV infection, also including the distribution of *Calomys callosus* and rice crops distribution in the region of the origin of the cases.

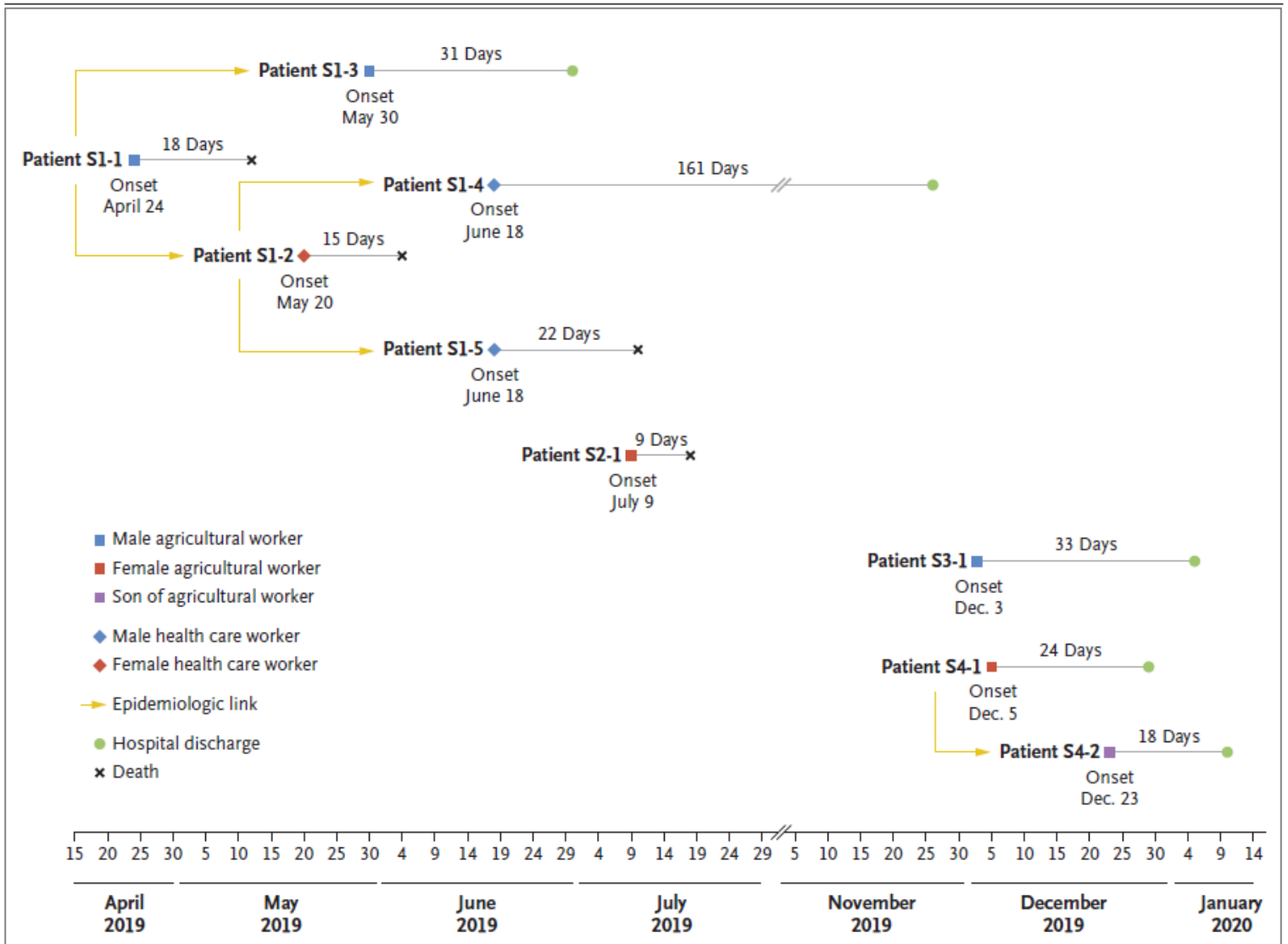


Figure 2. Transmission Chains Indicating Epidemiologic Linkages of Probable and Confirmed CHHF Cases in 2019.

Loayza Mafayle R, et al. Chapare Hemorrhagic Fever and Virus Detection in Rodents in Bolivia in 2019. N Engl J Med. 2022 Jun 16;386(24):2283-2294. doi: 10.1056/NEJMoa2110339. PMID: 35704480.

9. Escalera-Antezana JP, Rodriguez-Villena OJ, Arancibia-Alba AW, Alvarado-Arnez LE, Bonilla-Aldana DK, Rodríguez-Morales AJ. Clinical features of fatal cases of Chapare virus hemorrhagic fever originating from rural La Paz, Bolivia, 2019: a cluster analysis. Travel Med Infect Dis 2020;36:101589.

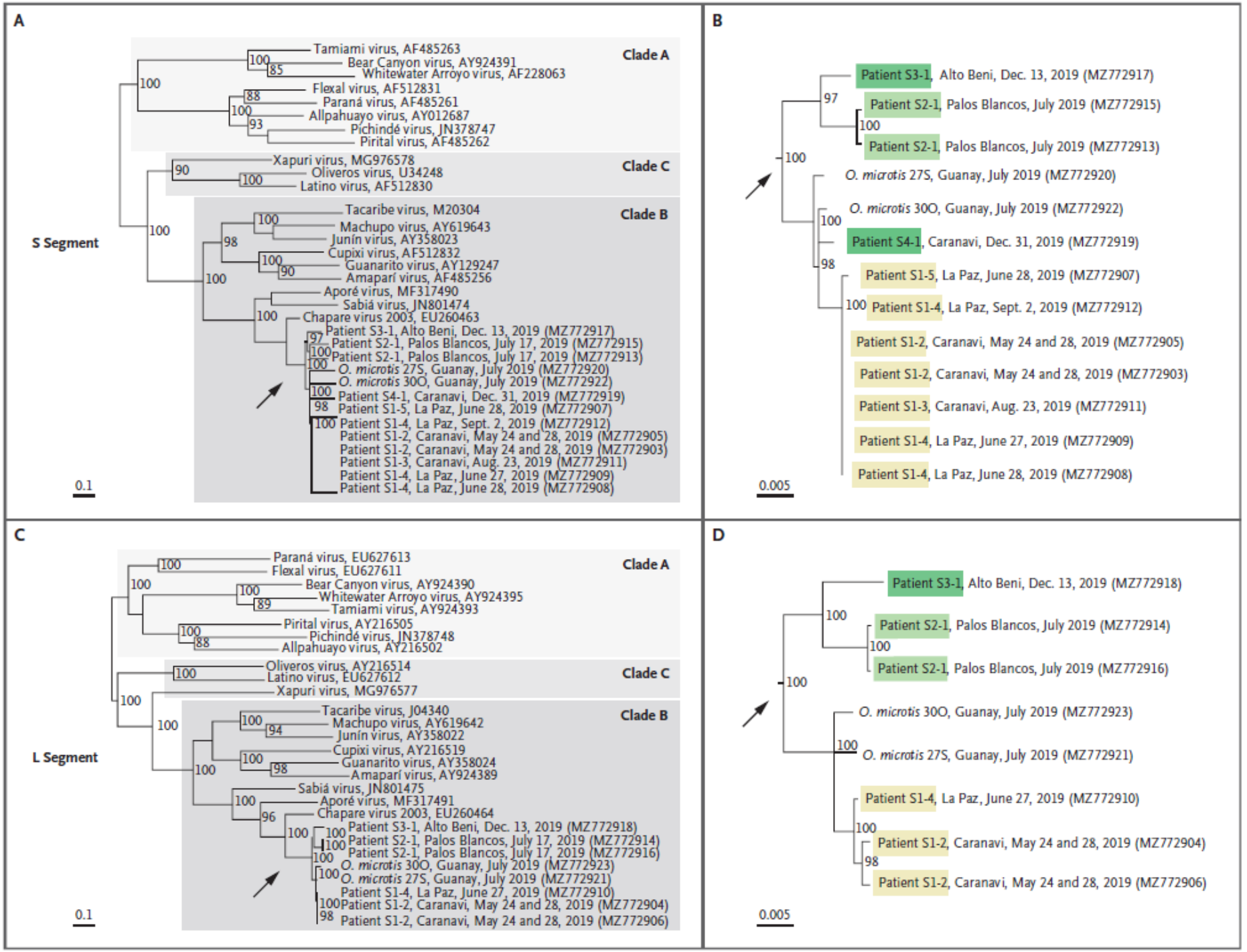
Table 1
Summary of sociodemographic data, signs and symptoms, clinical evolution, and outcomes for New World Arenavirus case-patients in La Paz Department, Bolivia, April–July 2019.

	Case				
	1	2	3	4	5
Sex	male	female	male	male	male
Age (in years)	65	25	21	48	42
Occupation	farmer	medical doctor	farmer	medical doctor	medical doctor
Type of transmission	zoonotic	nosocomial	zoonotic	nosocomial	nosocomial
Time to admission[a]	8	7	7	2	2
Time from illness onset to bleeding manifestations[b]	13	10	7	0	12
Duration of admission[c]	13	15	30	153	22
Conditions at discharge	died	died	recovered	recovered	died
Bleeding manifestations					
Gastrointestinal bleeding	(−)	(+)	(+)	(+)	(+)
Gingivorraghia	(+)	(+)	(−)	(+)	(−)
CNS bleeding	(−)	(−)	(+)	(−)	(−)

[a] Time to admission, defined as days from illness onset to hospital admission.
[b] Bleeding manifestations, described as gastrointestinal bleeding, hematemesis, melena, gingivorrhagia, epistaxis, or central nervous system bleeding.
[c] Duration of admission, defined as days in healthcare facility until death or discharge.

Toledo J, Torrez AP, Terrazas A, Molina Gutiérrez JT, Ramírez AM, Romero C, Condori D, de la Vega GA, Swanson KC, Kortepeter MG, Aldighieri S. Public health implications of a new world arenavirus outbreak that occurred in Bolivia, 2019. Travel Med Infect Dis. 2021 Sep-Oct;43:102124. doi: 10.1016/j.tmaid.2021.102124. Epub 2021 Jun 16. PMID: 34144179.

Loayza Mafayle R, et al. Chapare Hemorrhagic Fever and Virus Detection in Rodents in Bolivia in 2019. N Engl J Med. 2022 Jun 16;386(24):2283-2294. doi: 10.1056/NEJMoa2110339. PMID: 35704480.



RESEARCH LETTERS

Sabiá Virus–Like Mammarenavirus in Patient with Fatal Hemorrhagic Fever, Brazil, 2020

Fernanda de Mello Malta,[1] Deyvid Amgarten,[1] Ana Catharina de Seixas Santos Nastri, Yeh-Li Ho, Luciana Vilas Boas Casadio, Marcela Basqueira, Gloria Selegatto, Murilo Castro Cervato, Amaro Nunes Duarte-Neto, Hermes Ryoiti Higashino, Felipe Arthur Faustino Medeiros, José Luiz Pinto Lima Gendler, Anna S. Levin, João Renato Rebello Pinho

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DOI: https://doi.org/10.3201/eid2606.200099

New World arenaviruses can cause chronic infection in rodents and hemorrhagic fever in humans. We identified a Sabiá virus–like mammarenavirus in a patient with fatal hemorrhagic fever from São Paulo, Brazil. The virus was detected through virome enrichment and metagenomic next-generation sequencing technology.

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journal homepage: www.elsevier.com/locate/tmaid

Understanding Sabiá virus infections (*Brazilian mammarenavirus*)

Ana Catharina Nastri, MD, PhD [a,1], Amaro Nunes Duarte-Neto, MD, PhD [b,c,1], Luciana Vilas Boas Casadio, MD [a,1,*], William Marciel de Souza, PhD [d], Ingra M. Claro, BSc [e,f,1], Erika R. Manuli, MSc [e,f], Gloria Selegatto, MD [a], Matias C. Salomão, MD, PhD [g], Gabriel Fialkovitz, MD [a], Mariane Taborda, MD [a], Bianca Leal de Almeida, MD [a,g], Marcello C. Magri, MD, PhD [a], Ana Rúbia Guedes [g], Lauro Vieira Perdigão Neto, MD, PhD [g], Fatima Mitie Sataki [a], Thais Guimarães, MD, PhD [g], Maria Cassia Mendes-Correa, MD, PhD [e,f], Tania R. Tozetto-Mendoza, PhD [f], Marcilio Jorge Fumagalli, MSc [h], Yeh-Li Ho, MD, PhD [a], Camila Alves Maia da Silva [e,f], Thaís M. Coletti, BSc [e,f], Jaqueline Goes de Jesus, PhD [e,f], Camila M. Romano, PhD [e,f], Sarah C. Hill, PhD [i,j], Oliver Pybus, PhD [k], João Renato Rebello Pinho, MD, PhD [f,l], Felipe Lourenço Ledesma, MD [b], Yuri R. Casal, MD [b], Cristina T. Kanamura [c], Leonardo José Tadeu de Araújo [c], Camila Santos da Silva Ferreira [c], Juliana Mariotti Guerra [c], Luiz Tadeu Moraes Figueiredo, MD, PhD [h], Marisa Dolhnikoff, MD, PhD [b], Nuno R. Faria, PhD [f,k,m,2], Ester C. Sabino, MD, PhD [e,f,2], Venâncio Avancini Ferreira Alves, MD, PhD [b,2], Anna S. Levin, MD, PhD [a,e,f,g,2]

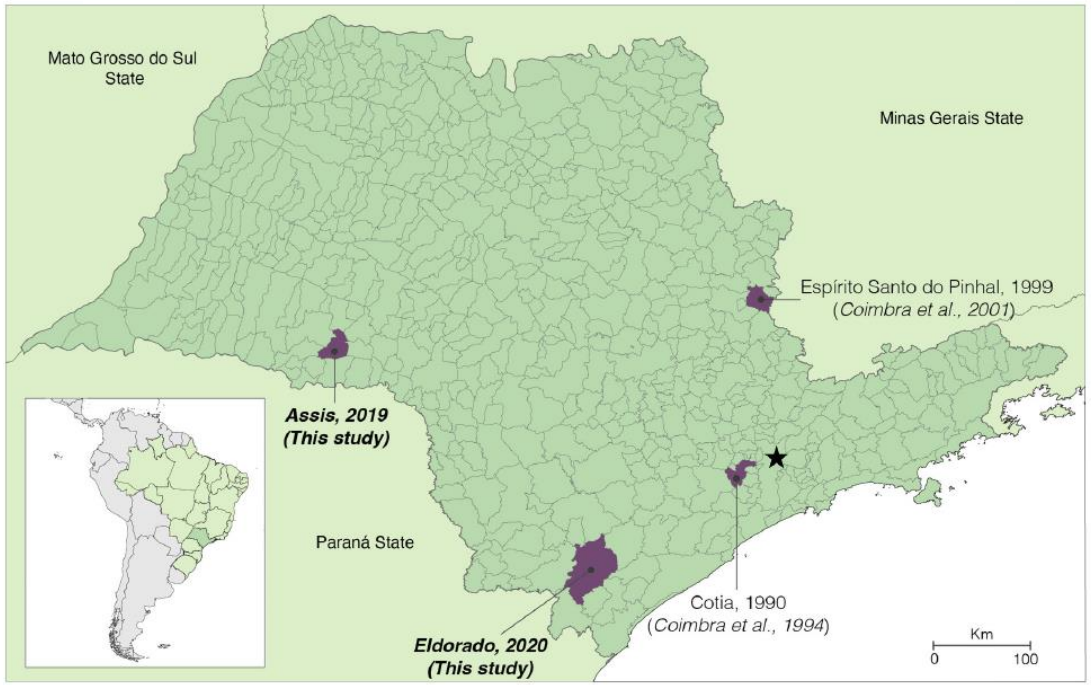
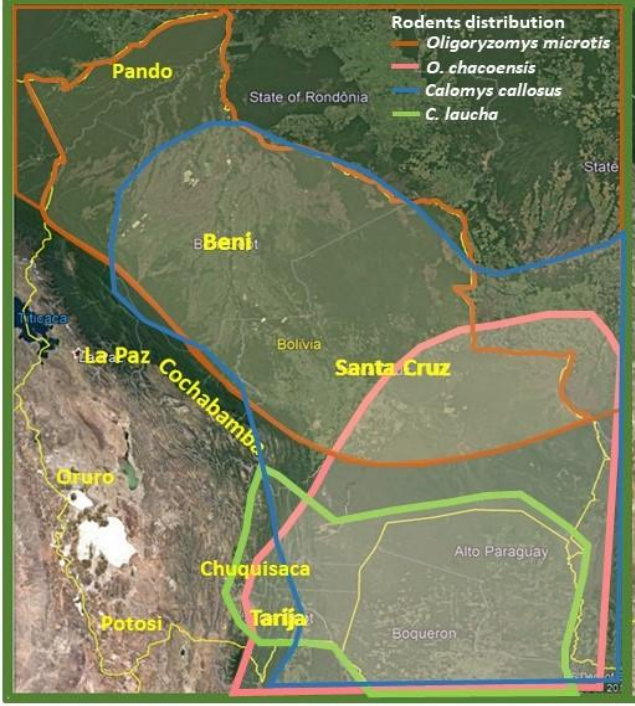
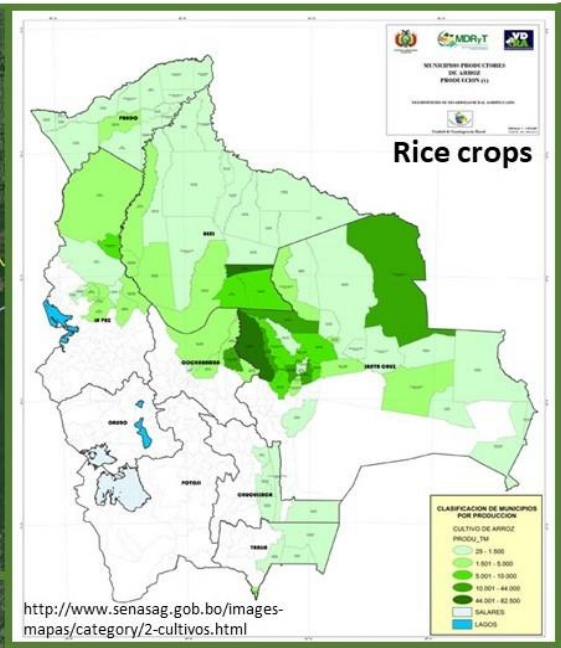


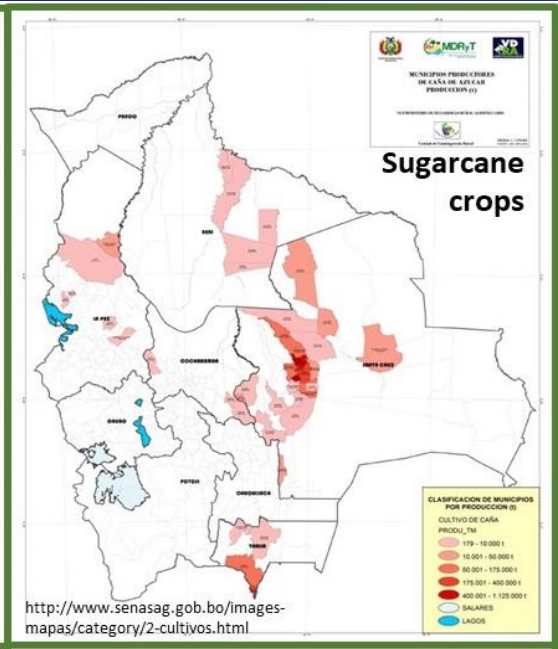
Fig. 1. State of São Paulo, Brazil, South America. In the figure's legend, the distance between the cities is in kilometers. The black star is for the city of São Paulo, the state capital, and where Hospital das Clínicas is located. The green line delimiters the State of São Paulo borders. The black lines show the probable localities of the autochthone SABV infections, and the year reported. #1 Cotia, 1990 (Coimbra et al., 1994); #2 Espírito Santo do Pinhal, 1999 (Coimbra et al., 2001); #3 Assis, 2019; #4 Eldorado, 2020. Distance between #1 to #2: 155 km; #2 to #3: 380 km; #3. #3 to #4: 315 km. Figure made by WMS with "Scientific colour maps" software [42]. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.).

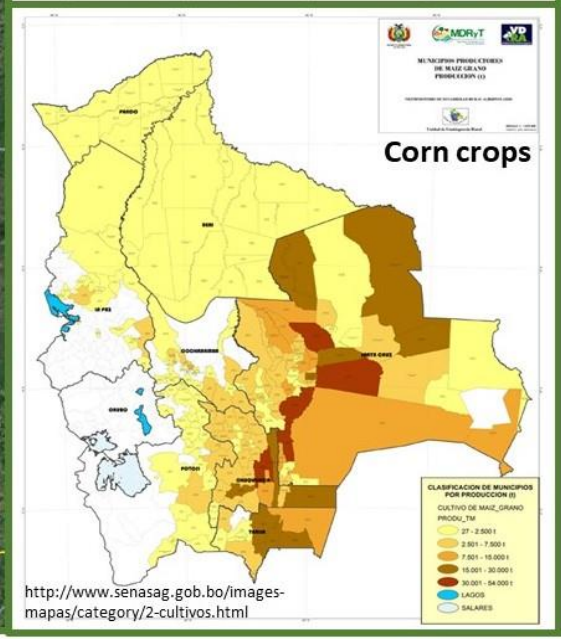
Ecoepidemiology of Hantavirus in Bolivia

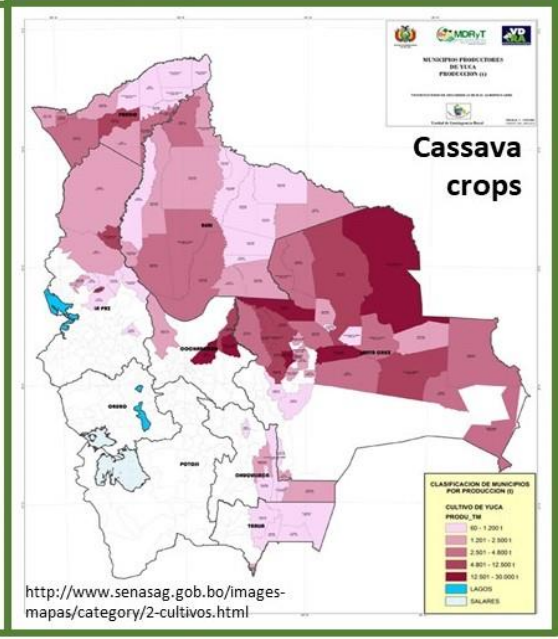
Roberto Torrez-Fernandez,1 Dagner Montalvan-Plata,2 Claudia Marcela Montenegro-Narváez,3,4 Jorge Luis Aviles-Sarmiento,5 Juan Pablo Escalera-Antezana,6 Lucia Elena Alvarado-Arnez,6 D. Katterine Bonilla-Aldana,7,8 Alfonso J. Rodríguez-Morales.6,7,*











International Journal of Infectious Diseases 90 (2020) 145–150

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Orthohantavirus pulmonary syndrome in Santa Cruz and Tarija, Bolivia, 2018

Juan Pablo Escalera-Antezana[a], Roberto Torrez-Fernandez[b], Dagner Montalvan-Plata[c], Claudia Marcela Montenegro-Narváez[d,e], Jorge Luis Aviles-Sarmiento[f], Lucia Elena Alvarado-Arnez[a], D. Katterine Bonilla-Aldana[g,h], Alfonso J. Rodríguez-Morales[a,h,*]

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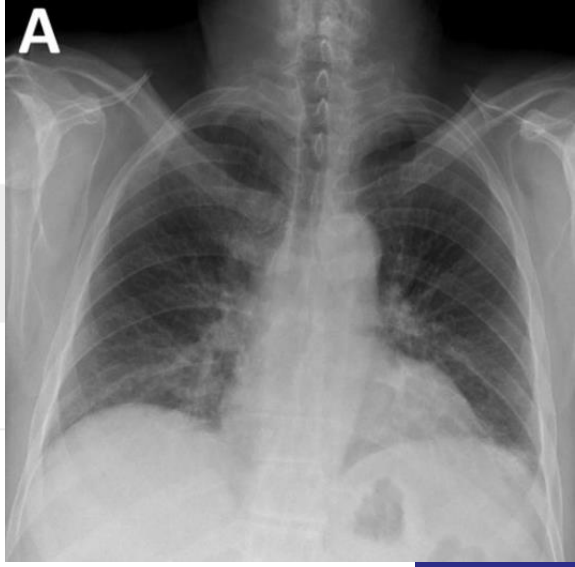
Volume 26, Number 2—February 2020



Research Letter

Hantavirus Infection with Renal Failure and Proteinuria, Colorado, USA, 2019

Swati Chand[1], Sangharsha Thapa[1], Shelley Kon, Steven C. Johnson, Eric M. Poeschla, Carlos Franco-Paredes, Alfonso J. Rodríguez-Morales, Salim Mattar, and Andrés F. Henao-Martínez

Author affiliations: Kathmandu University School of Medical Sciences, Kathmandu, Nepal (S. Chand, S. Thapa); University of Colorado School of Medicine, Aurora, Colorado, USA (S. Kon, S.C. Johnson, E.M. Poeschla, C. Franco-Paredes, A.F. Henao-Martínez); Hospital Infantil de México Federico Gómez, Mexico City, Mexico (C. Franco-Paredes); Universidad Tecnológica de Pereira, Pereira, Colombia (A.J. Rodríguez-Morales); Universidad de Córdoba, Montería, Colombia (S. Mattar)

Cite This Article

Abstract

In North America, hantaviruses commonly cause hantavirus pulmonary syndrome (HPS). Clinical descriptions of hantavirus-associated renal disease in the Americas are scarce. Herein, we discuss the case of a 61-year-old man whose predominant manifestations were acute kidney injury and proteinuria. Clinical recognition of renal signs in hantavirus infections can reduce risk for death.

Revista da Sociedade Brasileira de Medicina Tropical
Journal of the Brazilian Society of Tropical Medicine
Vol.:53:e20190132: 2020
doi: 10.1590/0037-8682-0132-2019

Short Communication

Seroprevalence of arenavirus and hantavirus in indigenous populations from the Caribbean, Colombia

***Amada Bolaños*[1], *Carolina Montoya-Ruiz*[2],[3], *Juan Camilo Perez-Peréz*[2], *Juan David Rodas*[2] *and Salim Mattar*[1]**

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[2]. Universidad de Antioquia, Grupo Centauro, Medellín, Antioquia, Colombia.
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TABLE 1: Results of individuals with IgG MCLV positivity on ELISA assay.

ID patient	ELISA Screening	Validation through titration (dilutions)		
	MCLV1/100	1/100	1/400	1/1600
Kankuamos 1	+	+	+	+
Kankuamos 2	+	+	+	-
Kankuamos 3	+	+	+	-
Tuchin 1	+	+	+	+
Tuchin 2	+	+	+	+

+: the titer of the serum was positive; -: the titer of the serum sample was negative. The cut off for the MCLV ELISA assay was OD 0.2 in a dilution of 1/400.

TABLE 2: Results of individuals with IgG JUNV positivity on ELISA assay.

ID patient	ELISA Screening	Validation through titration (dilutions)		
	JUNV 1/100	1/100	1/400	1/1600
Kankuamos 4	+	+	+	-
Kankuamos 5	+	+	+	-

+: the titer of the serum was positive; -: the titer of the serum sample was negative. The cut off for the JUNV ELISA assay is OD 0.2 in a dilution of 1/400.

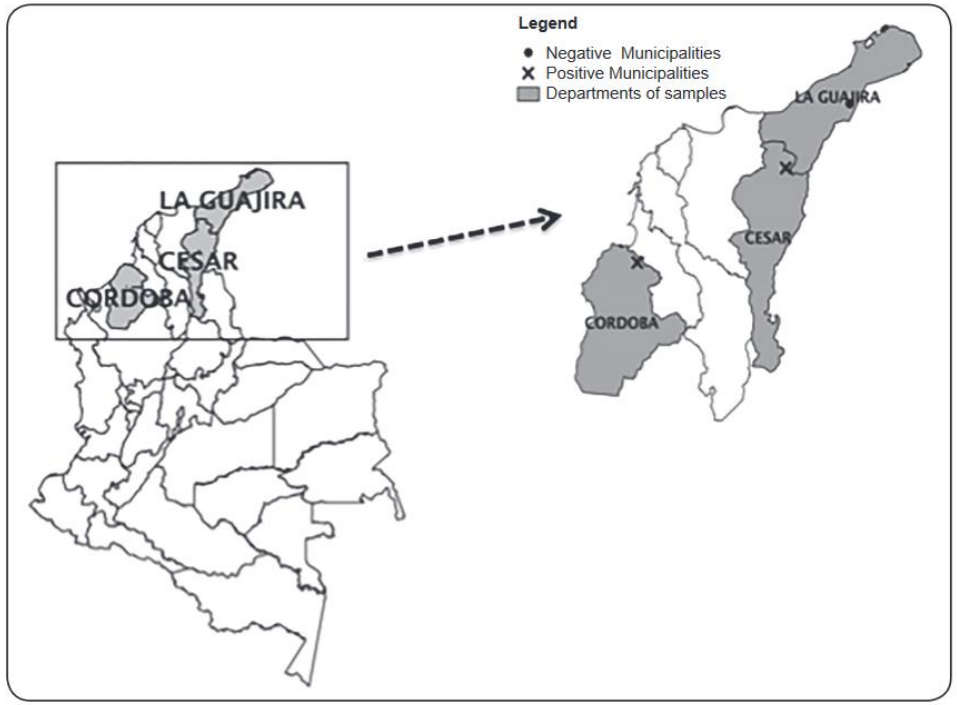

FIGURE 1. Geographical location of departments in which the sampled indigenous communities live.

Contents

- Socio-environmental overview of Latin America: importance of climate change, OneHealth approach and determinants
- Arboviruses in the region
- We have not just mosquitoes, but many rodents involved in emerging viral infections in the region: Mammarenaviruses and Orthohantaviruses
- **Cocirculation during COVID-19 pandemic, mpox, and avian influenza**
- Some conclusions - mitigation

Travel Medicine and Infectious Disease
Volume 43, September–October 2021, 102129

A fatal case of triple coinfection: COVID-19, HIV and Tuberculosis

Yeimer Ortiz-Martínez, Julie Melissa Mogollón-Vargas, Marggie López-Rodríguez, Alfonso J. Rodriguez-Morales

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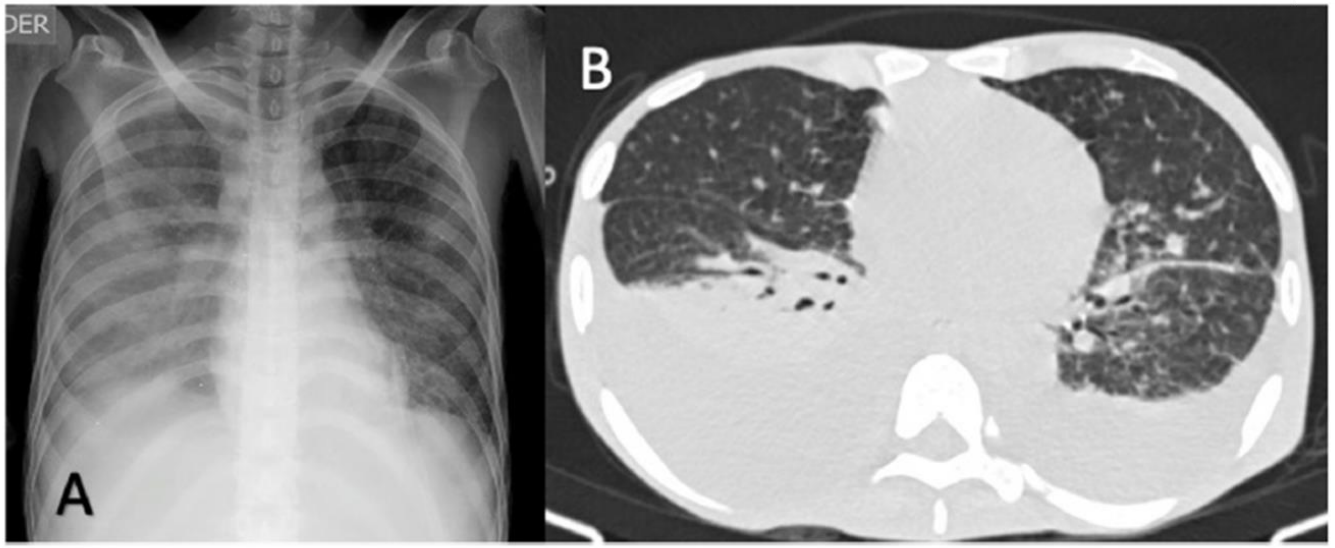

Fig. 1. Thorax radiography (A) demonstrates bilateral diffuse micronodular and reticular interstitial opacities. Chest computed tomography (B) axial thin-section unenhanced CT image showing randomly distributed (miliary) nodules in both lungs associated with glass-ground opacities in the left lower lobe and bilateral pleural effusion.

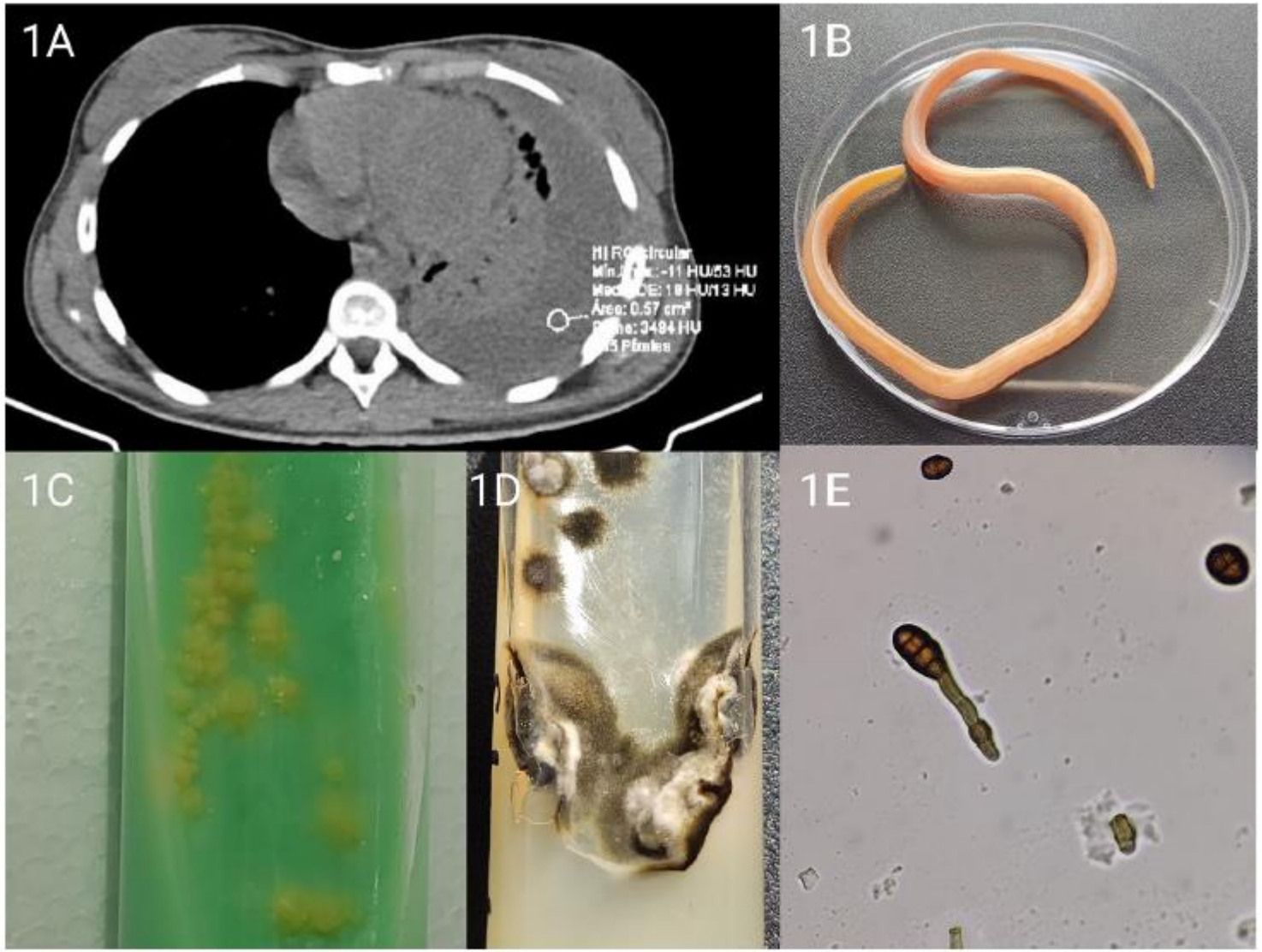

Fig. 1 Relevant radiological and microbiological findings of the case. **A** Thoracic tomography shows pleural effusion in the left hemithorax, approximate volume 485 mL, maximum density 38 hu, parietal and visceral pleura thickening, and mediastinal calcifications. Left anterior apical calcified granuloma, subpleural laminar and segmental atelectasis left basal consolidation with aerial bronchogram. Pre-aortic and subcarinal reactive nodules. Small right pericardial effusion. **B** Female helminth of *A. lumbricoides* obtained from the patient's vomit. **C** *Mycobacterium tuberculosis* isolated from lung biopsy on Lowenstein Jensen agar. **D** Culture of a lung biopsy on Sabouraud agar with chloramphenicol showing filamentous growth of *Curvularia hawaiiensis*. **E** Microscopic view of *C. hawaiiensis* ha colony with ellipsoid conidia, rounded at the ends, pale brown, medium reddish brown to dark brown, three septa

Aguirre *et al. Ann Clin Microbiol Antimicrob* (2023) 22:36
https://doi.org/10.1186/s12941-023-00593-z

Annals of Clinical Microbiology
and Antimicrobials

CASE REPORT Open Access

Necrotising pneumonia caused by *Curvularia hawaiiensis* (syn. *Bipolaris hawaiiensis*) and *Mycobacterium tuberculosis* coinfection in a patient with ascariasis: a case report and review

Cristina Aguirre[1,2†], Jaime David Acosta-España[3,4*†], Sheila Jissela Patajalo-Villata[2,5] and Alfonso J. Rodriguez-Morales[6,7]

- La COVID-19 ha revertido los avances alcanzados en la última década en la lucha contra la TB.
- Debido a esta pandemia se ha afectado seriamente el acceso a los servicios esenciales de prevención y atención de la TB en el 2020.
- A nivel mundial, en 2020, se estimaron que **9.9 millones** de personas enfermaron de tuberculosis, con un estimado de **1.5 millones de muertes** por esta infección, de ellas, **214.000 (14,3%) tenían VIH**.
- En las Américas, en 2020, se estimaron **291.000** casos de tuberculosis.
- Las muertes estimadas para la región fue **27.000**, de las cuales el **29% (7.900) corresponde a la co-infección por TB/VIH.**

- Se diagnosticaron **4.007 casos** de TB RR/MDR.
- De estos, tan solo el 89% inició tratamiento.
- La proporción de **casos de TB-RR estudiados** para resistencia a las fluoroquinolonas disminuyó al **29%** en comparación con el 53% del año anterior.
- La Estrategia Fin de la TB tiene como propósito terminar con la epidemia de tuberculosis en el mundo y está vinculada con los Objetivos de Desarrollo Sostenible (ODS), bajo tres indicadores de alto nivel:
  - reducir el número de muertes por tuberculosis en un **95%**,
  - reducir los nuevos casos en un **90% entre 2015 y 2035**, y
  - garantizar que ninguna familia enfrente costos catastróficos debidos a la tuberculosis.

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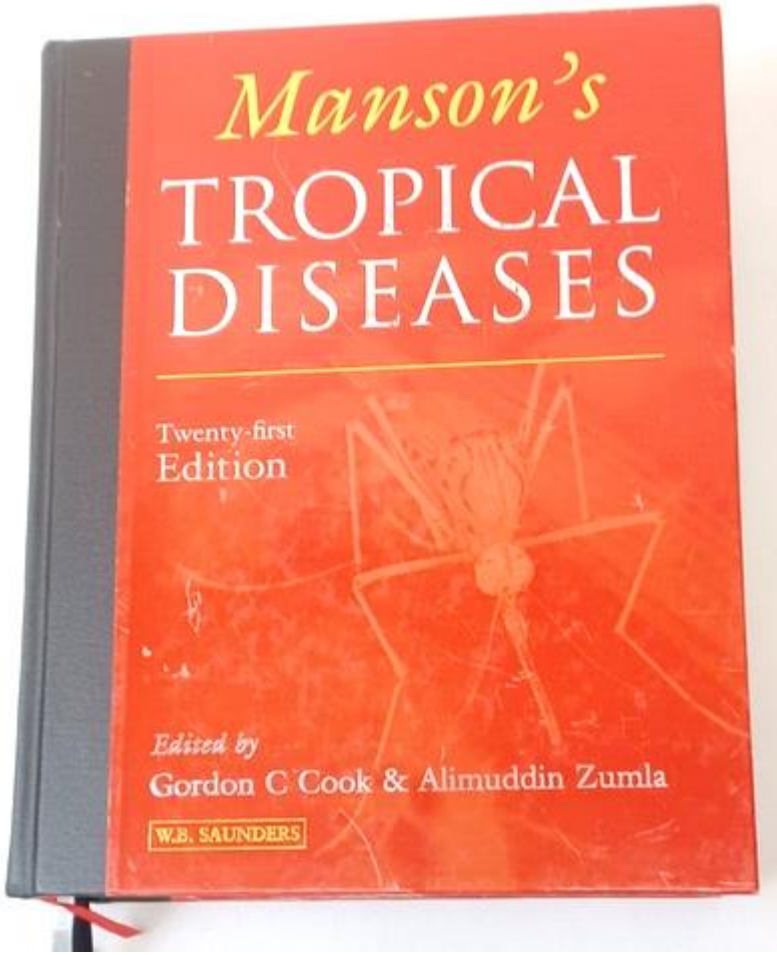
Volume 53, May–June 2023, 102568



World tuberculosis day 2023 – Reflections on the spread of drug-resistant tuberculosis by travellers and reducing risk in forcibly displaced populations

Alfonso J. Rodriguez-Morales [1], Aula Abbara, Francine Ntoumi, Nathan Kapata, Peter Mwaba, Dorothy Yeboah-Manu, Markus Maeurer, Osman Dar, Ibrahim Abubakar, Alimuddin Zumla

THE LANCET

Volume 402, Issue 10398, 22–28 July 2023, Pages e5-e7

Comment

Globalisation of antibiotic-resistant bacteria at recurring mass gathering events

Avinash Sharma [a] ✉, Alfonso J Rodriguez-Morales [b c], Tieble Traore [d], Shuja Shafi [e], Sherif A El-Kafrawi [f], Esam I Azhar [f], Alimuddin Zumla [g h]

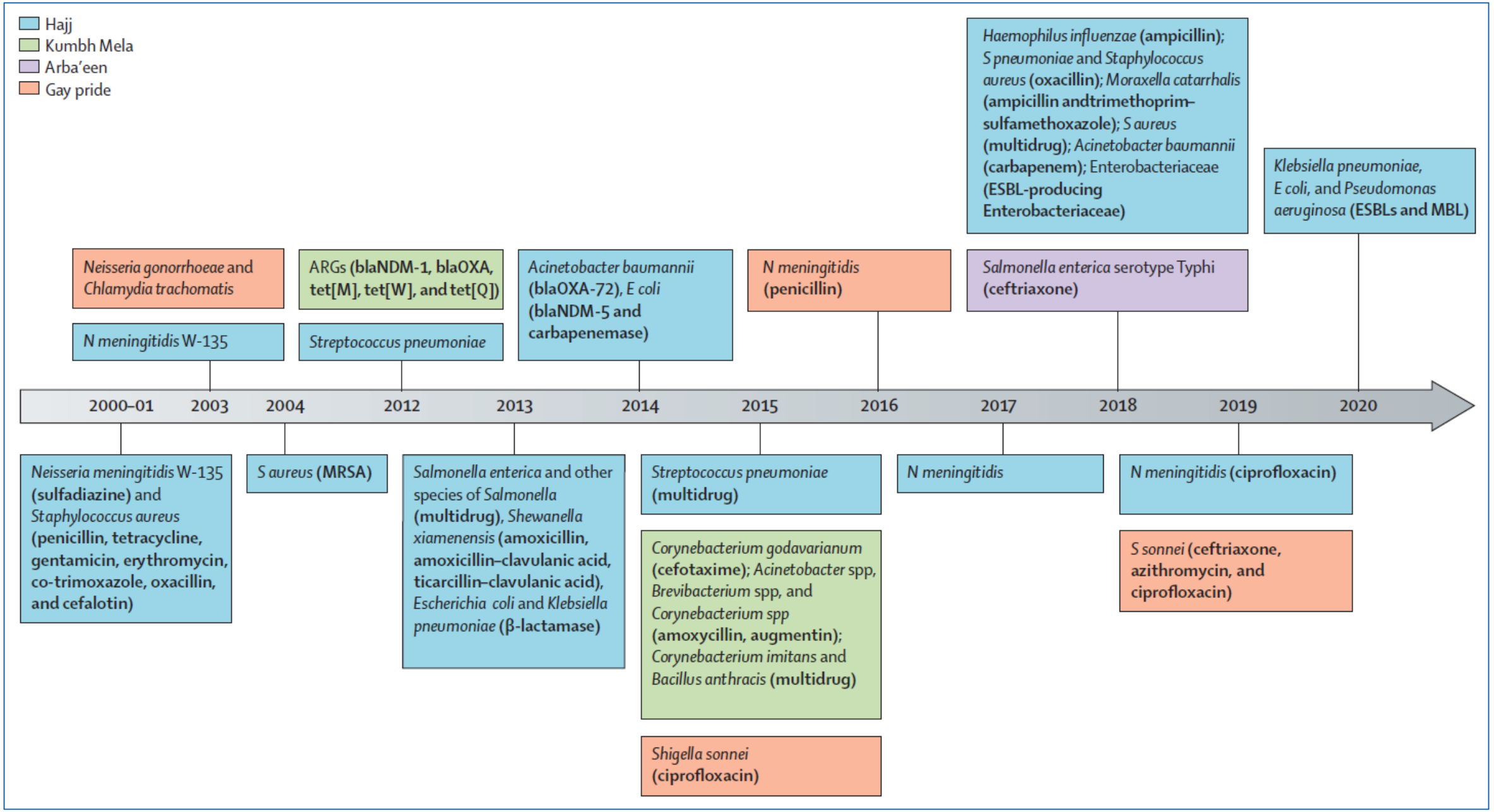


Figure: **Bacterial pathogens and antimicrobial resistance associated with religious and gay pride events**

The studies that inform this figure are listed in the appendix. Text in bold denotes the antibiotics to which the bacteria are resistant. ARGs=antibiotic resistance genes. ESBL=Extended-spectrum beta-lactamase. MBL=metallo beta-lactamase. MRSA=methicillin-resistant *Staphylococcus aureus*.

New Microbes and New Infections, Volume 49-50 Number C, ■■■ 2022

Clinical challenges of managing advanced AIDS in the tropics: Histoplasmosis, COVID-19, and shigellosis coinfections

4 en 1

Yeimer Ortiz-Martínez[1], **Luis Daniel Cabeza-Ruiz**[1], **Andrés F. Henao-Martínez**[2] and **Alfonso J. Rodriguez-Morales**[3,4,5]

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Keywords: COVID-19, HIV, Shigella, Histoplasma, Histoplasmosis
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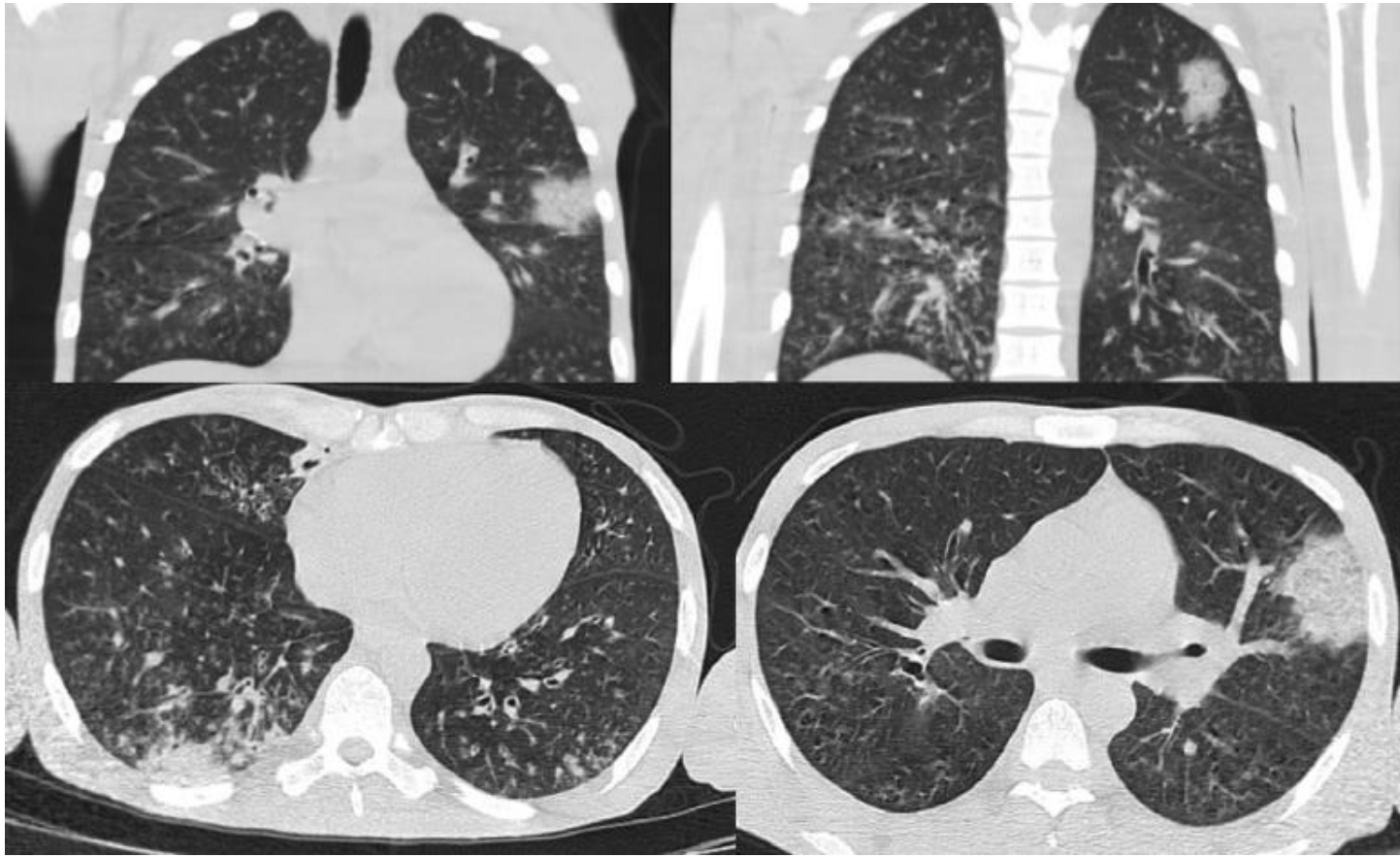

FIG. 1. Chest CT scan with diffuse branching opacities and upper segment of the lower lobe consolidation patches, and multiple bronchiectases in the middle and lower left lobes.

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New Microbes and New Infections
Volumes 49–50, November–December 2022, 101041

Systematic Review

COVID-19 and dengue coinfection in Latin America: A systematic review

Darwin A. León-Figueroa [a b], Sebastian Abanto-Urbano [c d], Mely Olarte-Durand [e f], Janeth N. Nuñez-Lupaca [g h], Joshuan J. Barboza [i], D. Katterine Bonilla-Aldana [j], Robinson A. Yrene-Cubas [k l], Alfonso J. Rodriguez-Morales [m n o]

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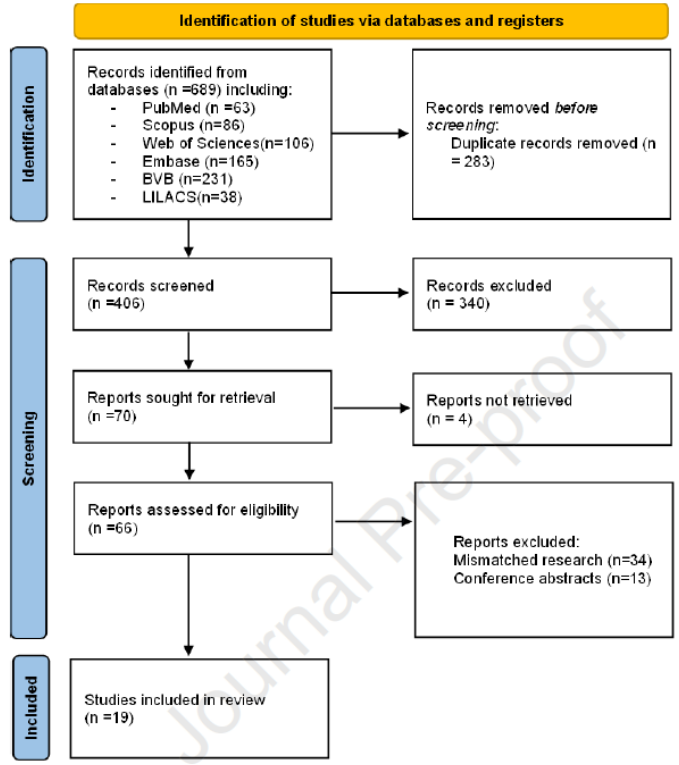
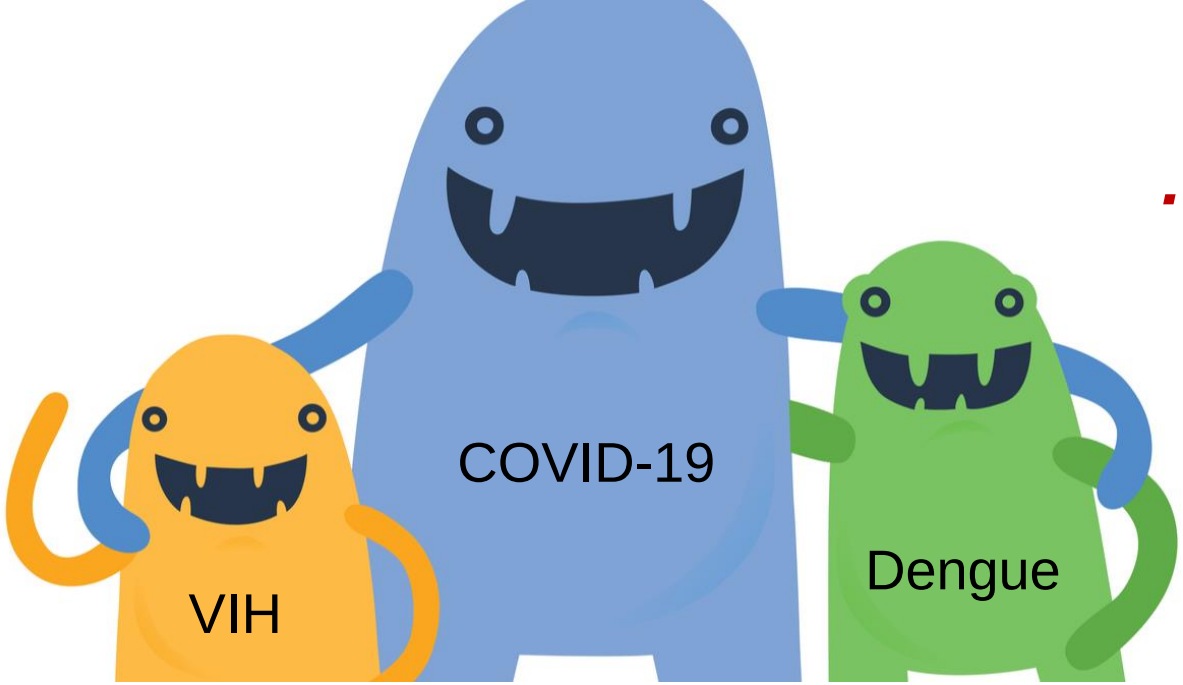


Figure 1. PRISMA flow chart of the studies selection process

Table 2. Main individual characteristics of the studies included.

Authors	Year	Design	Country	Participants (N)	Age (Years)	Sex	Diagnosis method		Serotype of dengue	Hospitalization (days)	Outcome
							COVID-19	Dengue			
Braatz M, et al.[23]	2021	Case series	Brazil	1	16	F	IgM, IgG, and PCR SARS-CoV-2 positive	PCR positive	NR	21	Discharged after 21 days of hospitalization
Reyes J, et al.[24]	2021	Case report	Mexico	1	42	F	PCR SARS-CoV-2 positive	PCR positive	DENV- 1	18	Discharged on day 24 after the onset of symptoms
Agudelo R, et al.[25]	2021	Case report	Colombia	2	24	F	PCR SARS-CoV-2 positive	IgM and IgG positive	DENV- 1	6	She was discharged after six days of hospitalization
					59	M	PCR SARS-CoV-2 positive	IgM/IgG positive	NR	63	Died
Bicudo N, et al.[26]	2020	Case report	Brazil	1	56	F	PCR SARS-CoV-2 positive	IgM/IgG positive	DENV- 1	6	Discharged after 6 days.
Lopes R.[27]	2020	Case report	Brazil	1	39	M	IgM, IgG and PCR SARS-CoV-2 positive	PCR positive	DENV- 1	NR	Clinical improvement
Salvo C, et al.[28]	2020	Case report	Argentina	1	43	M	PCR SARS-CoV-2 positive	IgM and NS1 positive.	NR	NR	Discharged.
Nakandakari et al.[29]	2021	Case report	Peru	1	13	F	IgM and IgG positive	NS1 positive.	NR	5	Discharged after five days
Rosso et al.[30]	2021	Cross-sectional	Colombia	2	NR	NR	PCR SARS-CoV-2 positive	PCR positive	DENV 1 - 4	NR	NR
					NR	NR	PCR SARS-CoV-2 positive	Seroconversion	NR	NR	NR
Estofolete et al. [31]	2020	Case report	Brazil	1	60	F	PCR SARS-CoV-2 positive	NS1, IgM and IgG positive	NR	NR	Died after five days
Villamil-Gomez WE, et al.[32]	2021	Case report	Colombia	1	52	M	PCR SARS-CoV-2 positive	IgG, IgM and PCR positive	DENV- 2	7	Discharged, after 7 days

Figure 2. Cases of co-infection between COVID-19 and dengue in Latin America. Only coinfection cases from Latin American countries reported in selected studies were included. Updated September 4, 2021.



…peor si es un trio letal..!!!

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COINFECCIÓN DENGUE Y SARS-COV-2 EN PACIENTE HIV POSITIVO

CAROLINA P. SALVO, NATALIA DI LELLA, FLORENCIA SOLVEYRA LÓPEZ, JORGE HUGO, JULIETA GIGENA ZITO, ANDRÉS VILELA

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Resumen El dengue es una arbovirosis confinada a las áreas geográficas donde habitan sus vectores, los mosquitos *Aedes aegypti* y *Aedes albopictus*. La transmisión ocurre principalmente durante el verano, pero la persistencia del insecto en el ambiente puede extenderla hasta el otoño en climas templados y cálidos. En nuestro país, este año la trasmisión estacional del dengue se superpuso temporalmente con la pandemia de COVID-19, producida por el SARS-CoV-2, un coronavirus causante de afecciones respiratorias graves con eventual desenlace fatal. Por otro lado, el HIV es un retrovirus que debilita el sistema inmune favoreciendo las infecciones por numerosos patógenos oportunistas. Presentamos el caso de un paciente con infección HIV sin tratamiento que desarrolló infección simultánea por dengue y SARS-CoV-2 con evolución favorable.

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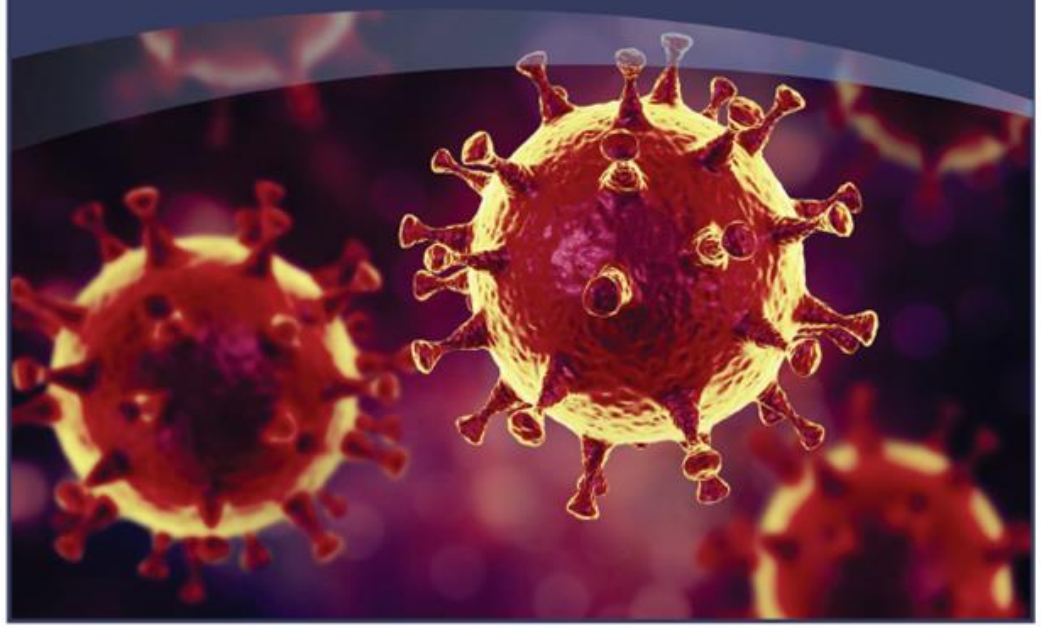
Instituto de Evaluación Tecnológica en Salud®

Volumen 24 Número 3 (S1). Marzo de 2020

CONSENSO COLOMBIANO DE ATENCIÓN, DIAGNÓSTICO Y MANEJO DE LA INFECCIÓN POR SARS-CoV-2/COVID-19 EN ESTABLECIMIENTOS DE ATENCIÓN DE LA SALUD

RECOMENDACIONES BASADAS EN CONSENSO DE EXPERTOS E INFORMADAS EN LA EVIDENCIA

(Resumen ejecutivo)



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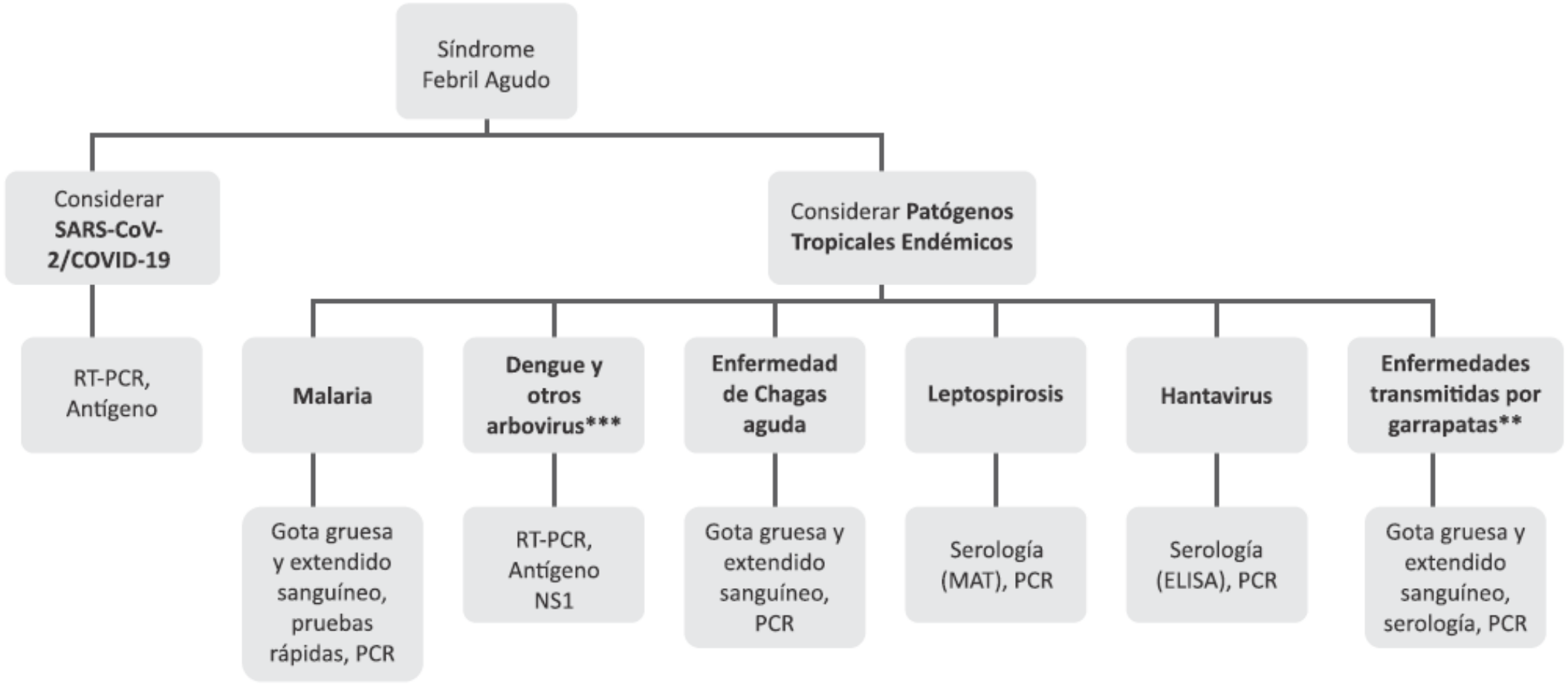

* Paciente febril que vive en zonas endémicas o procede de ellas durante el último mes, de acuerdo a la patología a sospechar (ej. Malaria hasta 1 mes, arbovirosis, últimos, últimos 14 días). Pueden presentarse coinfecciones entre estospatógenos y con la infección SARS-CoV-2/COVID-19. **Incluye babesiosis, rickettsiosis, ehrliquiosis, anaplasmosis, entre otras. ***Chikunguhya, Zika, Fiebre Amarilla, Encefalitis Equinas (EEV, EE, Madariaga), Mayaro, Oropouche.

Table 1 - Data on case reports of zoonotic febrile illnesses misdiagnosed as COVID-19.

Reference	*Case*	*Age (gender)*	*Origin*	*Diagnosis*	*Clinical manifestations*	*Laboratory parameters*	*Treatment*	*Outcome*
Vogel N et al. 2020 [14]	1	35 (M)	Germany	Leptospirosis	Fever, cough, sore throat, body ache, tachycardia, jaundice, myalgia	Thrombocytopenia, leukocytosis, hypoalbuminemia, ↑Cr, ↑Urea, ↑uric acid, ↑AST, ↑ALT, ↑GGT; ↑TBil, ↑DBil,	Hydration, ceftriaxone	Recovered
Patel HM 2020 [15]	2	25 (M)	United States	Murine typhus	Fever, headache, myalgia, chills, vomiting, diarrhea, cough, congestion, fatigue, dizziness, back pain, tachycardia, body aches	Bandemia, lymphopenia, ↑ESR	Doxycycline	Recovered
Alamarat Z 2020 [16]	3 to 8	9, 11, 11, 13, 13, 14*	United States (6/6)	Murine typhus (6/6)	Fever (6/6), tachycardia (6/6), tachypnea (6/6), rash (6/6), myalgia (5/6), cough (5/6), abdominal pain (5/6), sore throat (4/6), vomiting (4/6), diarrhea (1/6), fatigue (1/6)	↑AST (6/6), ↑ALT (6/6), ↑LDH (6/6), ↑Ferritin (6/6), ↑D-dimer (6/6), ↑CRP (6/6), ↑Procalcitonin (6/6), leucopenia (3/6), neutrophilia (3/6), thrombocytopenia (3/6), lymphopenia (2/6)	Doxycycline (4/6) None (2/6)	Recovered (6/6)
Wormser GP et al. 2021 [17]	9	36 (M)	United States	Lyme borreliosis and Babesiosis	Fever, erythematous skin lesion, myalgia, stiff neck, fatigue,	ND	Ceftriaxone, doxycycline	Recovered

Reference	*Case*	*Age (gender)*	*Origin*	*Diagnosis*	*Clinical manifestations*	*Laboratory parameters*	*Treatment*	*Outcome*
Tendulkar P et al. 2021 [18]	12	23 (M)	India	Leptospirosis	Fever, shortness of breath, yellowish expectoration, loose stools, tachypnea, respiratory failure	Leukocytosis, neutrophilia, lymphopenia, ↑Urea, ↑Cr, ↑TBil, ↑DBil, ↑AST, ↑ALT, ↑ALP, ↑GGT	Doxycycline	Deceased
Cetin S and Sahin AM 2021 [19]	13	57 (M)	Turkey	Hantavirus infection	Fever, fatigue, hyporexia, myalgia, arthralgia, tachycardia, oliguria	Leukocytosis, thrombocytopenia, ↑Urea, ↑Cr, ↑CRP, ↑D-dimer, ↑Ferritin, ↑AST	Hydration, Supportive therapy	Recovered
de Lemos ERS et al. 2022 [20]	14	24 (M)	Brazil	Hantavirus Cardiopulmonary Syndrome	Fever, headache, dry cough, diarrhea, hyporexia, respiratory discomfort, dry cough, hemoptysis, tachycardia, prostration, nausea, vomiting, dyspnea	Normal WBC with left shift, bandemia, thrombocytopenia, ↑AST, ↑ALT	Oxygen therapy, amoxicillin/ clavulanic acid, oseltamivir	Deceased
Mardani M et al. 2022 [21]	15	41 (M)	Iran	Crimean-Congo hemorrhagic fever	Fever, myalgia, malaise, coffee ground vomitus, melena,	Thrombocytopenia, ↑PTT, ↑AST, ↑ALT, ↑Ferritin, ↑LDH, ↑D-dimer, ↑CRP	Ribavirin	Recovered
Turmel JM et al. 2022 [22]	16	83 (F)	Martinique	Leptospirosis	Fever, dyspnea, myalgia, arthralgia, diarrhea	Lymphopenia, thrombocytopenia, ↑Cr, ↑BUN, ↑CRP, ↑AST, ↑ALT	Amoxycilin, steroid therapy	Recovered
Elçi H and Orhan Ö 2022 [23]	17	3 (M)	Turkey	Leptospirosis	Fever, cough, weakness, abdominal pain, tachycardia, tachypnea	Thrombocytopenia, ↑CRP	Hydration, cefotaxime, doxycycline	Recovered
Barbina S et al. 2022 [24]	18	72 (F)	United States	Spotted fever group rickettsiosis	Fever, myalgia, fatigue, dry cough, nausea,	Hyponatremia, ↑AST, ↑ALT, ↑CRP,	Doxycycline	Recovered

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Zoonotic febrile illnesses misdiagnosed as COVID-19: a review of reported clinical cases

Carlos Ramiro Silva-Ramos[1], Julián A. Mejorano-Fonseca[1], Alfonso J. Rodríguez-Morales[2,3], Marylin Hidalgo[1], Álvaro A. Faccini-Martínez[4,5]

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Annals of Clinical Microbiology
and Antimicrobials

REVIEW Open Access

Pan-American Guidelines for the treatment of SARS-CoV-2/COVID-19: a joint evidence-based guideline of the Brazilian Society of Infectious Diseases (SBI) and the Pan-American Association of Infectious Diseases (API)

Alexandre Naime Barbosa[1,17*], Alberto Chebabo[2,3], Carlos Starling[4], Clevy Pérez[5], Clóvis Arns Cunha[3,6], David de Luna[7], Estevão Portela Nunes[8], Gabriela Zambrano[9,23], Juliana Carvalho Ferreira[10,11], Julio Croda[12], Maicon Falavigna[13], Monica Maria Gomes-da-Silva[14], Monica Thormann[15], Sergio Cimerman[3,16], Suena Medeiros Parahiba[13], Suzana Tanni[17], Wanderley Marques Bernardo[18] and Alfonso J. Rodriguez-Morales[19,20,21,22*]

Conclusions

Since the beginning of the COVID-19 pandemic, studies have been conducted to provide the evidence necessary to formulate recommendations. This guideline presents a set of drugs that have proven effective in the prophylaxis and treatment of COVID-19 following the principles of evidence-based medicine, emphasising the strong recommendation for the use of nirmatrelvir/ritonavir in outpatients. Evidence has shown the lack of benefit of hydroxychloroquine and ivermectin, contraindicating their use in both outpatient and inpatient settings. It is strongly advised that these recommendations be adopted in the Americas to optimise the use of health resources and reduce the heterogeneity of procedures, as well as to reduce the progression to long COVID-19 [65].

Infection
https://doi.org/10.1007/s15010-022-01788-w

ORIGINAL PAPER

Post-COVID-19 syndrome: assessment of short- and long-term post-recovery symptoms in recovered cases in Saudi Arabia

Mohammed A. Garout[1] · Saleh A. K. Saleh[2,3] · Heba M. Adly[1] · Altaf A. Abdulkhaliq[2] · Abdullah A. Khafagy[1] · Magda R. Abdeltawab[4] · Ali A. Rabaan[5,6,7] · Alfonso J. Rodriguez-Morales[8,9,10] · Jaffar A. Al-Tawfiq[11,12,13] · Maher N. Alandiyjany[14,15]

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Online ahead of print.

The global challenges of the long COVID-19 in adults and children

Alfonso J Rodriguez-Morales [1], María Camila Lopez-Echeverri [2], Maria Fernanda Perez-Raga [2], Valentina Quintero-Romero [2], Valentina Valencia-Gallego [2], Nicolas Galindo-Herrera [2], Santiago López-Alzate [2], Juan Diego Sánchez-Vinasco [2], Juan José Gutiérrez-Vargas [2], Percy Mayta-Tristan [3], Rola Husni [4], Rima Moghnieh [4], Joseph Stephan [4], Wissam Faour [4], Samah Tawil [4], Hanane Barakat [4], Toufic Chaaban [4], Andre Megarbane [4], Youssef Rizk [4], Rania Sakr [4], Juan Pablo Escalera-Antezana [5], Lucia E Alvarado-Arnez [6], D Katterine Bonilla-Aldana [7], German Camacho-Moreno [8], Henry Mendoza [9], Ivan Arturo Rodriguez-Sabogal [10], Jose Millán-Oñate [11], Gustavo Lopardo [12], Alexandre Naime Barbosa [13], Sergio Cimerman [14], Tânia do Socorro Souza Chaves [15], Tomas Orduna [16], Susana Lloveras [16], Andrea G Rodriguez-Morales [17], Monica Thormann [18], Patricia Gabriela Zambrano [19], Clevy Perez [20], Nancy Sandoval [21], Lysien Zambrano [22], Carlos A Alvarez-Moreno [23], Enrique Chacon-Cruz [24], Wilmer E Villamil-Gomez [25], Vicente Benites-Zapata [26], Eduardo Savio-Larriera [27], Jaime A Cardona-Ospina [28], Alejandro Risquez [29], David A Forero-Peña [30], Andrés F Henao-Martínez [31], Ranjit Sah [32], Joshuan J Barboza [33], Darwin A León-Figueroa [34], Jaime David Acosta-España [35], Carmen María Carrero-Gonzalez [36], Jaffar A Al-Tawfiq [37], Ali A Rabaan [38], Hakan Leblebicioglu [39], Jose A Gonzales-Zamora [40], Rolando Ulloa-Gutiérrez [41]

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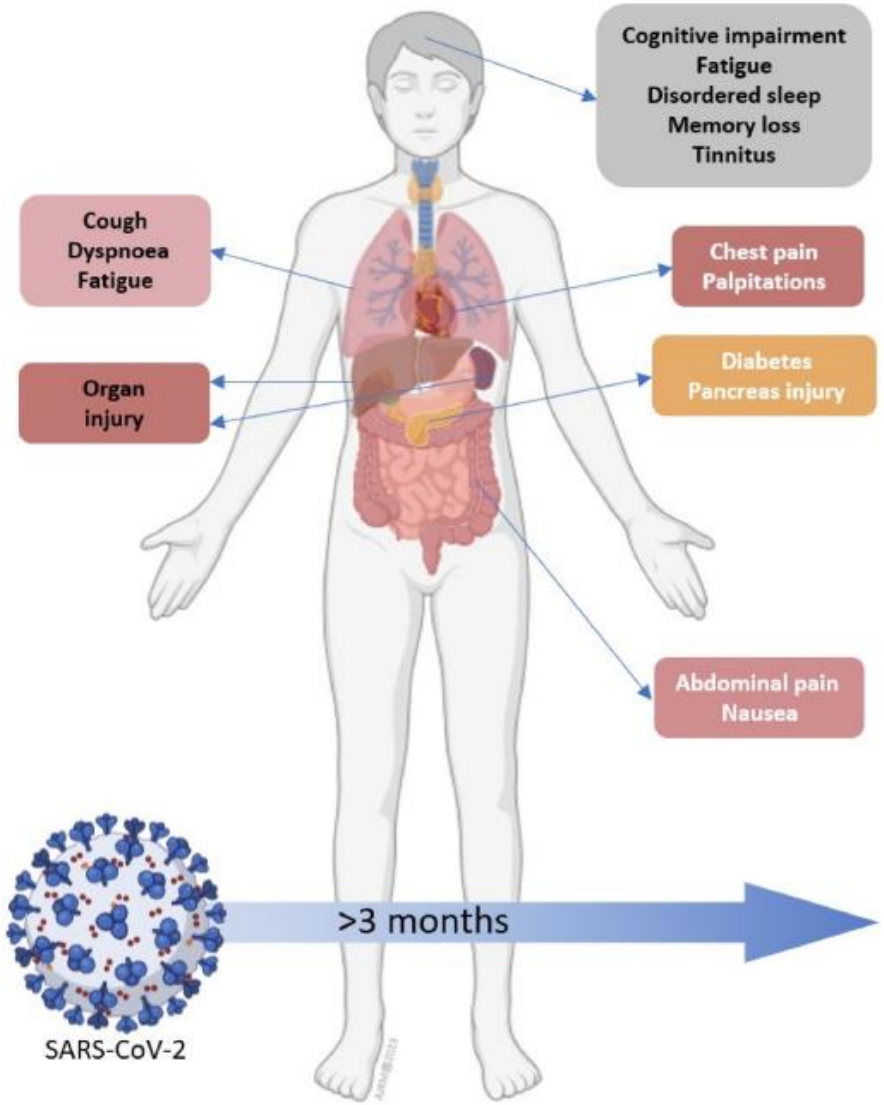

Fig. 1. Some of the clinical findings associated with long COVID-19, modified from Davis et al. [63].

A.J. Rodriguez-Morales et al. Travel Medicine and Infectious Disease 54 (2023) 102606

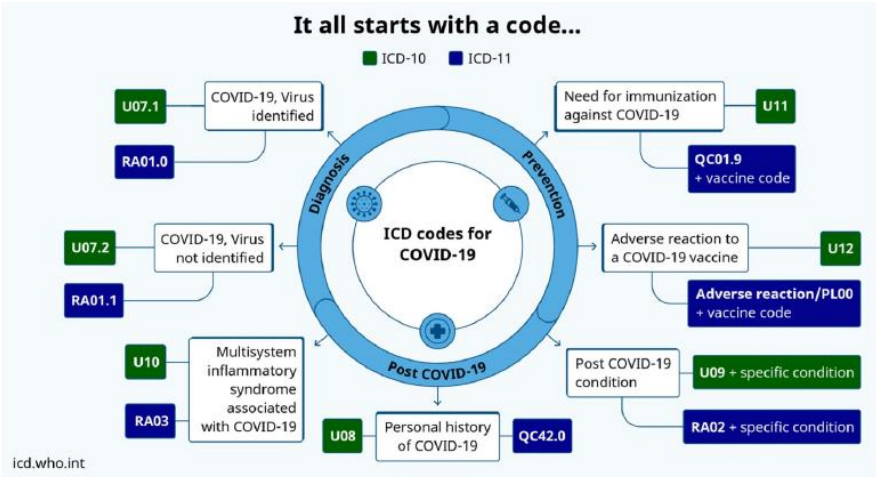

Fig. 2. ICD codes for COVID-19, according the WHO (https://www.who.int/standards/classifications/classification-of-diseases/emergency-use-icd-codes-for-covid-19-disease-outbreak).

Rodriguez-Morales AJ, Lopez-Echeverri MC, Perez-Raga MF, Quintero-Romero V, Valencia-Gallego V, Galindo-Herrera N, López-Alzate S, Sánchez-Vinasco JD, Gutiérrez-Vargas JJ, Mayta-Tristan P, Husni R, Moghnieh R, Stephan J, Faour W, Tawil S, Barakat H, Chaaban T, Megarbane A, Rizk Y, Sakr R, Escalera-Antezana JP, Alvarado-Arnez LE, Bonilla-Aldana DK, Camacho-Moreno G, Mendoza H, Rodriguez-Sabogal IA, Millán-Oñate J, Lopardo G, Barbosa AN, Cimerman S, Chaves TDSS, Orduna T, Lloveras S, Rodriguez-Morales AG, Thormann M, Zambrano PG, Perez C, Sandoval N, Zambrano L, Alvarez-Moreno CA, Chacon-Cruz E, Villamil-Gomez WE, Benites-Zapata V, Savio-Larriera E, Cardona-Ospina JA, Risquez A, Forero-Peña DA, Henao-Martínez AF, Sah R, Barboza JJ, León-Figueroa DA, Acosta-España JD, Carrero-Gonzalez CM, Al-Tawfiq JA, Rabaan AA, Leblebicioglu H, Gonzales-Zamora JA, Ulloa-Gutiérrez R. The global challenges of the long COVID-19 in adults and children. Travel Med Infect Dis. 2023 Jun 8;54:102606. doi: 10.1016/j.tmaid.2023.102606. Epub ahead of print. PMID: 37295581; PMCID: PMC10247301.

ELSEVIER

Travel Medicine and Infectious Disease

Available online 26 May 2022, 102362

In Press, Journal Pre-proof

The never ending global emergence of viral zoonoses after COVID-19? The rising concern of monkeypox in Europe, North America and beyond

Darwin A. León-Figueroa [1], D. Katterine Bonilla-Aldana [1], Monica Pachar [1], Luccio Romaní, Hortencia M. Saldaña-Cumpa, Claudia Anchay-Zuloeta, Milagros Diaz-Torres, Carlos Franco-Paredes, José Antonio Suárez, Juan David Ramirez, Alberto Paniz-Mondolfi, Alfonso J. Rodriguez-Morales

Table 1
Key features of Smallpox and Monkeypox.

Orthopoxvirus	
Smallpox	Monkeypox
More infectious	Less infectious
Vaccines used until used up to four decades ago	No specific vaccine is available yet (cross-immunity with Smallpox vaccine)
Eradicated in 1980 (last known case in 1977 in Somalia)	Known circulation in Africa since 1958 (1970 first human case in DRC)
Similar transmission routes	
CFR:	CFR
Variola minor: 1%	West African clade: 1%
Variola major: 30%	Central African clade: 10%

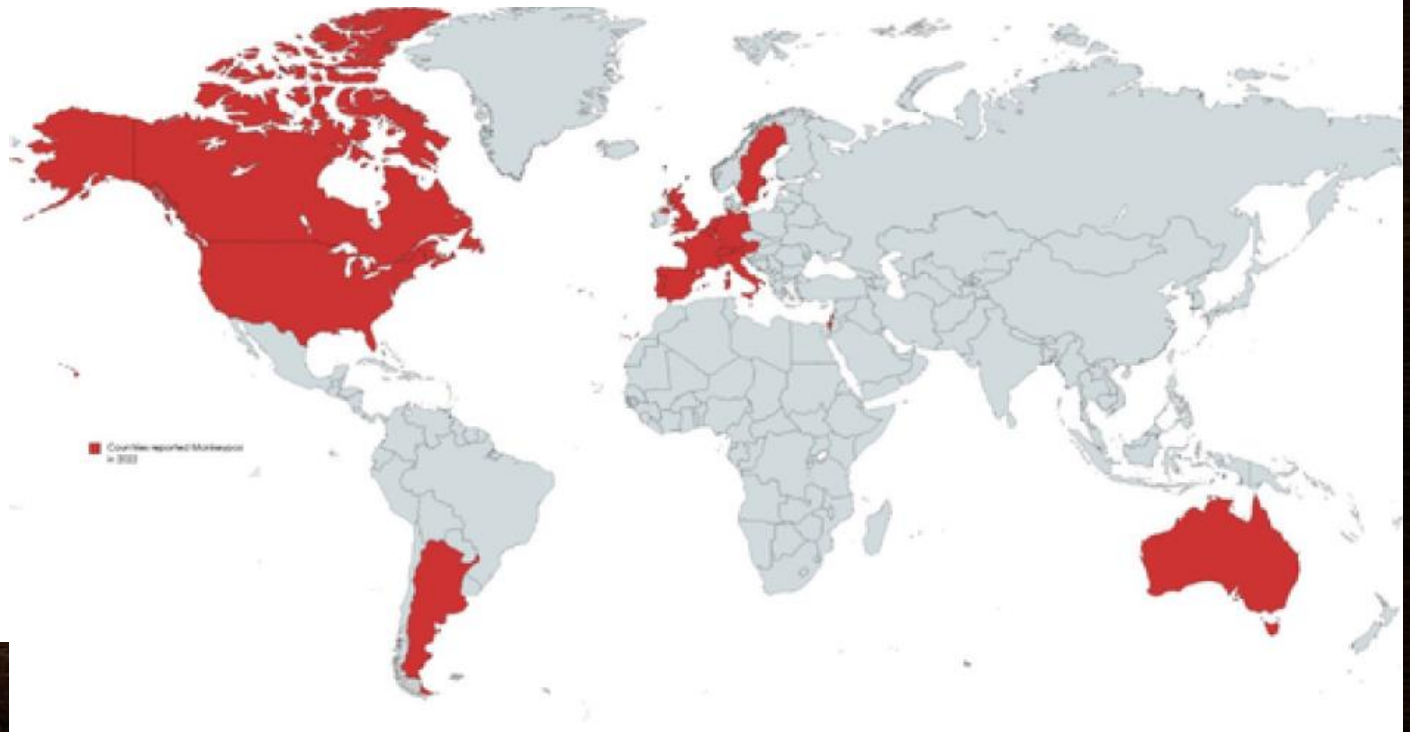

Fig. 1. Countries that have reported Monkeypox in 2022, up to May 23.

Latin America: Situation and preparedness facing the multi-country human monkeypox outbreak

Alfonso J. Rodriguez-Morales,[a,b,c*] Gustavo Lopardo,[d] Sergio Verbanaz,[e] Tomas Orduna,[d,f] Susana Lloveras,[d,f] Jose María Azeñas-Burgoa,[g] Juan Pablo Escalera-Antezana,[h] Lucia Elena Alvarado-Arnez,[i] Alexandre Naime Barbosa,[j] Fredi Diaz-Quijano,[k] Sergio Cimerman,[l] Tânia do Socorro Souza Chaves,[m] Andrea G. Rodriguez-Morales,[n] Cecilia Perret,[o] Claudio A. Méndez,[p] Jorge A. Riera,[q] D. Katterine Bonilla-Aldana,[a] German Camacho,[r] Henry Mendoza,[s] Ivan Rodriguez,[t] Jose Oñate,[u] Angel A. Escobedo,[v] Monica Thormann,[w] Yori Roque,[x] Gabriela Zambrano,[y] Yenddy Carrero,[z] Nancy Sandoval,[aa] Lysien Zambrano,[ab] Carlos Franco-Paredes,[ac] Enrique Chacon-Cruz,[ad] Iván Lopez-Delgado,[ad] Cesar Cuadra-Sánchez,[ae] Monica Pachar,[af] Ricardo Correa,[ag] Hernan D. Rodriguez-Enciso,[ah] Veronica Rotela-Fisch,[ai] Julio Maquera-Afaray,[aj] Percy Herrera-Añazco,[ak] Vicente Benitez-Zapata,[al] Eduardo Savio-Larriera,[am] Juan David Ramírez,[an,ao] Alberto Paniz-Mondolfi,[am,ap] Alejandro Risquez,[aq] David A. Forero-Peña,[aq,ar] Jaime R. Torres,[as] and Jose Antonio Suarez[at]

ID-IRI Monkeypox Survey

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- Sociedad Venezolana de Infectolgía

THE LANCET Regional Health Americas

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Centers for Disease Control and Prevention

CDC 24/7: Saving Lives, Protecting People™

Confirmed Cases

89,581
Total Cases

87,688
in locations that have not historically reported mpox

1,893
in locations that have historically reported mpox

Locations with cases

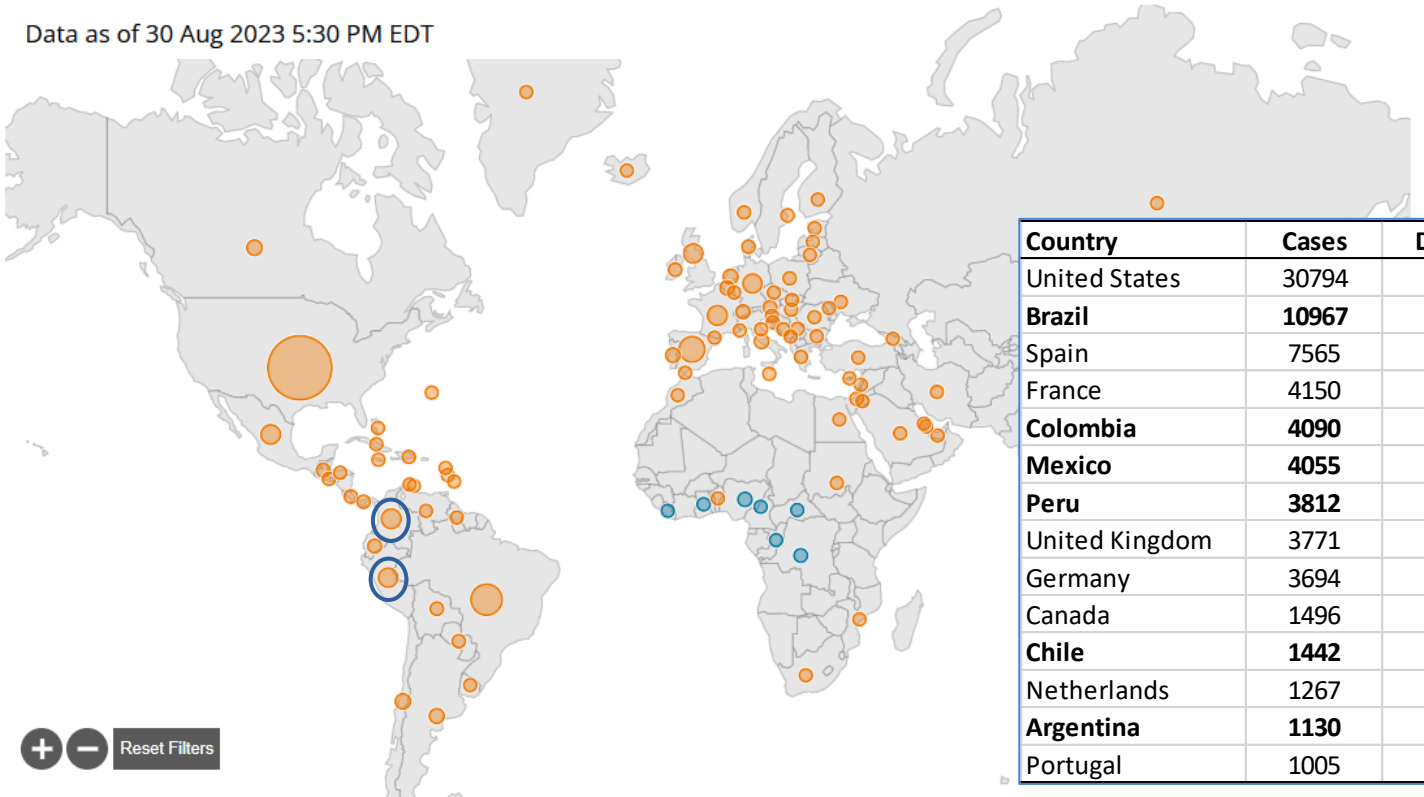
114
Total

107
Has not historically reported mpox

7
Has historically reported mpox

2022 Mpox Outbreak Global Map

Data as of 30 Aug 2023 5:30 PM EDT



Country	Cases	Deaths
United States	30794	53
Brazil	**10967**	**16**
Spain	7565	3
France	4150	0
Colombia	**4090**	**0**
Mexico	**4055**	**30**
Peru	**3812**	**20**
United Kingdom	3771	0
Germany	3694	0
Canada	1496	0
Chile	**1442**	**3**
Netherlands	1267	0
Argentina	**1130**	**2**
Portugal	1005	1

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New Microbes and New Infections

Available online 20 May 2023, 101154

In Press, Journal Pre-proof What's this?

Original Article

Features of Mpox infection: The analysis of the data submitted to the ID-IRI network

Gulden Eser-Karlidag [a], Enrique Chacon-Cruz [b], Yasemin Cag [c], Jose Arturo Martinez-Orozco [d], Humberto Gudino-Solorio [d], Raul Adrian Cruz-Flores [d], Andrea Gonzalez-Rodriguez [d], Daniela Martinez-Nieves [d], Mario Gomez-Zepeda [d], Andrea Calderon-Suarez [d], Hülya Çaşkurlu [c], Antonio Cascio [e], Ricardo Fernandez [f], Greisha M. Gonzales [f], Pedro Palma [g], Corneliu Petru Popescu [h], Roman Stebel [i], Botond Lakatos [j], Eva Nagy [j], Massimiliano Lanzafame [k], Amani El-Kholy [l], Buse Tuncer [a], Iva Christova [m], Stefka Krumova [m], Alexandre Naime Barbosa [n], Juan Pablo Escalera-Antezana [o], Ruben Castillo-Quino [p], Carlos Eduardo Gonzales-Flores [p], Miriam Moreira-Flores [p], Marcelo Felipe Batallanos-Huarachi [p], Christian Gomez-Davila [p], Rusmir Baljic [q], Tarsila Vieceli [r], Olumuyiwa Elijah Ariyo [s], Mireia Cairo Llobell [t], Osasona Oluwadamilola Gideon [u], Augustus Osborne [v], Umran Elbahr [w], Philippe Bossi [x], Antonella Tammaro [y], Alfonso J. Rodriguez-Morales [z aa ab], Hakan Erdem [ac]

Symptom/s	614	95.3
Fever	337	54.9
Headache	190	30.9
Sore throat	130	21.2
Fatigue	246	40.1
Itching	203	33.1
Cough	16	2.6
Mental deterioration	4	0.7
Muscle pain	224	36.4
Abdominal pain	6	0.9
Nausea-vomiting	17	2.8
Rectal pain	67	10.9
Rectal bleeding	12	1.9
Ulcers in the mouth	38	6.2
Genital ulcers	220	35.8
Lymphadenopathy	419	65.1
Region of lymphadenopathy		
Inguinal	327	78
Cervical	144	34.4
Axillary	23	5.5
Mixed	75	17.9

THERAPEUTIC ADVANCES in
Infectious Disease

Brief Report

Hospitalization risk among patients with Mpox infection—a propensity score matched analysis

Andrés F. Henao-Martínez, Chloe M. Orkin, Boghuma K. Titanji, Alfonso J. Rodriguez-Morales, Jorge L. Salinas, Carlos Franco-Paredes, Jose Tuells and Daniel B. Chastain

Abstract

Background: Monkeypox (Mpox) is a reemerging, neglected viral disease. By May 2023, worldwide Mpox cases surpassed 87,000. Predictive factors for hospitalization with Mpox are lacking.

Objective: We aim to compare clinical characteristics and outcomes in hospitalized and nonhospitalized patients with Mpox infection.

Design: A multicenter retrospective case-control cohort of patients with Mpox infection.

Methods: We performed a propensity score match analysis from a global health network (TrinetX). We compare clinical characteristics and outcomes between hospitalized and nonhospitalized patients with Mpox.

Results: Of 1477 patients, 6% were hospitalized, 52% required an ED visit, and 29% received treatment at urgent care. After propensity score matching, 80 patients remained in each group. Hospitalizations were more common among Black persons (51% *versus* 33%, $p = 0.01$), people with HIV (50% *versus* 20%, $p < 0.0001$), and those with proctitis (44% *versus* 12.5%, $p < 0.001$).

Conclusion: Independent predictive factors of hospitalization in our cohort for Mpox included people who are Black with a diagnosis of HIV, severe proctitis, pain requiring opioids, and elevated lactate dehydrogenase. Greater recognition of factors associated with increased risk of Mpox severity and hospitalization is paramount.

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Table 1. Clinical characteristics of Mpox patients by hospitalization status.

Variable, Mean ± SD, *N* (%)	N	Overall, *N* = 1477	Hospitalized, *N* = 89	Nonhospitalized, *N* = 1388	*p*-Value
Demographics					
Age (years),	1477	35 ± 11.8	34 ± 11	35.1 ± 11.9	0.3882
Men	1477	1323 (90%)	80 (90%)	1243 (90%)	0.9203
White	1477	436 (30%)	38 (43%)	398 (29%)	0.0049
Hispanic	1477	212 (14%)	15 (17%)	197 (14%)	0.4877
Black	1477	438 (30%)	45 (51%)	393 (28%)	<0.0001
Symptoms					
Rash	1477	204 (14%)	49 (55%)	155 (11%)	<0.0001
Fever	1477	81 (5%)	20 (22%)	61 (4%)	<0.0001
Nausea	1477	35 (2%)	11 (12%)	24 (2%)	<0.0001
Headaches	1477	32 (2%)	10 (11%)	22 (2%)	<0.0001
Comorbidities*					
HIV	1477	487 (33%)	51 (57%)	436 (31%)	<0.0001
History of Syphilis	1477	267 (18%)	31 (35%)	236 (17%)	<0.0001
Neoplasm	1477	185 (13%)	17 (19%)	168 (12%)	0.0532
Aplastic anemia	1477	83 (6%)	17 (19%)	66 (5%)	<0.0001
DM2	1477	71 (5%)	12 (14%)	59 (4%)	<0.0001
Transplant status	1477	<10 (<1%)	<10 (<11%)	<10 (<1%)	<0.0001
Complications					
Proctitis	1477	143 (10%)	29 (33%)	114 (8%)	<0.0001
Cellulitis	1477	33 (2%)	15 (17%)	21 (2%)	<0.0001
Tonsillitis	1477	22 (2%)	10 (11%)	12 (1%)	<0.0001
Pneumonia	1477	<10 (<1%)	<10 (<11%)	<10 (<1%)	<0.0001
Labs**					
Creatinine (mg/dL)	315	1.0 ± 10.7	0.9 ± 0.4	1.0 ± 0.3	0.0188
AST (IU/mL)	175	29.1 ± 20	51.5 ± 103	29.2 ± 20.4	0.0052
Leukocytes (10^3/μL)	260	10.8 ± 87.1	10.3 ± 7.0	11.3 ± 64	0.9015
Lymphocytes (10^3/μL)	227	3.0 ± 1.2	2.5 ± 2.2	2.2 ± 2.5	0.5384
Hemoglobin (mg/dL)	254	14.5 ± 1.64	13.6 ± 1.8	14.5 ± 1.6	0.0004
Hemoglobin A1c (%)	43	5.87 ± 1.68	5.4 ± 1.1	5.9 ± 1.7	0.3609
CD4 count (cells/μL)	107	600 ± 336	286 ± 283	618 ± 337	0.0003
HIV RNA (copies/mL)	33	39k ± 81k	248k ± 200k	31k ± 73k	<0.0001
LDH (U/L)	24	254 ± 121	304 ± 131	261 ± 125	0.3823
Ferritin (ng/mL)	28	196 ± 90.6	234.6 ± 254.4	175.1 ± 88.6	0.635

First Monkeypox deaths outside Africa: no room for complacency

Ranjit Sah, Aroop Mohanty, Abdelaziz Abdelaal, Abdullah Reda, Alfonso J. Rodriguez-Morales and Andres F. Henao-Martinez

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2022, Vol. 9: 1–3
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Keywords: case fatality rate, deaths, international concern, monkeypox, mortality, outbreak, public health emergency

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As of 16 August 2022, there are 37,632 confirmed cases of monkeypox in more than 85 non-endemic countries, plus those in endemic African areas, making a total of 38,019 in 93 countries.[1] The disease was always considered endemic in the African continent, with only a few sporadic outbreaks in the rest of the world since 2003.[2] Surprisingly, the present epidemic has wholly changed the epidemiology of the disease, with Europe and the American continent contributing more than 90% of the total confirmed cases.[3]

From the beginning of 2022 until 8 June 2022, 72 deaths were reported, all belonging to the African region. Of the total 72, the Democratic Republic of Congo (DRC) had the largest proportion with 64 deaths.[4] The disease remained confined to the African continent until the beginning of May 2022, when the first case was seen in the United Kingdom on 8 May 2022.[5] The World Health Organization (WHO) reported on 22 July 2022 that only five deaths were due to monkeypox, with all of them again from Africa.

The first death from monkeypox outside Africa was reported in Brazil on 29 July 2022, when a 41-year-old man undergoing treatment for lymphoma died of septic shock.[6] Shortly after, Europe had its first death from a monkeypox case in Spain. The identity of the deceased was not disclosed. However, according to the Spanish health authorities, the individual was a middle-aged man from Alicante (Valencia region), who died due to encephalitis.[7] Within 24 hours of the first case, Spain again confirmed its second death from monkeypox. The second case reportedly is a young man, and more details are yet to be known. Spain is the worst hit country in Europe, with more than 4,200 confirmed cases and 120 monkeypox hospitalizations.

On 31 July 2022, India reported its first monkeypox death.[8] He was a 22-year-old man who had returned from United Arab Emirates (UAE) on 21 July to Thrissur district in Kerala. Kerala is a state in the south of India that has reported the first three confirmed cases of monkeypox. He was admitted to a private hospital on 27 July 2022, with fever, encephalitis and lymph node swelling. At admission, he did not have any body rash, and therefore, there was no suspicion of monkeypox. It was only after he died that he tested positive for monkeypox at Ras Al-Khaimah (UAE) on July 19, just before his return to Kerala. According to health authorities, the deceased patient was healthy and did not have any other illness. Given the unexpected death, a high-level task force has been constituted to review the ongoing country public health preparedness.

On 1 August 2022, death due to monkeypox was also confirmed in Lima, Peru, in a 41-year-old man with HIV and tuberculosis that was not under antiretroviral treatment. He was admitted to the ICU with respiratory failure, acute renal failure and septic shock, and confirmed monkeypox virus (MPXV) infection.[9] One death has been also reported in Guayaquil, Ecuador.

Possible causes of death triggered by monkeypox infection include MPXV central nervous system (CNS) invasion with encephalitis,[10] an infrequent complication, but where cell-mediated immunity defects may play a role. Also, sepsis from a skin and soft tissue infection can complicate the associated skin lesions. During prior African outbreaks – especially with the Congo basin strain – mortality was common among young children.[11] In those cases, researchers hypothesize the potential role of occasional co-infection with Varicella zoster virus (VZV). Experimental aerosolized MPXV infection among cynomolgus monkeys produced a fatal fibrinonecrotic bronchopneumonia 1–2 weeks after exposure.[12] In animal models, high MPXV viremias and neutropenias have been implicated in fatal gramme-positive sepsis.[13] Future autopsy histopathology analyses from fatal cases are needed to elucidate specific viral mechanisms of death.

Five deaths, among 37,632 cases in non-endemic countries represents, theoretically, a case fatality rate (CFR%) of 0.01%, compared with 1.81% in endemic countries during 2022 (183 times higher) (Table 1). Nevertheless, there are regional differences (Table 1). The difference would be higher when comparing with recent systematic reviews of African cases before 2022,[14] reporting 10.6% [95% confidence interval (CI), 8.4–13.3%] for clade 1 (formerly Congo basin or Central African) and 4.6% (95% CI 2.1–8.6%) for clade 2 (formerly West African). The differences may be related to multiple factors, including difference in the host (e.g. nutrition, comorbidities, immunosuppression, among others), but also to the quality of the health care systems as well as the viral evolution. In addition, transmission has primarily been between men who have sex with men (MSM), and they have generally been of a young age (20- to 40-years-old) with few comorbidities; this has changed the epidemiology and likely reduced the CFR%.

More deaths due to monkeypox are yet to come during this outbreak, especially among immunosuppressed patients. Mortality risk factors and interventions should be researched immediately to prevent, control and mitigate the disease burden.

Table 1. Comparison of CFR% among non-endemic and endemic countries during 2022, up to 16 August.

Country	Cases	Deaths	CFR%
Non-endemic countries			
India	9	1	11.11
Ecuador	17	1	5.88
Spain	5719	2	0.03
Brazil	2893	1	0.03
Subtotal non-endemic countries	37,632	5	0.01
Endemic countries			
Central African Republic	8	2	25.00
Nigeria	157	4	2.55
Ghana	47	1	2.13
Subtotal endemic countries	387	7	1.81
Total (World)	38,019	12	0.03

CFR, case fatality rate.

Declarations

Ethics approval and consent to participate
Not applicable.

Consent for publication
Not applicable.

Author contributions
Ranjit Sah: Writing – original draft.

Aroop Mohanty: Writing – review & editing.

Abdelaziz Abdelaal: Writing – review & editing.

Abdullah Reda: Writing – review & editing.

Alfonso J. Rodriguez-Morales: Writing – review & editing.

Andres F. Henao-Martinez: Writing – review & editing.

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Competing interests
The authors declared the following potential conflicts of interest with respect to the research, authorship, and/or publication of this article: The

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CFR, case fatality rate.

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Comment

Monkeypox virus infection in women and non-binary people: uncommon or neglected?

Alfonso J Rodriguez-Morales [a b c] ✉, Fatma A Amer [d e]

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REVIEW

WILEY

A meta-analysis and mapping of global mpox infection among children and adolescents

Tarun Kumar Suvvari[1,2] | Mokanpally Sandeep[3] | Jogender Kumar[4] | Prakasini Satapathy[5] | Santenna Chenchula[6] | Aravind P. Gandhi[7] | Muhammad Aaqib Shamim[8] | Patricia Schlagenhauf[9] | Alfonso J. Rodríguez-Morales[10,11] | Ranjit Sah[12,13] | Keerti Bhusan Pradhan[14] | Sarvesh Rustagi[15] | Alaa Hamza Hermis[16] | Bijaya K. Padhi[17]

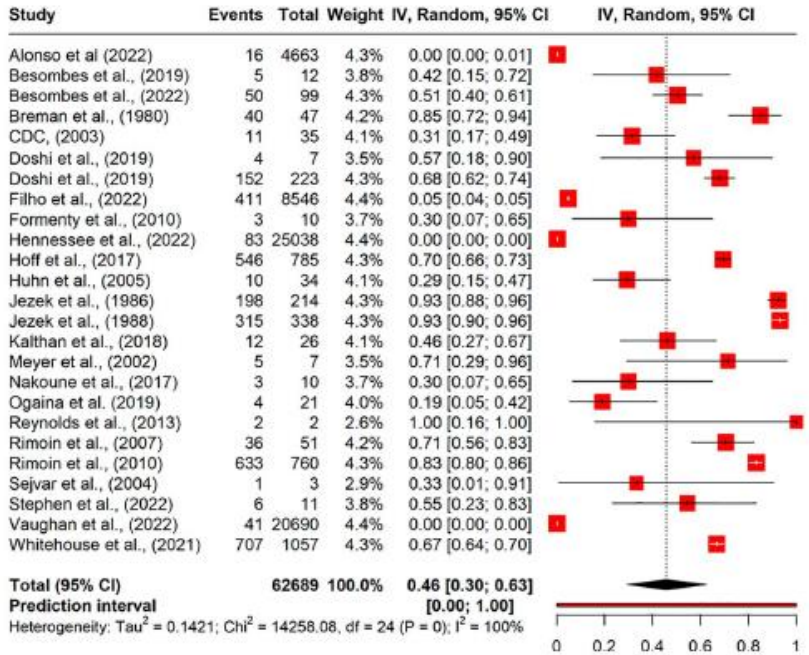

FIGURE 2 Forest plots showing overall effect size and its confidence interval; and heterogeneity statistics of proportion of children with mpox.

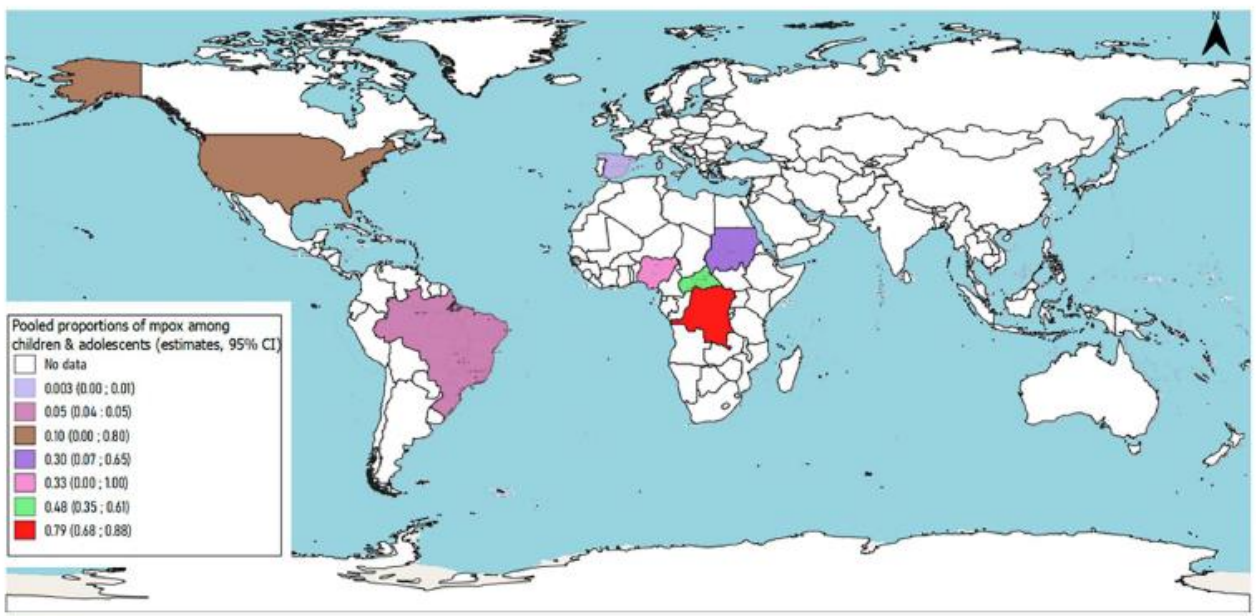

FIGURE 3 Choropleth map depicting the global outbreak of mpox among children and adolescents.

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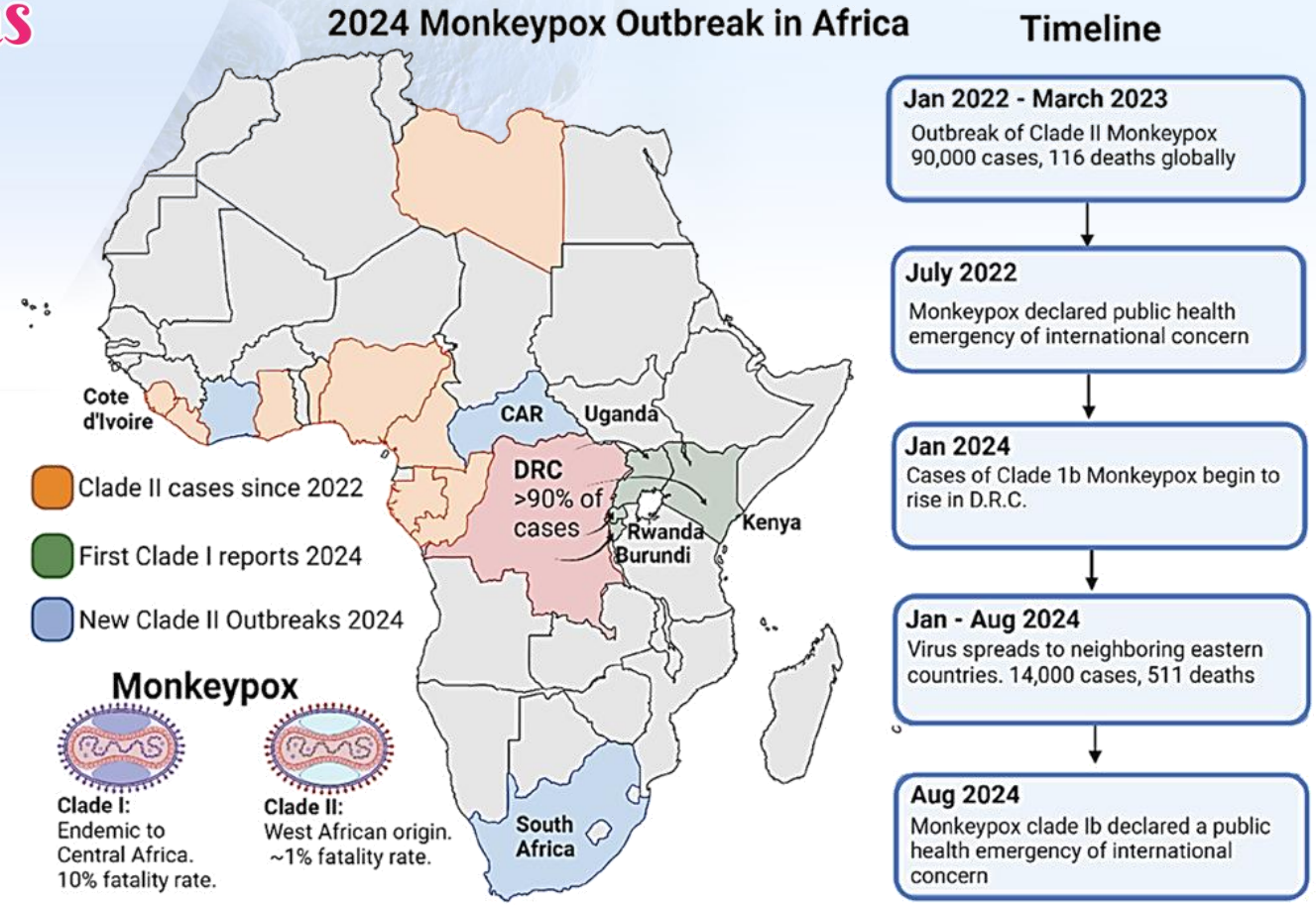

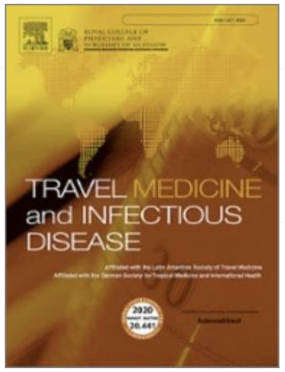

SLAMVI Sociedad Latinoamericana de Medicina del Viajero

Fig. 1. Mpox outbreaks in Africa since 2022 highlighting re-emerging outbreaks (blue) in Central African Republic (CAR), Cote d'Ivoire and South Africa, with new outbreaks (green) in Burundi, Kenya, Rwanda and Uganda for the first time, declaring the African outbreak as a Public Health Emergency of Continental Security by the African CDC; and the WHO as a Public Health Emergency of International Concern. The Demographic Republic of Congo reports >90 % of the cases. (For interpretation of the references to colour in this figure legend, the reader is referred to the Web version of this article.)

Sah R, Apostolopoulos V, Mehta R, Rohilla R, Sah S, Mohanty A, Mehta V, Feehan J, Luna C, Membrillo de Novales FJ, Al-Tawfiq JA, Cascio A, Samayoa-Bran AJ, Bonilla-Aldana DK, **Rodriguez-Morales AJ. Mpox Strikes Once More in 2024: Declared Again as a Public Health Emergency of International Concern**. *Travel Med Infect Dis* 2024 Epub Ahead Aug 23; https://www.sciencedirect.com/science/article/pii/S147789392400070X

CORRESPONDENCE · Online first, September 23, 2024

Renaming mpox in Spanish, French, and Portuguese: using language to address stigma and racism

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Enfermedades Infecciosas y Microbiología Clínica

Editorial · Full text access

Proponiendo el cambio de denominación de la viruela del mono (Mpox) en español a viruela M

Francisco Javier Membrillo de Novales, Jaime García Iglesias, Miriam J. Álvarez-Martínez, Luis E. Cuellar, ... Alfonso J. Rodriguez-Morales

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XIV Encuentro Nacional de investigación e innovación en Enfermedades Infecciosas
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EDITORIAL

The Resurgence of Mpox: A New Global Health Crisis

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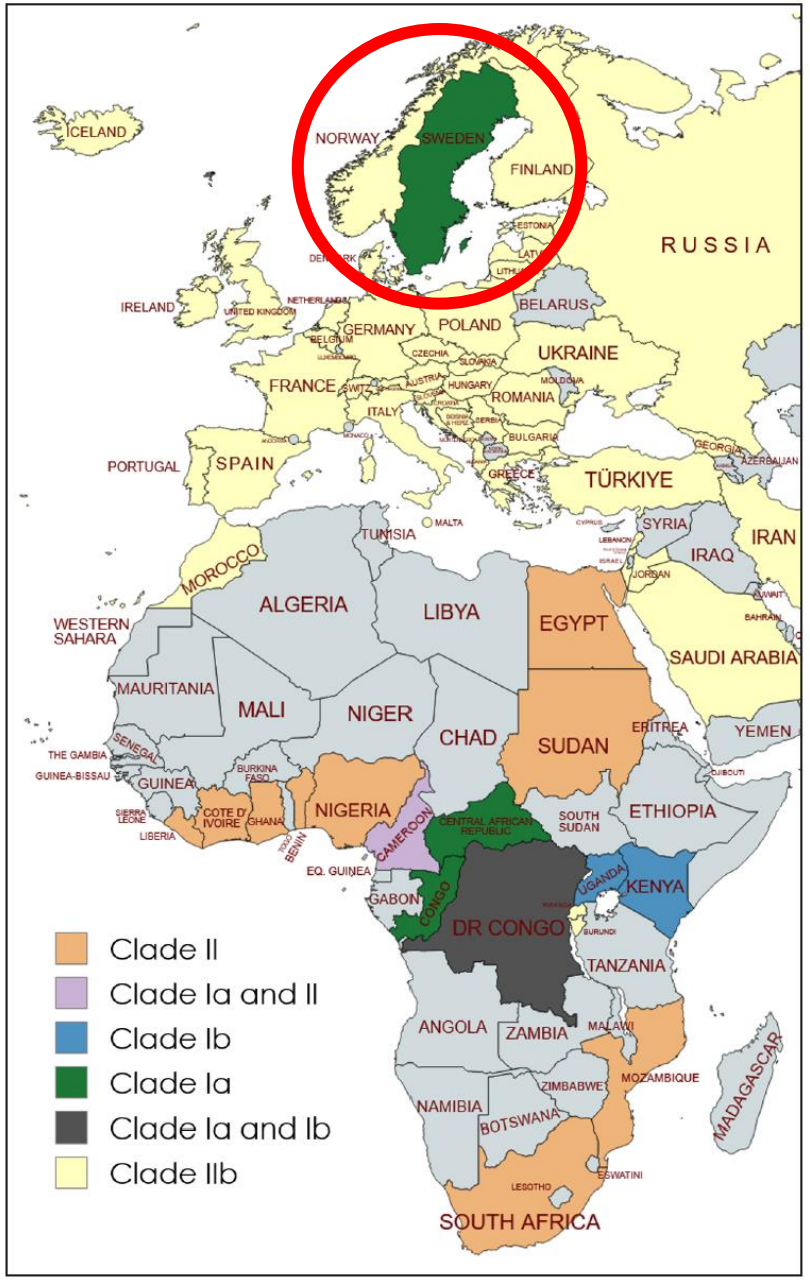
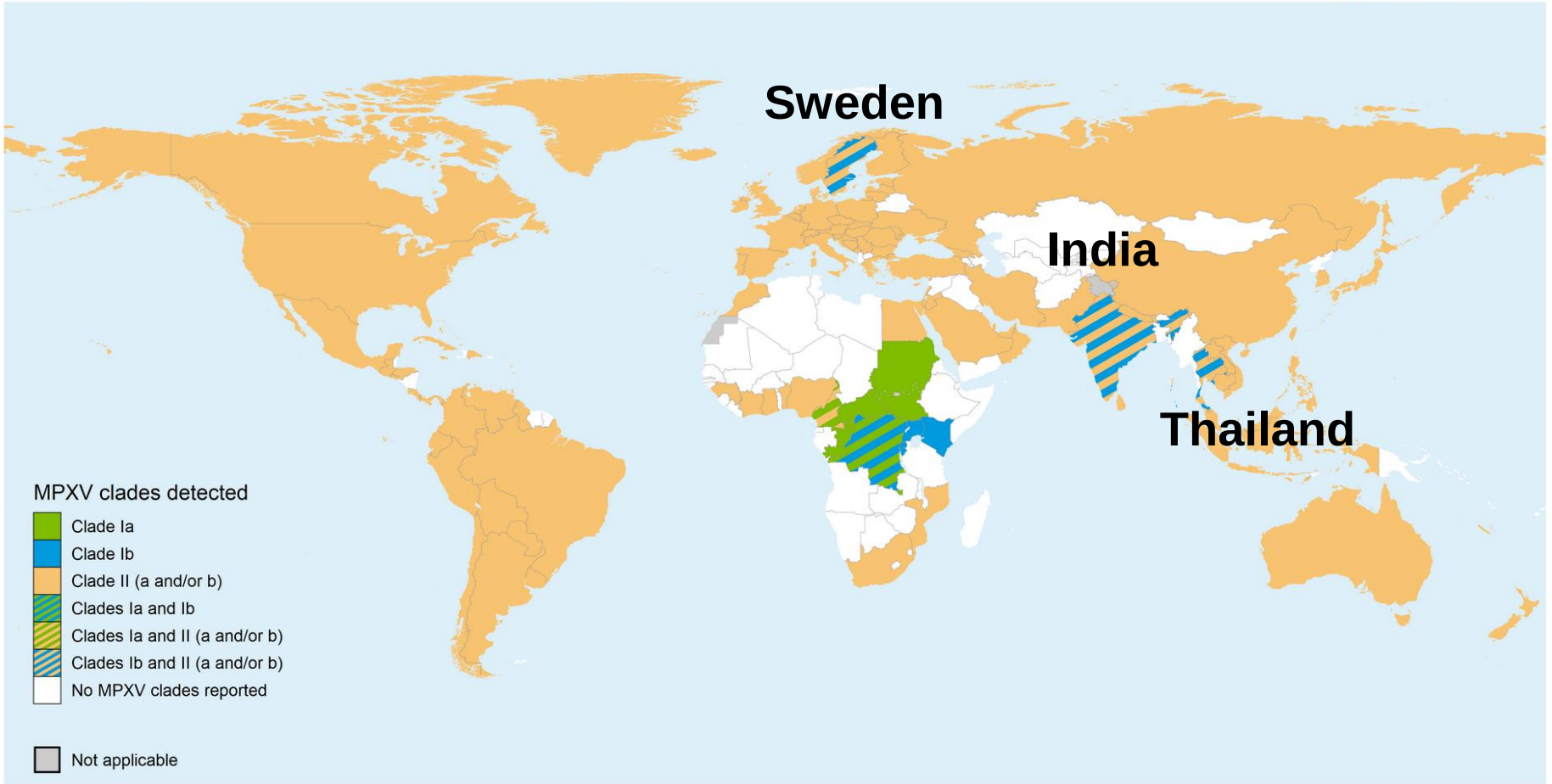


Figure 1 - African countries where monkeypox virus clade I and/or clade II have been detected, and European countries that have previously reported clade IIb; including Sweden recently reported clade Ib (2024).

MPXV clades detected globally

includes imported cases; from 1 Jan 2022, as of 29 Sep 2024

World Health Organization



The designations employed and the presentation of the material in this publication do not imply the expression of any opinion whatsoever on the part of WHO concerning the legal status of any country, territory, city or area or of its authorities, or concerning the delimitation of its frontiers or boundaries. Dotted and dashed lines on maps represent approximate border lines for which there may not yet be full agreement.

Data Source: World Health Organization
Map Production: WHO Health Emergencies Programme

World Health Organization

Health Topics | Countries | Newsroom | Emergencies | Data | About WHO

Home / News / WHO approves first mpox diagnostic test for emergency use, boosting global access

WHO Emergency Use List: Monkeypox virus IVDs/ Nucleic Acid Tests

Last updated October 3 2024

Date Listed	Manufacturer name	Product name	Product code(s)	Regulatory version	EUL application number	Packaging	Link to access public report
3 October 2024	Abbott Molecular Inc	Alinity m MPXV assay (Alinity m MPXV Amplification (AMP) Kit & Alinity m MPXV Control (CTRL) Kit)	QTP	USFDA EUA	MPXV-12644-027-00	Alinity m MPXV Amplification (AMP) Kit: 48 tests/tray, 192 tests/kit Alinity m MPXV Control (CTRL) Kit: 12 tubes per level	To be published

WHO approves first mpox diagnostic test for emergency use, boosting global access

ChikDenMaZika Yellow Monkey

REV. CM HNAAA

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Editorial

Arboviral diseases and monkeypox - An epidemiological overlapping differential diagnosis?

Arbovirosis y Viruela del Mono - ¿Un diagnóstico diferencial de solapamiento epidemiológico?

DOI

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Alfonso J. Rodriguez-Morales[1,2,3,4,a,*], Darwin A. León-Figueroa[5,6,b], Ranjit Sah[7,8,c], Wilmer E. Villamil-Gomez[8,9,d]

Over the last decades, the epidemiological importance of different arboviral diseases in the world has been significant, especially in Latin America and South-East Asia[1]. Dengue, chikungunya, Zika, yellow fever, but also Venezuelan Equine Encephalitis, Mayaro, and Oropouche, among others, have been significantly important in the case of Latin America[2,3]. Multiple dengue epidemics and the recent 2014-2015 epidemics of chikungunya[4,5] or 2015-2016 of Zika[2,4,6,7] have been a matter of concern. Furthermore, during the COVID-19 pandemic, coinfections with arboviruses and other tropical pathogens have also been relevant[4-6]. That is important to consider as a differential diagnosis and the possibility of coinfections.

FILIATION

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Indexed in Scopus

Table 1. Clinical comparison between arboviral diseases and monkeypox.

	CHIK	DEN	MA	ZIKA	YELLOW	MONKEY
Fever	+++	++++	++++	++/0[a]	+++	++++/0[d]
Myalgia/arthralgia	++++	+++	+++	++	+	++/0[d]
Edema in limbs	0	0	0	++	0	0
Maculopapular rash	++	++	++	+++ [b]	0	+++[e]
Vesiculopapular rash	0	0	0	0	0	++++[e]
Retro-ocular pain	+	+++	++	++	0	0
Conjunctivitis, non-purulent	+	0	0	+++	0	+/0[d]
Lymphadenopathies	++	++	+	+	0/+	++++/0[d]
Hepatomegaly	++	0	+	0	+++	0
Leukopenia/ thrombocytopenia	++	++++	++	0/+[c]	+++	Leukocytosis/ Thrombocytopenia++
Haemorrhages	+	+++	0	0/+[c]	++++	+/0[d]
Headache	+	+++	+	+	+++	++/0[d]
Lumbago	++	+	+	0	+++	0
Asthenia	+	++	+	0	++	+++/0[d]

CHIK, chikungunya; DEN, dengue; MA, mayaro; ZIKA, Zika; YELLOW, yellow fever; MONKEY, Monkeypox.

Bold indicates which of the arboviruses is the highest frequency of the clinical finding.

[a] Depends on the geography and phylogeny of the virus, in some areas, patients do not present fever.

[b] Pruriginous (mild to severe).

[c] In some cases, these findings have been reported.

[d] In the 2022 clinical phenotype, such a finding may not be present.

[e] In these cases, with intense pruritus and pain.

After SARS-CoV-2, will H5N6 and other influenza viruses follow the pandemic path?

D. Katterine Bonilla-Aldana[1,2], Mateo Aguirre-Florez[2], Rhuvi Villamizar-Peña[2], Estefanía Gutiérrez-Ocampo[2], Juan F. Henao-Martínez[2], Aleksandar Cvetkovic-Vega[3,4], Kuldeep Dhama[5], Ali A. Rabaan[6], Ranjit Sah[7], Alfonso J. Rodriguez-Morales[2,3,8], Patricia Schlagenhauf[9], Alberto Paniz-Mondolfi[10,11,12]

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SUMMARY

While the world is focused on attending, controlling, and mitigating the current pandemic of COVID-19, caused by the SARS-CoV-2, other viral threats are possibly emerging and reemerging especially in Asia, posing a risk for the spread in that region and beyond. A predictable threat is the avian influenza virus, especially H5N6, which has recently led to significant outbreaks in China and the Philippines, deserving more attention and control. In the current review, we assess the history of this highly pathogenic reemerging virus, as well as the contemporary implications of poultry outbreaks occurring in some Asian countries. We also look at outbreaks due to other strains not only in Asia but also across Europe and Africa, according to recent reports from the World Organization of Animal Health (OIE).

Keywords: Avian influenza, H5N6; SARS-CoV-2, emerging, pandemic, emergency.

INTRODUCTION

Avian Influenza (AI) is a highly contagious viral respiratory disease that affects all species of birds, including commercial, wild, and pet birds [1-3]. Its causal agent, the Avian influenza virus (AIV) is a single-stranded segmented negative-sense RNA virus. Classification is based on the antigenic properties of their Hemagglutinin (HA) and Neuraminidase (NA) [4, 5]. According to the ability of the virus to cause significant disease, the different strains could be further divided into Non-Pathogenic AIV (NPAIV), Low-Pathogenic AIV (LPAIV), and Highly-pathogenic AIV (HPAIV) [6]. Spillover to human beings and other animal species may occur, leading to an infection that may be life-threatening [1].

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Throughout history, most AIV did not infect humans. However, sporadic cross-species infections did occur, triggering mild outbreaks, and even pandemics (Spanish flu, 1918-1920 caused by H1N1) [7]. From 2010 to date, over 400 cases and more than 150 human deaths by an HPAI have been reported in Egypt, Ghana, Hong Kong, Indonesia, Nigeria, Bangladesh, Cambodia, Vietnam, and Canada [8, 9]. The threat of a new HPAI strain has been latent over the years, with occasional outbreaks in poultry associated with severe consequences on livelihoods, international trade, and also severely impacting public health systems [2, 10]. Recently, lineages of the H5Nx (H5N1, H5N2, H5N6, H5N8) have proven to pose a severe risk to the veterinarian and human health due to the capacity for the zoonotic spread and the genomic interactions amongst this viral group (Figure 1) [11]. One example was the 2003 H5N1 epidemic, spreading from Asia to Europe and Africa, causing millions of animal deaths and hundreds of people infected, with reported case fatality rate close to 60% [2, 12].

The AIV H5N6 was an LPAIV first reported decades ago [11]. However, the first reported case of human infection with a novel HPAIV H5N6 dates from 2014 in China, with symptoms that included fever and sore throat [4, 12, 13]. The association with live bird markets (LBM) or wet markets was established, confirming once more the threat that these markets pose to public health as they provide a perfect scenario for the spread, but also the modification of the AIV genes due to the close

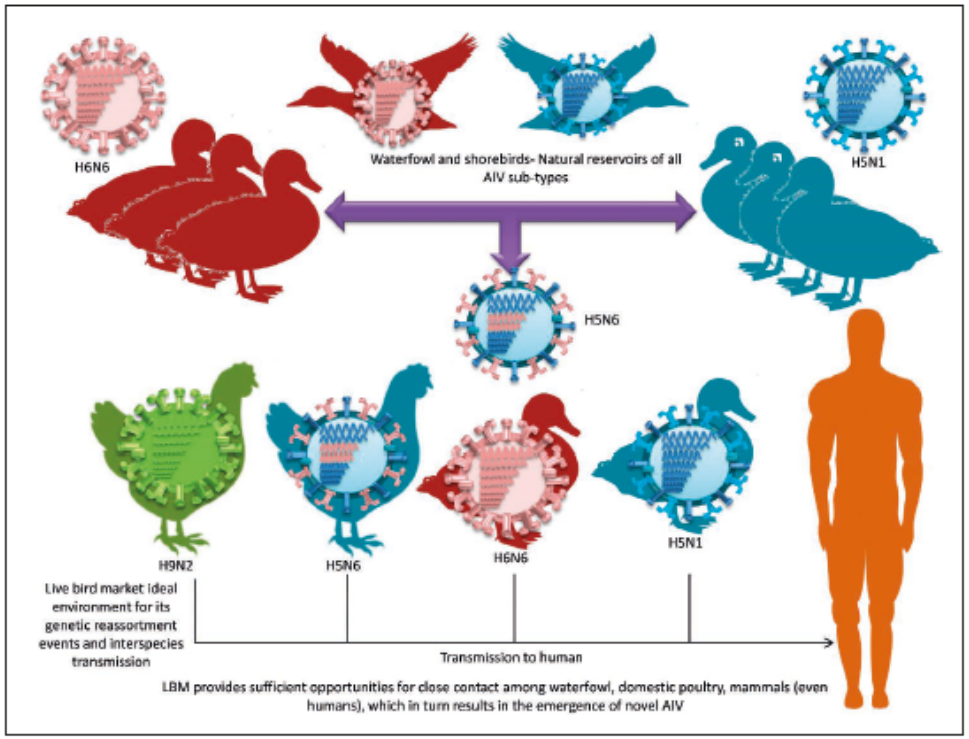

Figure 1 - Origin of H5N6 and other Avian Influenza viruses.

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Prevalence of Avian Influenza H5N6 in Birds: A Systematic Review and Meta-analysis of Other Viral Zoonosis

D. Katterine Bonilla-Aldana[1,2], Yeimer Holguin-Rivera[2], Isabella Cortes-Bonilla[2], María C. Cardona-Trujillo[2], Alejandra García-Barco[2], Hugo A. Bedoya-Arias[2], Leidy Jhoana Patiño-Cadavid[2], Mateo Aguirre-Florez[2], Graciela J. Balbin-Ramon[3,4], Delcy C. Erazo-Arana[2], Lysien I. Zambrano[5], Luis Perez-Garcia[6], Alfonso J. Rodriguez-Morales[2,3,7]*, and Alberto Paniz-Mondolfi[6,8,9,10]

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SYSTEMATIC REVIEW
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ABSTRACT

Avian influenza viruses (AIV) are zoonotic pathogens that can potentially affect humans and potentially be epidemic in a region. Birds (such as poultry and wild birds) serve as potential reservoirs for these viruses, highlighting the importance of determining AIV prevalence in the avian population. No systematic reviews have been published on this issue in the world so far. The present systematic literature review following the PRISMA standard, with meta-analysis, used three databases to globally assess the Influenza H5N6 infection in birds (including poultry and wild birds). A model of random-effects meta-analysis was performed to calculate the pooled prevalence and 95% Confidence Interval (95% CI) for the prevalence of Influenza H5N6 infection in birds. A total number of 14,605 articles published from 2015 to 2020 were retrieved. After screening the abstract/title, 37 articles were selected for full-text assessment, and 15 were included for qualitative and quantitative analyses. Of the total number of birds (n = 13,416 birds), the pool prevalence by RT-PCR was 3.5% (95% CI: 2.8-4.3%). From the total, 39.67% of the birds assessed were ducks (family Anatidae), in which pool prevalence was 7.7% (95% CI: 4.4-11.0). In chickens (*Gallus gallus domesticus*), the pool prevalence was 3.3% (95% CI 1.9-4.8). Vietnam was the country with the highest pool prevalence; 7.9% (95% CI 4.0-11.7%). Bangladesh was the country with the lowest pool prevalence of 0.4% (95% CI 0.2-0.7%). A considerable proportion of infected birds tested positive highlighted the relevance of individual animals as reservoirs of H5N6. Ducks and chickens were found to be positive by RT-PCR in over 3% of the cases. These data suggest their relevance in maintaining zoonotic transmission and their potential implications for epidemics and even pandemics in the near future.

Keywords: H5N6, Influenza, Meta-Analysis, Molecular diagnosis, RT-PCR, Systematic Review

INTRODUCTION

Avian influenza viruses (AIV) belong to the Alphainfluenzavirus genus in the Orthomyxoviridae family (Lefkowitz et al., 2018). They can be classified into Low-Pathogenic Avian Influenza Viruses (LPAIVs) with water birds as primary host reservoirs and Highly Pathogenic Avian Influenza Viruses (HPAIVs) with poultry as the main host reservoirs (Dhingra et al., 2018). These viruses can be brought long distances by aquatic birds, transmitted at chicken farms, and infect naive poultry (Bi et al., 2016). Highly Pathogenic Avian Influenza Viruses (HPAIVs) remain an underlying threat to global health and the economy. Some of these viruses carry potential pandemic risks (Swayne et al., 2017; Shin et al., 2020; Shittu et al., 2020).

H5N6, an AIV subtype, was first isolated from mallards in 1975 (Garcia et al., 1997). This virus has continuously evolved and reasserted to generate novel HPAIVs that have led to several epidemics incidents; in 2014, Laos and Vietnam reported an Influenza H5N6 outbreak that killed hundreds of birds (Shen et al., 2015), possibly imported from live poultry from China (Wong et al., 2015). In the same year, China reported the first fatal case of Influenza H5N6

To cite this paper: Bonilla-Aldana DK, Holguin-Rivera Y, Cortes-Bonilla I, Cardona-Trujillo M.C., García-Barco A, Bedoya-Arias HA, Patiño-Cadavid LJ, Aguirre-Florez M, Balbin-Ramon GJ, Erazo-Arana DC, Zambrano LI, Perez-Garcia L, Rodriguez-Morales AJ, and Paniz-Mondolfi A (2021). Prevalence of Avian Influenza H5N6 in Birds: A Systematic Review and Meta-analysis of Other Viral Zoonosis. *World Vet. J.*, 11 (2): 146-156.

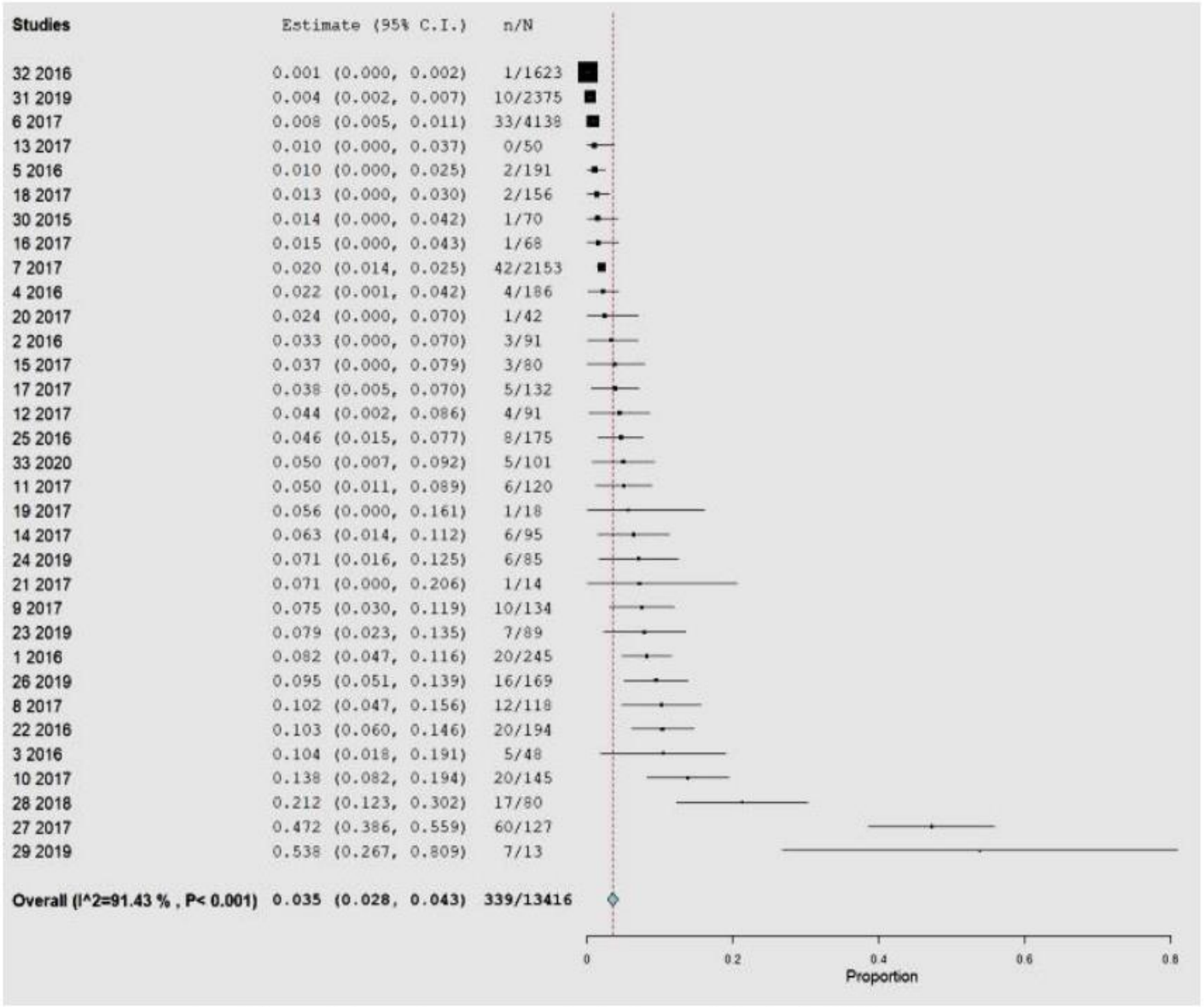

Figure 3. Forrest plot of the pooled prevalence meta-analysis of H5N6 infection in birds

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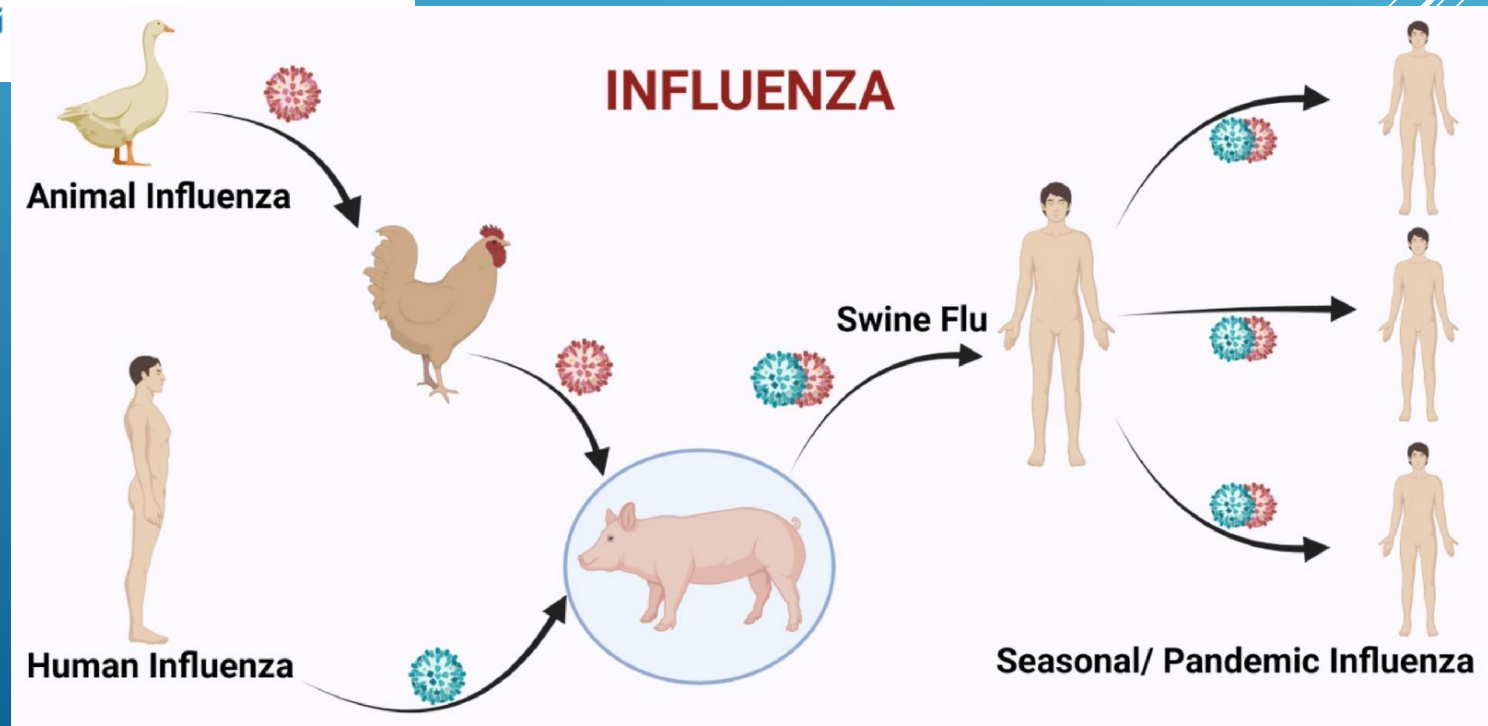
Letter to the Editor

The re-emergence of H3N2 influenza: An update on the risk and containment

Priyanka, Rekha Khandia, Hitesh Chopra, Om Prakash Choudhary ✉,
D. Katterine Bonilla-Aldana, Alfonso J. Rodriguez-Morales ✉



Travel Medicine and Infectious Disease

Volume 41, May–June 2021, 102054

Editorial

Concerns about influenza H5N8 outbreaks in humans and birds: Facing the next airborne pandemic?

Alfonso J. Rodriguez-Morales, D. Katterine Bonilla-Aldana, Alberto E. Paniz-Mondolfi

Show more

https://doi.org/10.1016/j.tmaid.2021.102054

REPORT PREVIEW

Colombia - Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-) - Immediate notification

GENERAL INFORMATION

COUNTRY/TERRITORY OR ZONE
ZONE

ANIMAL TYPE
TERRESTRIAL

DISEASE CATEGORY
OIE-listed

DISEASE
Influenza A viruses of high pathogenicity (Inf. with) (non-poultry including wild birds) (2017-)

CAUSAL AGENT
Highly pathogenic avian influenza virus

GENOTYPE / SEROTYPE / SUBTYPE
H5N1

REASON FOR NOTIFICATION
First occurrence in the country

DATE OF LAST OCCURRENCE
-

CONFIRMATION DATE
2022/10/18

END DATE
-

SELF-DECLARATION
NO

MEASURING UNIT

Animal

Species		Susceptible	Cases	Deaths	Killed and Disposed of	Slaughtered/ Killed for commercial use	Vaccinated
Blue winged teal (WILD)	NEW	5	0	0	5	0	0
	TOTAL	5	0	0	5	0	0
Birds (DOMESTIC)	NEW	194	136	86	108	0	0
	TOTAL	194	136	86	108	0	0
All species	NEW	199	136	86	113	0	0
	TOTAL	199	136	86	113	0	0

DIAGNOSTIC DETAILS

CLINICAL SIGNS

YES

METHOD OF DIAGNOSTIC

Diagnostic test

Test name	Laboratory	Species sampled	Outbreaks	First result date	Last result date	Result
Real-time polymerase chain reaction (real-time PCR)	Laboratorio nacional de diagnóstico veterinario (LNDV)	Birds	1	2022/10/18	2022/10/18	Positive

After SARS-CoV-2, will H5N6 and other influenza viruses follow the pandemic path?

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Throughout history, most AIV did not infect humans. However, sporadic cross-species infections did occur, triggering mild outbreaks, and even pandemics (Spanish flu, 1918-1920 caused by H1N1) [7]. From 2010 to date, over 400 cases and more than 150 human deaths by an HPAI have been reported in Egypt, Ghana, Hong Kong, Indonesia, Nigeria, Bangladesh, Cambodia, Vietnam, and Canada [8, 9]. The threat of a new HPAI strain has been latent over the years, with occasional outbreaks in poultry associated with severe consequences on livelihoods, international trade, and also severely impacting public health systems [2, 10]. Recently, lineages of the H5Nx (H5N1, H5N2, H5N6, H5N8) have proven to pose a severe risk to the veterinarian and human health due to the capacity for the zoonotic spread and the genomic interactions amongst this viral group (Figure 1) [11]. One example was the 2003 H5N1 epidemic, spreading from Asia to Europe and Africa, causing millions of animal deaths and hundreds of people infected, with reported case fatality rate close to 60% [2, 12].

The AIV H5N6 was an LPAIV first reported decades ago [11]. However, the first reported case of human infection with a novel HPAIV H5N6 dates from 2014 in China, with symptoms that included fever and sore throat [4, 12, 13]. The association with live bird markets (LBM) or wet markets was established, confirming once more the threat that these markets pose to public health as they provide a perfect scenario for the spread, but also the modification of the AIV genes due to the close

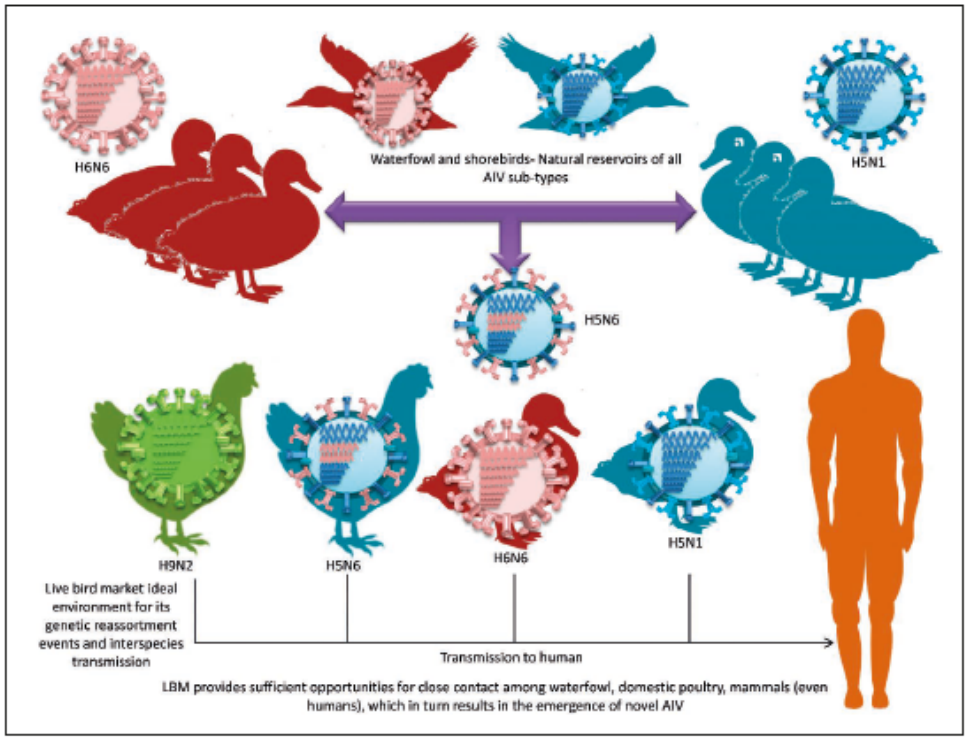

Figure 1 - Origin of H5N6 and other Avian Influenza viruses.

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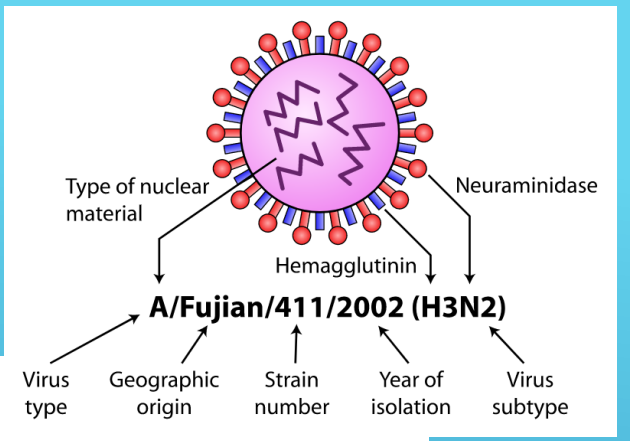
Reported Human Infections with Avian Influenza A Viruses



Low Pathogenic Avian Influenza A Virus Infections*

Subtypes of low pathogenic avian influenza (LPAI) A viruses that have been virologically confirmed to have infected people include A(H6), A(H7), A(H9), and A(H10) viruses.

- A(H6) Virus Infections
- A(H7) Virus Infections
- A(H9) Virus Infections
- A(H10) Virus Infections

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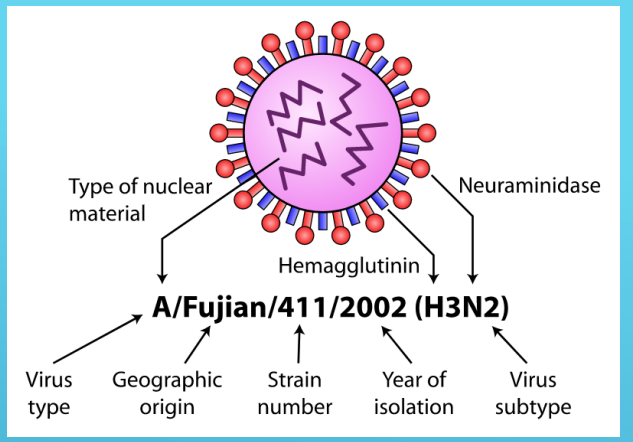
Reported Human Infections with Avian Influenza A Viruses



Highly Pathogenic Avian Influenza A Virus Infections*

Subtypes of highly pathogenic avian influenza (HPAI) A viruses that have been virologically confirmed to have infected people include A(H5) and A(H7) viruses.

- A(H5) Virus Infections
- A(H7) Virus Infections

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Prevalence of Avian Influenza H5N6 in Birds: A Systematic Review and Meta-analysis of Other Viral Zoonosis

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[2]*Grupo colaborativo de investigación en Enfermedades Transmitidas por vectores, Zoonóticas y tropicales de Risaralda (GETZ), Pereira, Risaralda, Colombia.*
[3]*Master of Clinical Epidemiology and Biostatistics, Universidad Científica del Sur, Lima, Peru*
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SYSTEMATIC REVIEW
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ABSTRACT

Avian influenza viruses (AIV) are zoonotic pathogens that can potentially affect humans and potentially be epidemic in a region. Birds (such as poultry and wild birds) serve as potential reservoirs for these viruses, highlighting the importance of determining AIV prevalence in the avian population. No systematic reviews have been published on this issue in the world so far. The present systematic literature review following the PRISMA standard, with meta-analysis, used three databases to globally assess the Influenza H5N6 infection in birds (including poultry and wild birds). A model of random-effects meta-analysis was performed to calculate the pooled prevalence and 95% Confidence Interval (95% CI) for the prevalence of Influenza H5N6 infection in birds. A total number of 14,605 articles published from 2015 to 2020 were retrieved. After screening the abstract/title, 37 articles were selected for full-text assessment, and 15 were included for qualitative and quantitative analyses. Of the total number of birds (n = 13,416 birds), the pool prevalence by RT-PCR was 3.5% (95% CI: 2.8-4.3%). From the total, 39.67% of the birds assessed were ducks (family Anatidae), in which pool prevalence was 7.7% (95% CI: 4.4-11.0). In chickens (*Gallus gallus domesticus*), the pool prevalence was 3.3% (95% CI 1.9-4.8). Vietnam was the country with the highest pool prevalence; 7.9% (95% CI 4.0-11.7%). Bangladesh was the country with the lowest pool prevalence of 0.4% (95% CI 0.2-0.7%). A considerable proportion of infected birds tested positive highlighted the relevance of individual animals as reservoirs of H5N6. Ducks and chickens were found to be positive by RT-PCR in over 3% of the cases. These data suggest their relevance in maintaining zoonotic transmission and their potential implications for epidemics and even pandemics in the near future.

Keywords: H5N6, Influenza, Meta-Analysis, Molecular diagnosis, RT-PCR, Systematic Review

INTRODUCTION

Avian influenza viruses (AIV) belong to the Alphainfluenzavirus genus in the Orthomyxoviridae family (Lefkowitz et al., 2018). They can be classified into Low-Pathogenic Avian Influenza Viruses (LPAIVs) with water birds as primary host reservoirs and Highly Pathogenic Avian Influenza Viruses (HPAIVs) with poultry as the main host reservoirs (Dhingra et al., 2018). These viruses can be brought long distances by aquatic birds, transmitted at chicken farms, and infect naive poultry (Bi et al., 2016). Highly Pathogenic Avian Influenza Viruses (HPAIVs) remain an underlying threat to global health and the economy. Some of these viruses carry potential pandemic risks (Swayne et al., 2017; Shin et al., 2020; Shittu et al., 2020).

H5N6, an AIV subtype, was first isolated from mallards in 1975 (Garcia et al., 1997). This virus has continuously evolved and reasserted to generate novel HPAIVs that have led to several epidemics incidents; in 2014, Laos and Vietnam reported an Influenza H5N6 outbreak that killed hundreds of birds (Shen et al., 2015), possibly imported from live poultry from China (Wong et al., 2015). In the same year, China reported the first fatal case of Influenza H5N6

To cite this paper: Bonilla-Aldana DK, Holguin-Rivera Y, Cortes-Bonilla I, Cardona-Trujillo M.C., García-Barco A, Bedoya-Arias HA, Patiño-Cadavid LJ, Aguirre-Florez M, Balbin-Ramon GJ, Erazo-Arana DC, Zambrano LI, Perez-Garcia L, Rodriguez-Morales AJ, and Paniz-Mondolfi A (2021). Prevalence of Avian Influenza H5N6 in Birds: A Systematic Review and Meta-analysis of Other Viral Zoonosis. *World Vet. J.*, 11 (2): 146-156.

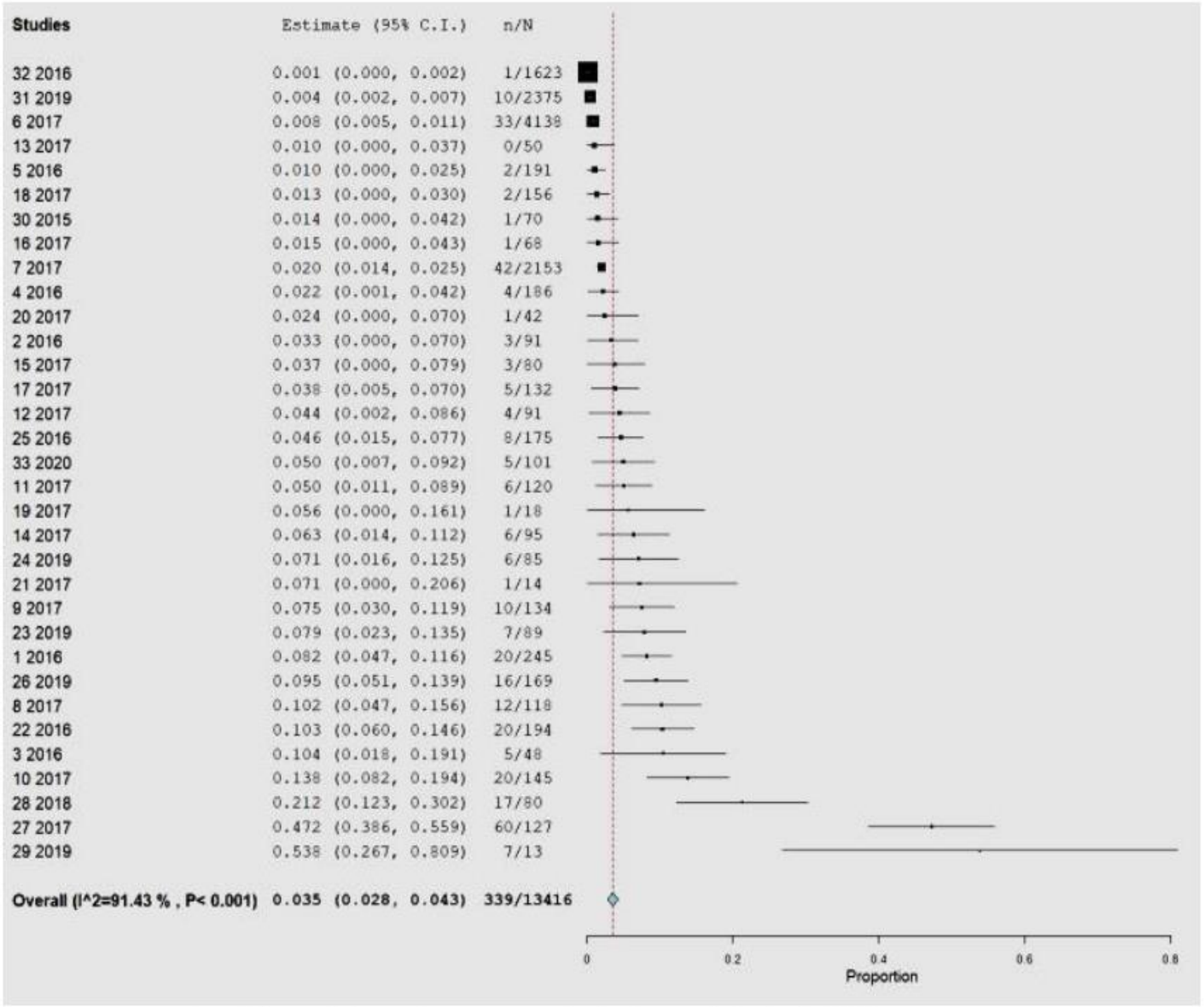

Figure 3. Forrest plot of the pooled prevalence meta-analysis of H5N6 infection in birds

To cite this paper: Bonilla-Aldana DK, Holguin-Rivera Y, Cortes-Bonilla I, Cardona-Trujillo M.C., García-Barco A, Bedoya-Arias HA, Patiño-Cadavid LJ, Aguirre-Florez M, Balbin-Ramon GJ, Erazo-Arana DC, Zambrano LI, Perez-Garcia L, Rodriguez-Morales AJ, and Paniz-Mondolfi A (2021). Prevalence of Avian Influenza H5N6 in Birds: A Systematic Review and Meta-analysis of Other Viral Zoonosis. *World Vet. J.*, 11 (2): 146-156.

Travel Medicine and Infectious Disease

Volume 41, May–June 2021, 102054

Editorial

Concerns about influenza H5N8 outbreaks in humans and birds: Facing the next airborne pandemic?

Alfonso J. Rodriguez-Morales, D. Katterine Bonilla-Aldana, Alberto E. Paniz-Mondolfi

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https://doi.org/10.1016/j.tmaid.2021.102054

Influenza A H5N1

Host & sialic acid \ Virus	H5N1	H7N9	H9N2
α-2,3-Gal	Mild / Moderate	Mild	Mild
α-2,3-Gal	Severe	Mild	Mild / Moderate
α-2,3-Gal, α-2,6-Gal	Moderate	Mild	Mild
α-2,6-Gal	Severe	Moderate / Severe	Mild / Moderate
α-2,6-Gal	Severe	Severe	Mild / Moderate

FIGURE 1 | Zoonotic influenza pathology is linked to host biology. H5N1, H7N9, and H9N2 avian influenza (AI) viruses causing varying

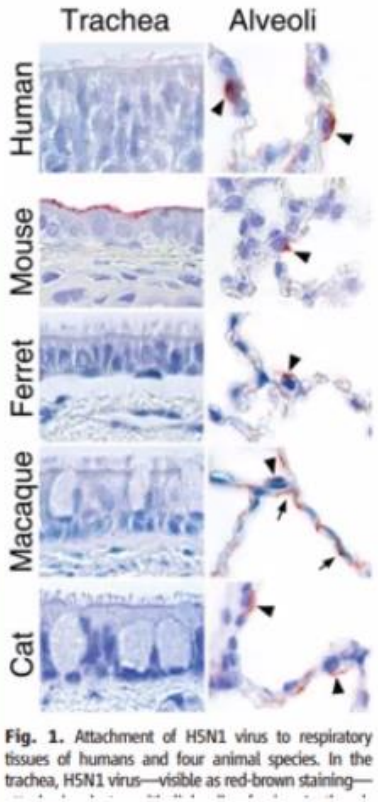
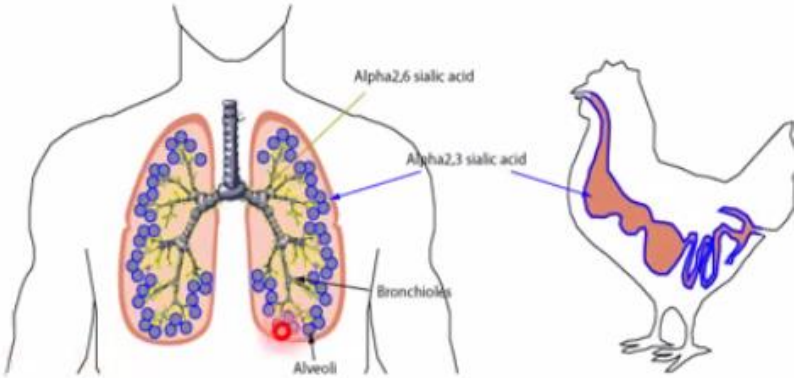


Fig. 1. Attachment of H5N1 virus to respiratory tissues of humans and four animal species. In the trachea, H5N1 virus—visible as red-brown staining—



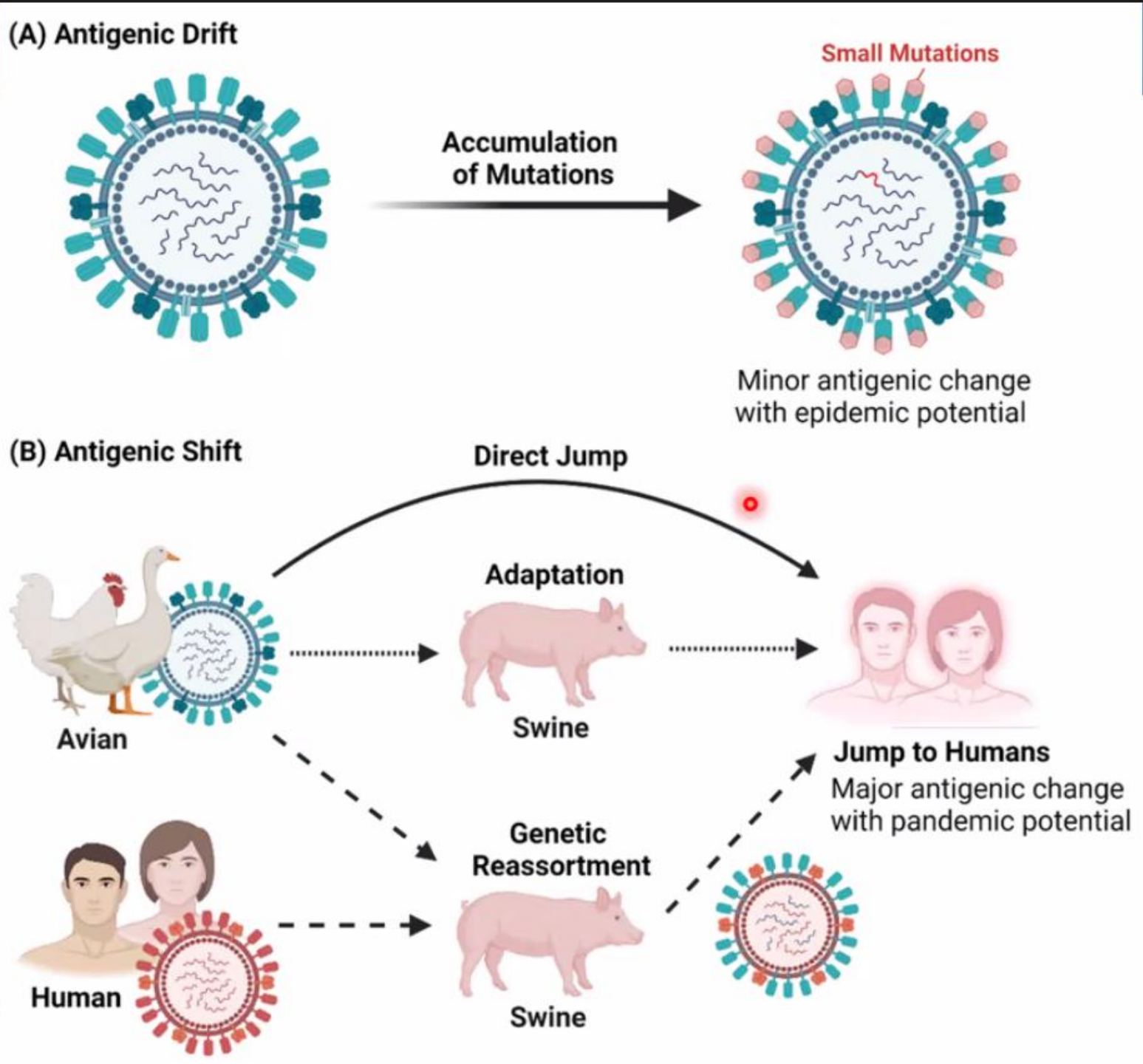
SCIENCE VOL 312 21 APRIL 2006

frontiers in Immunology

REVIEW
published: 08 August 2018
doi: 10.3389/fimmu.2018.01812

DE COLOMBIA

Influenza A



Viruses **2021**, *13*, 2276. https://doi.org/10.3390/v13112276

Influenza A H5N1

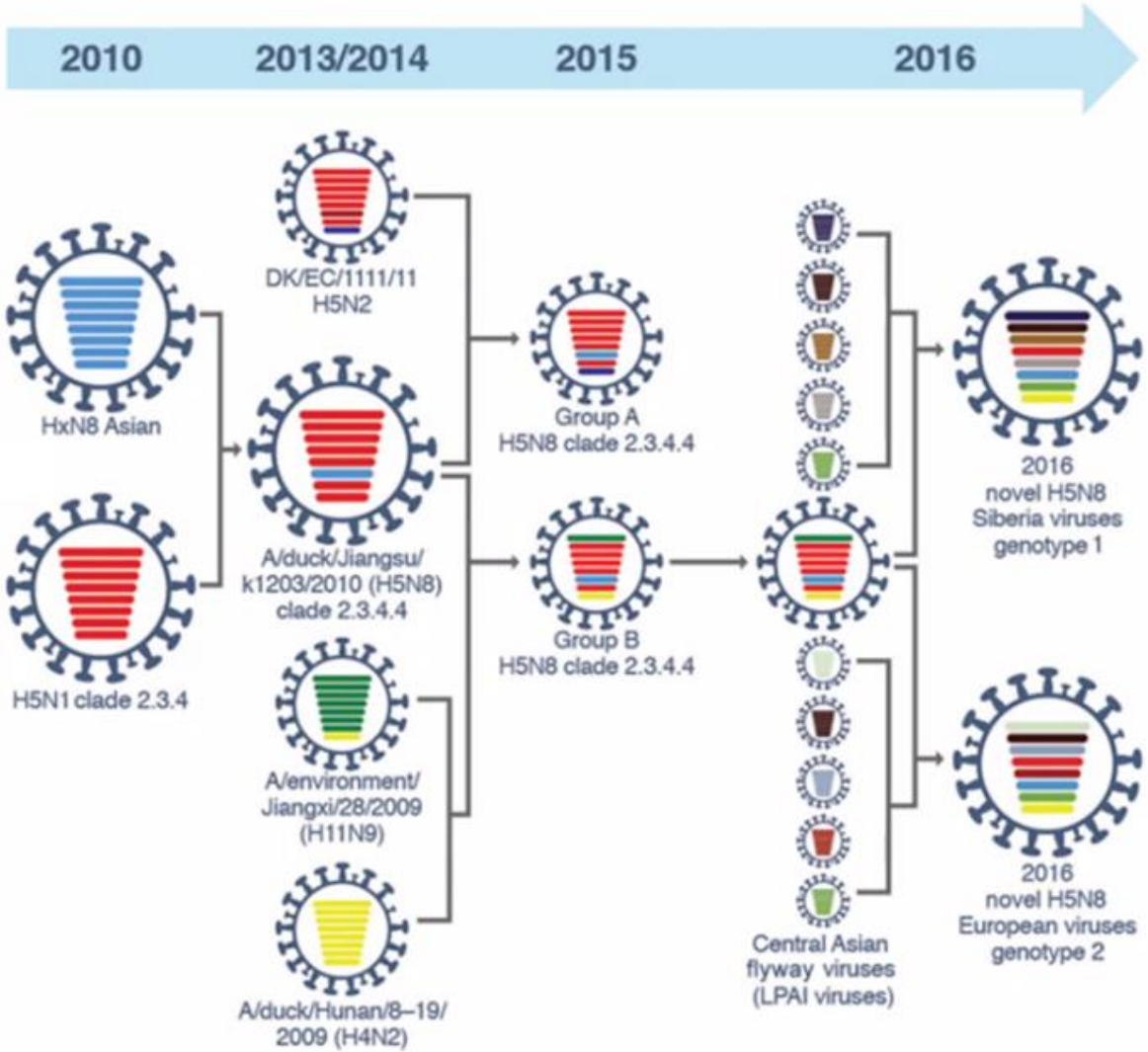
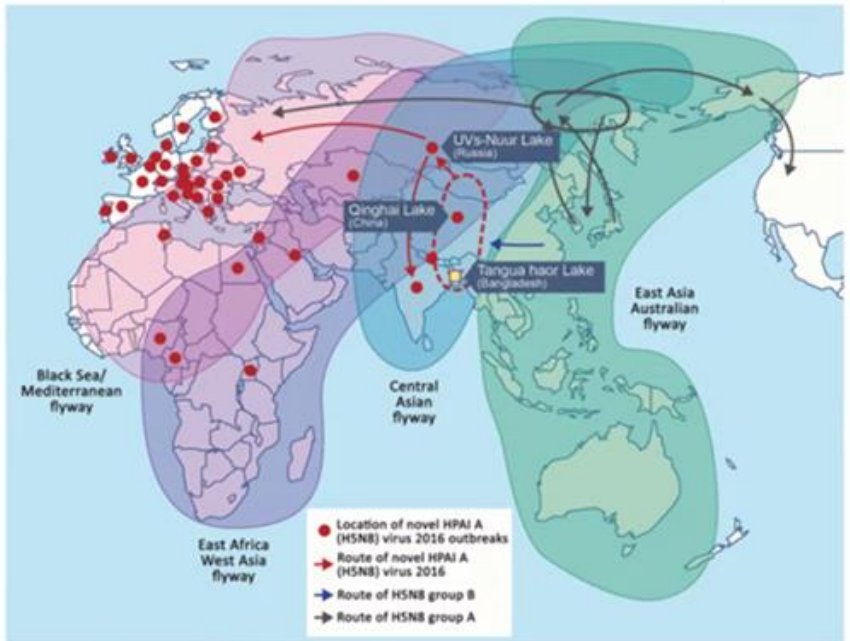


Figure 2. Illustration of original reassortment events of novel highly pathogenic avian influenza (HPAI) A(H5N8) viruses isolated from Siberia and Europe in 2016. The 8 gene segments (from top to bottom) in each virus are polymerase basic 2, polymerase basic 1, polymerase acidic, hemagglutinin, nucleoprotein, neuraminidase, matrix, and nonstructural. Each color indicates a separate virus background. In 2010, HPAI A(H5N1) clade 2.3.4 viruses reassorted with subtype N8 viruses from Eurasia and produced A/duck/Jiangsu/k1203/2010(H5N8). Until late 2013, HPAI viruses with H5N8 subtypes circulated in eastern China and South Korea. In 2014, HPAI A(H5N8) viruses reassorted with A/duck/Hunan/8–19/2009(H4N2) and A/environment/Jiangxi/28/2009(H11N9) to generate group B viruses. The subsequent reassortment between HPAI A(H5N8) group B viruses and low pathogenicity (LPAI) viruses circulating along the central Asian flyway led to generation of the novel HPAI A(H5N8) genotype 1 and 2 viruses.



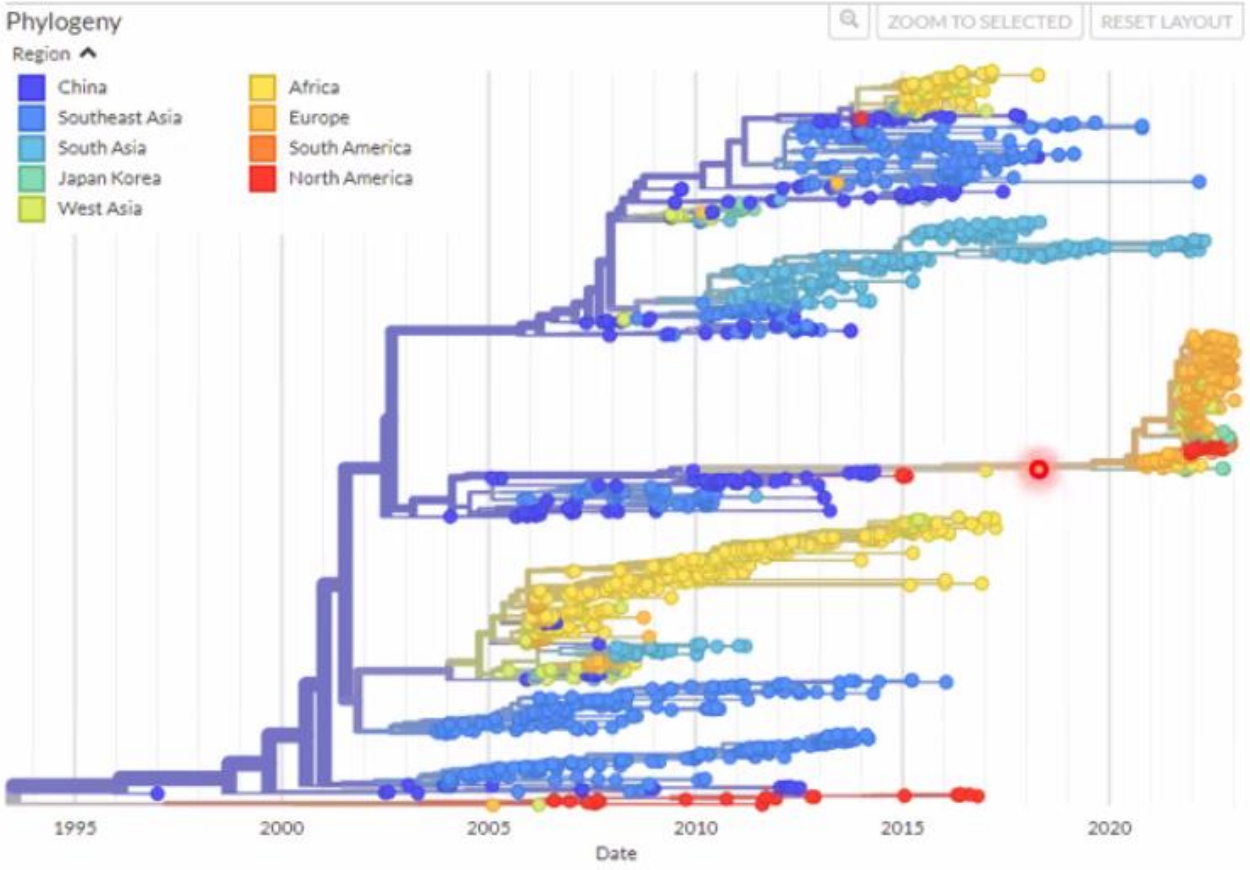
Jiangxi/28/2009(H11N9) to generate group B viruses. The subsequent reassortment between HPAI A(H5N8) group B viruses and low pathogenicity (LPAI) viruses circulating along the central Asian flyway led to generation of the novel HPAI A(H5N8) genotype 1 and 2 viruses.

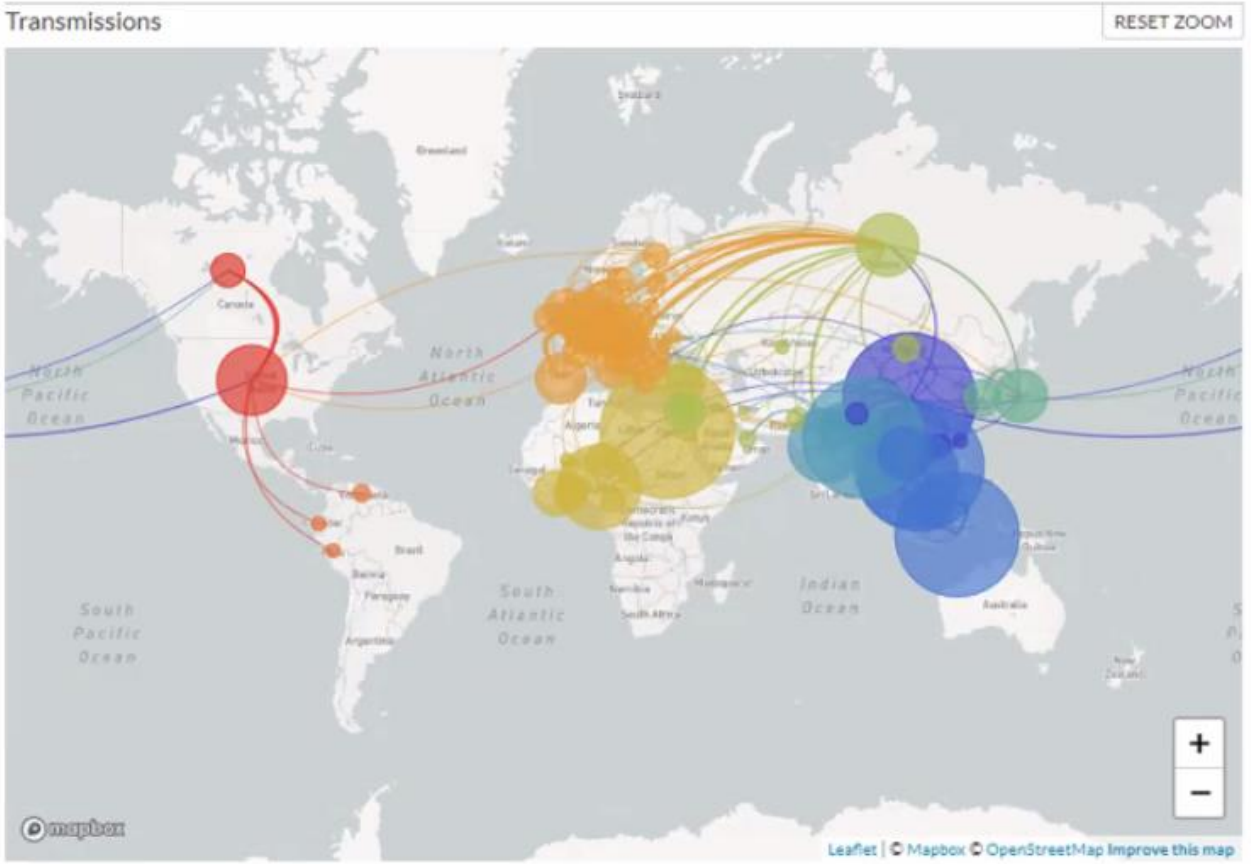
Influenza A H5N1

Real-time tracking of influenza A/H5N1 virus evolution

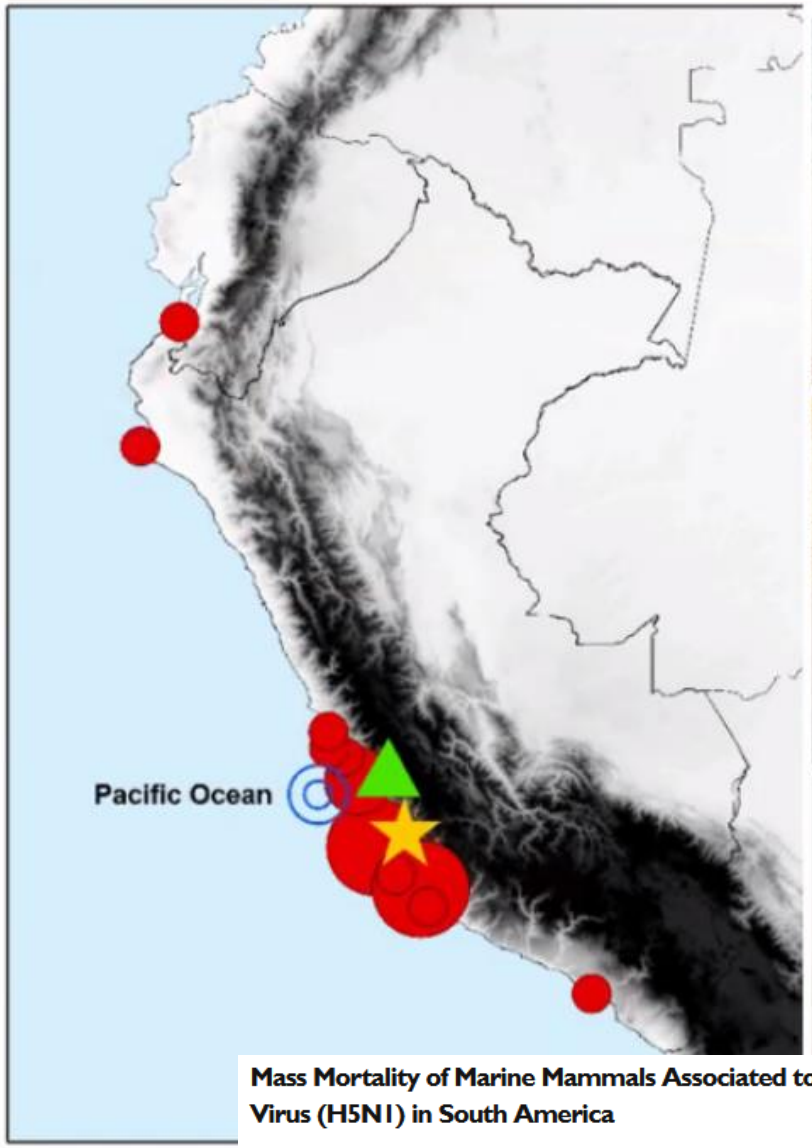
Built with nextstrain/avian-flu. Maintained by Louise Moncla.

Showing 1773 of 1773 genomes sampled between Dec 1996 and Jan 2023.





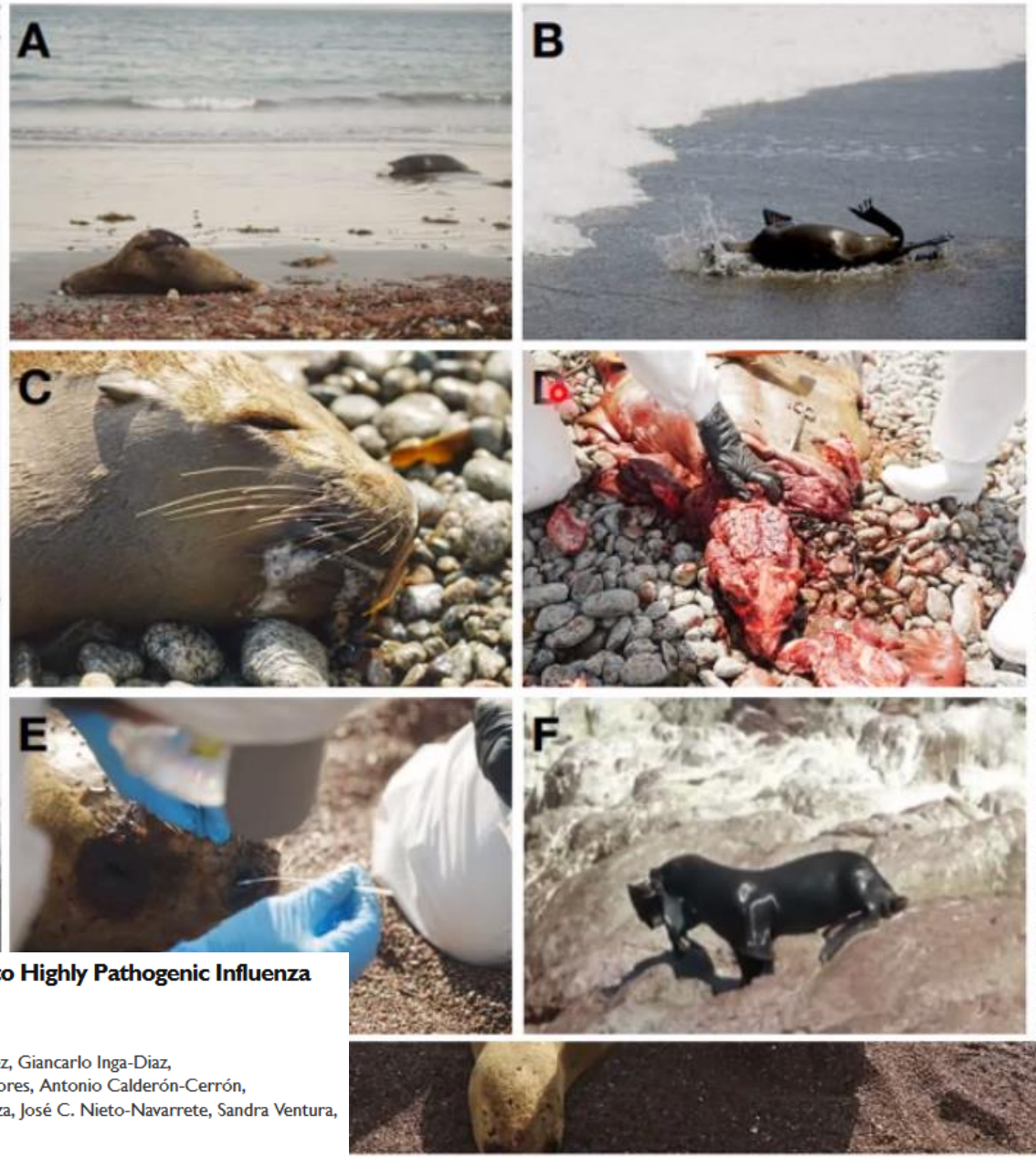
Influenza



Sea lion mortality (number of individuals)

- 1-73
- 120-145
- 216-217

- Samples taken by SERFOR
- Samples taken by SERNANP
- Sea lion carcasses floating in the sea (n=100)



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Mass Mortality of Marine Mammals Associated to Highly Pathogenic Influenza Virus (H5N1) in South America

Víctor Gamarra-Toledo, Pablo I. Plaza, Roberto Gutiérrez, Giancarlo Inga-Diaz, Patricia Saravia-Guevara, Oliver Pereyra-Meza, Elver Coronado-Flores, Antonio Calderón-Cerrón, Gonzalo Quiroz-Jiménez, Paola Martinez, Deyvis Huamán-Mendoza, José C. Nieto-Navarrete, Sandra Ventura, Sergio A. Lambertucci

doi: https://doi.org/10.1101/2023.02.08.527769

The Lancet Regional Health - Americas 2024;35: 100785

Published Online 23 May 2024
https://doi.org/10.1016/j.lana.2024.100785

THE LANCET *Regional Health* Americas

Comment

Concerns on H5N1 avian influenza given the outbreak in U.S. dairy cattle

Ranjit Sah,[a,b,c] Shriyansh Srivastava,[d,e] Sachin Kumar,[d] Rachana Mehta,[f,g] Suzanne Donovan,[h] Leandro Sierra-Carrero,[i] Camila Luna,[j] Laila Woc-Colburn,[k] Jaime A. Cardona-Ospina,[l,m,n] Monica Hinestroza-Jordan,[o] Mireya Wessolossky,[p] and Alfonso J. Rodriguez-Morales[j,m,q,]*

[a]Green City Hospital, Tokha, Kathmandu, Nepal
[b]Department of Microbiology, Dr. D.Y. Patil Medical College, Hospital and Research Centre, Dr. D.Y. Patil Vidyapeeth, Pune, India
[c]Department of Public Health Dentistry, Dr. D.Y. Patil Dental College and Hospital, Dr. D.Y. Patil Vidyapeeth, Pune, Maharashtra, India
[d]Department of Pharmacology, Delhi Pharmaceutical Sciences and Research University (DPSRU), New Delhi, India
[e]Department of Pharmacy, School of Medical and Allied Sciences, Galgotias University, Greater Noida, India
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[g]Medical Laboratories Techniques Department, AL-Mustaqbal University, 51001, Hillah, Babil, Iraq
[h]David Geffen School of Medicine at UCLA Medical Center, Los Angeles, CA, USA
[i]Department of Internal Medicine, Cleveland Clinic Foundation, Cleveland, OH, USA
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[k]Division of Infectious Diseases, Emory University, Atlanta, GA, USA
[l]Division of Infectious Diseases and Vaccinology, School of Public Health, University of California, Berkeley, Berkeley, CA, USA
[m]Grupo de Investigación Biomedicina, Facultad de Medicina, Fundación Universitaria Autónoma de las Américas-Institución Universitaria Visión de las Américas, Pereira, Colombia
[n]Emerging Infectious Diseases and Tropical Medicine Research Group, Instituto para la Investigación en Ciencias Biomédicas - Sci-Help, Pereira, Colombia
[o]Division of Infectious Diseases, Department of Medicine, University of Arizona College of Medicine, Tucson, AZ, USA
[p]Department of Medicine, Division of Infectious Diseases and Immunology, University of Massachusetts Chan Medical School, Worcester, MA, USA
[q]Gilbert and Rose-Marie Chagoury School of Medicine, Lebanese American University, Beirut, Lebanon

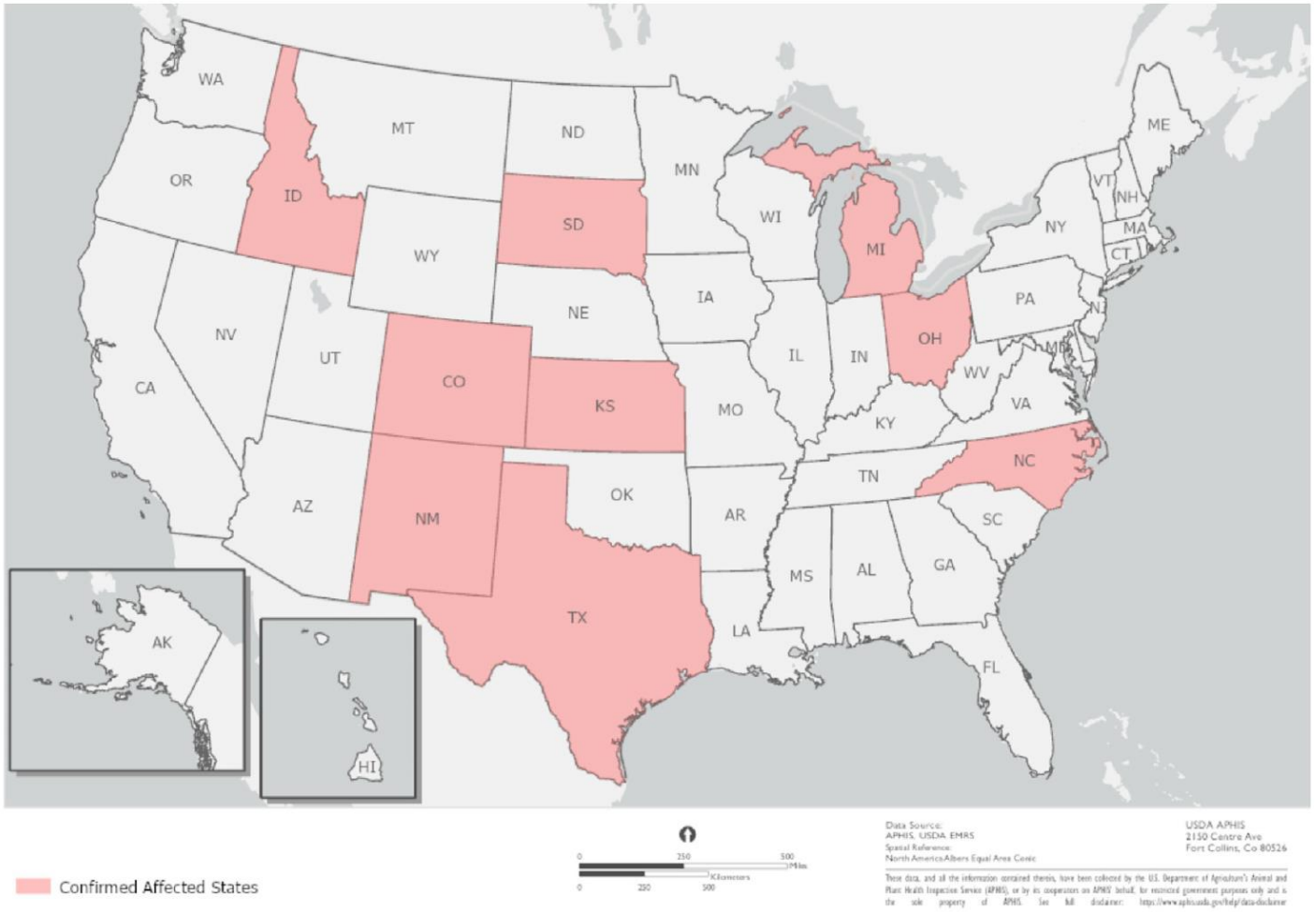


Fig. 1: Confirmed cases of HPAI in domestic livestock in the USA, May 16, 2024, according to the animal and plant health inspection service (APHIS) of the U.S. Department of agriculture (USDA). Reproduced from https://www.aphis.usda.gov/livestock-poultry-disease/avian/avian-influenza/hpai-detections/livestock.

to detect and act upon any human risks as soon as possible. Proactive surveillance, early detection, and collaboration among local, state, and federal health agencies, as well as cattle farmers and dairy distributors, are essential to effectively manage and contain the current outbreak of H5N1 avian influenza in U.S. dairy cattle. Before crossing state lines, dairy cattle must undergo testing for the Influenza A virus at a designated National Animal Health Laboratory Network (NAHLN) facility and receive a negative result. In the event of a positive test among dairy cattle intended for interstate travel, herd owners will need to furnish epidemiological details, such as tracing the movement of animals. Compliance with conditions outlined by the Animal and

to detect and act upon any human risks as soon as possible. Proactive surveillance, early detection, and collaboration among local, state, and federal health agencies, as well as cattle farmers and dairy distributors, are essential to effectively manage and contain the current outbreak of H5N1 avian influenza in U.S. dairy cattle. Before crossing state lines, dairy cattle must undergo testing for the Influenza A virus at a designated National Animal Health Laboratory Network (NAHLN) facility and receive a negative result. In the event of a positive test among dairy cattle intended for interstate travel, herd owners will need to furnish epidemiological details, such as tracing the movement of animals. Compliance with conditions outlined by the Animal and

Case summary	Description
Human case	01
Age	18 Year
Date of report	March 25, 2024
Location	United States, Texas
Virus strain	Highly Pathogenic Avian Influenza (HPAI) A (H5N1)
Symptoms	Eye redness (consistent with conjunctivitis)
Genetic clade	Clade 2.3.4.4b
Detection method	Throat swab, Unpasteurized milk samples
Detection in dairy cattle	Texas, Kansas, Michigan, Idaho, South Dakota, New Mexico, Ohio, North Carolina and Colorado.
Treatment	Isolation, Antiviral medication
Vaccine availability	Candidate vaccine viruses (CVVs) available for manufacturing if necessary
Prevention	Avoidance of unprotected exposures to infected animals, raw milk products, use of personal protective equipment (PPE)
Public health assessment	Low for the general public, Increased risk for those with close or prolonged, unprotected exposures to infected birds or animals

Table 1: **Analysis of HPAI avian influenza A (H5N1) human case and outbreak dynamics.**[3,4]

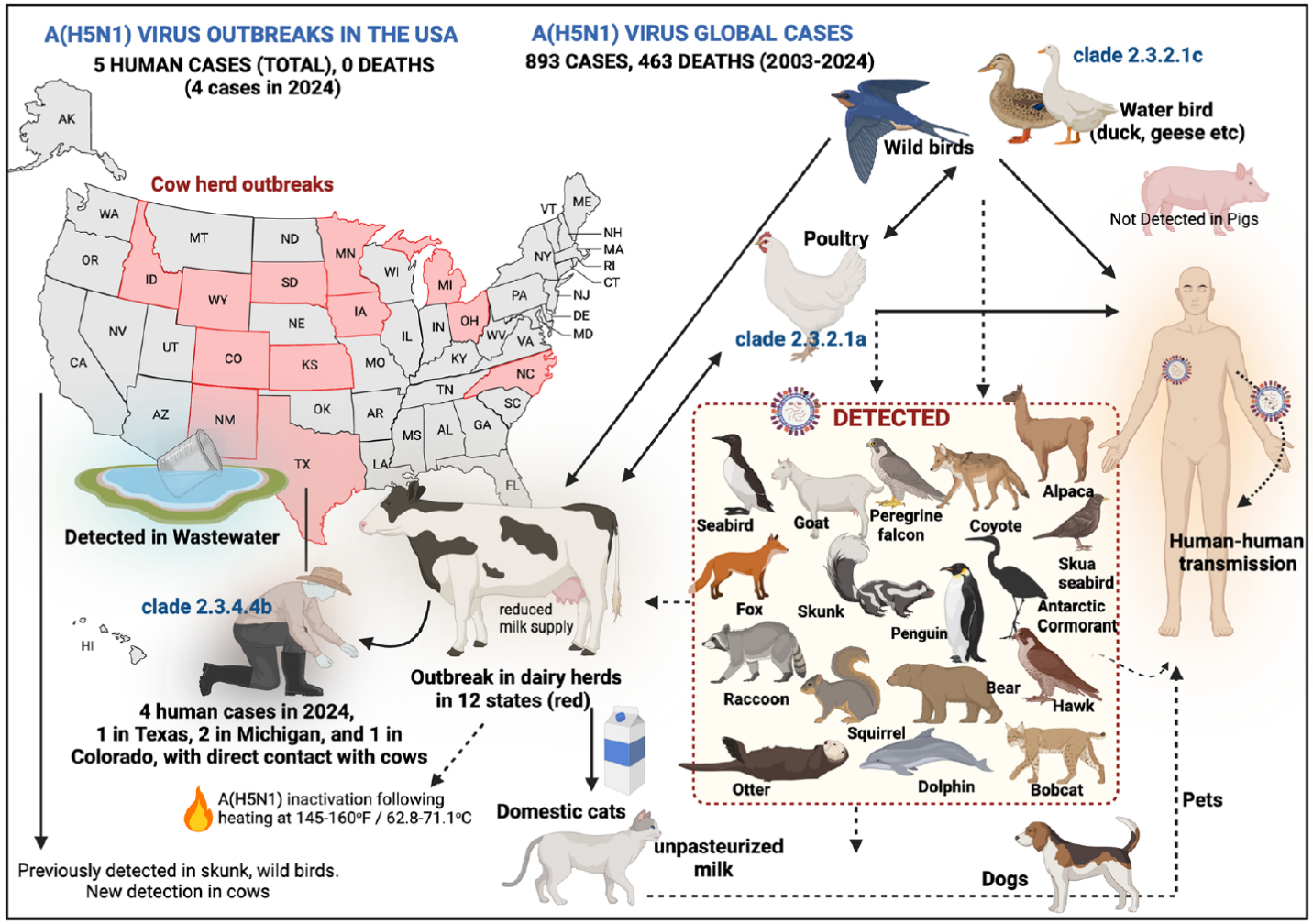


Figure 1. Is H5N1 the next pandemic? Since 2003, A(H5N1) has accounted for 893 global human cases with 463 deaths in 24 countries, including 11 cases in 2024. Antarctica has seen the first-ever cases of A(H5N1) virus in animals. In 2024, a man in Texas, two in Michigan, and one in Colorado, contracted H5N1 after contact with dairy cattle. H5N1 has been detected in several states across United States in wastewater, and there have been 145 cowherd outbreaks in 12 states across the United States (as of 8 July 2024), as shown. Cats contracted H5N1 from infected cow's milk, and hunting dogs have also been found to be positive after retrieving wild waterfowl. The virus's ability to infect pets is concerning, as wild birds transmit it to poultry and cattle. Other animals, as shown in the inset, have also been detected with A(H5N1) virus infection, but their role in transmission remains unclear. Solid lines depict confirmed transmission routes, while dotted lines depict uncertain transmission pathways.
Source: The bio-render (https://www.biorender.com/) was used for developing this figure.

First published Jul 24, 2024

Apostolopoulos V, Chavda VP, Mehta R, Rodriguez-Morales AJ, Henao-MartÍnez AF, Sah R. Alert and surveillance on H5N1 influenza virus: risks to agriculture and public health. Therapeutic Advances in Infectious Disease. 2024;11. doi:10.1177/20499361241266521

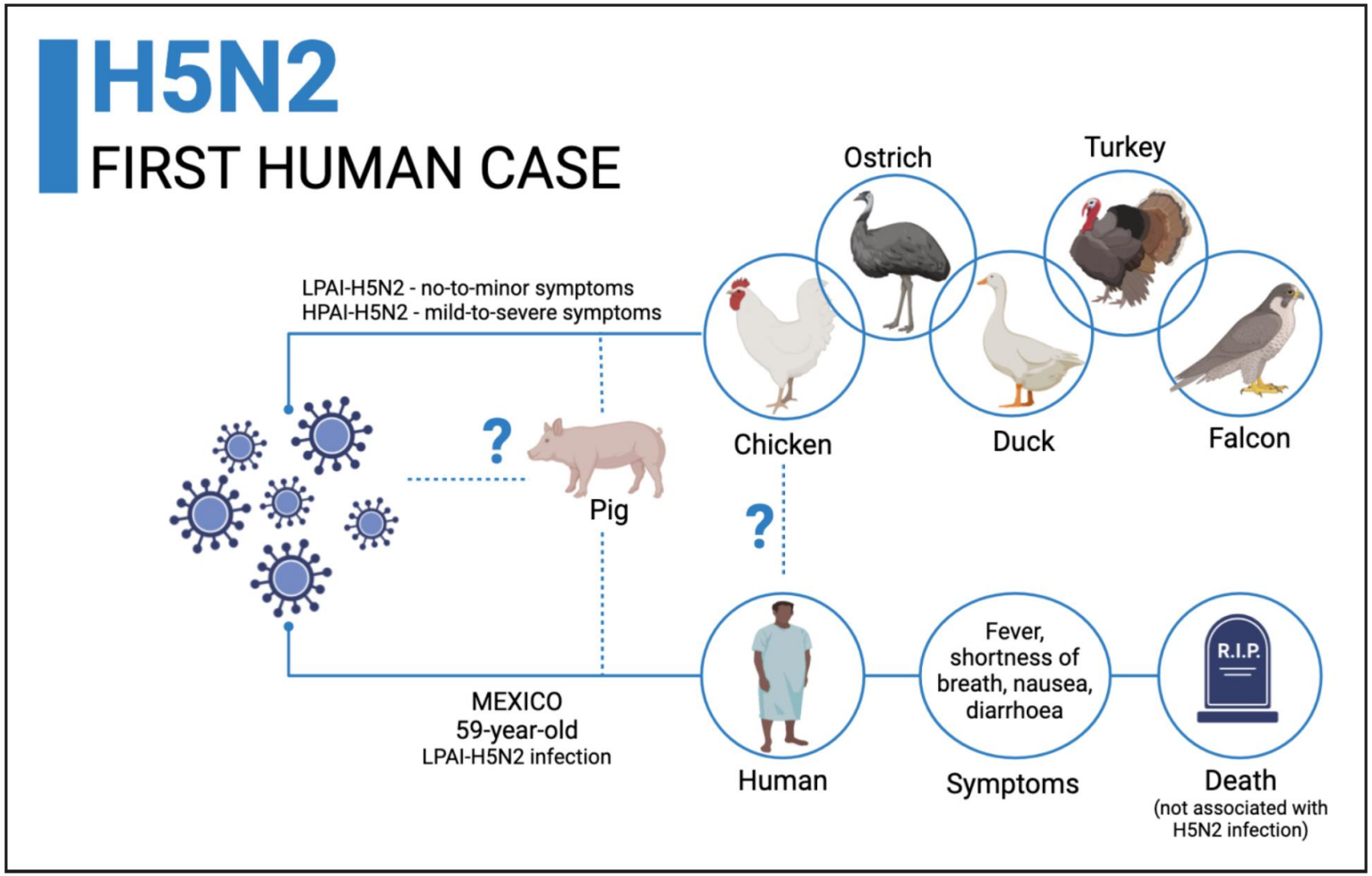
First confirmed human case of H5N2 virus infection in Mexico: an emerging zoonotic concern.

Apostolopoulos V, Sah R, Mehta R, Diaz B, Rodriguez-Morales AJ.

Infez Med. 2024 Sep 1;32(3):413-416. doi: 10.53854/liim-3203-16. eCollection 2024.

Figure 1
The first recorded H5 virus was in Mexico, and the first globally recorded human H5N2 infection was on May 23, 2024. In Mexico, a 59-year-old who presented with shortness of breath, fever, and diarrhoea was admitted to the hospital on April 24, 2024, and died the same day; an LPAI-H5N2 virus infection was confirmed but not associated with the death. This infection highlights a potential new zoonotic threat to humans. Figure made using biorender.com.

Abbreviations: HPAI-H5N2, highly pathogenic avian influenza virus subtype H5N2; LPAI-H5N2, low pathogenic avian influenza virus subtype H5N2.



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Travel Medicine and Infectious Disease

Volume 55, September–October 2023, 102634

Avian influenza spillover to humans: Are we prepared to deal with another potential pandemic?

Faraz Ahmad, Shafiul Haque, Samah Tawil, Rola Husni, D. Katterine Bonilla-Aldana, Juan Jose Montenegro-Idrogo, Alfonso J. Rodriguez-Morales [1]

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Fig. 1. Global alerts on avian influenza at HealthMap during the last six months (February–August, 2023).

Ahmad F, Haque S, Tawil S, Husni R, Bonilla-Aldana DK, Montenegro-Idrogo JJ, Rodriguez-Morales AJ. **Avian influenza spillover to humans: Are we prepared to deal with another potential pandemic?** *Travel Med Infect Dis*. 2023 Aug 19;55:102634. doi: 10.1016/j.tmaid.2023.102634. Epub ahead of print. PMID: 37598877.

Contents

- Socio-environmental overview of Latin America: importance of climate change, OneHealth approach and determinants
- Arboviruses in the region
- We have not just mosquitoes, but many rodents involved in emerging viral infections in the region: Mammarenaviruses and Orthohantaviruses
- Cocirculation during COVID-19 pandemic, mpox, and avian influenza
- **Some conclusions - mitigation**

frontiers in Tropical Diseases

SPECIALTY GRAND CHALLENGE
published: 04 May 2021
doi: 10.3389/fitd.2021.676905

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The Constant Threat of Zoonotic and Vector-Borne Emerging Tropical Diseases: Living on the Edge

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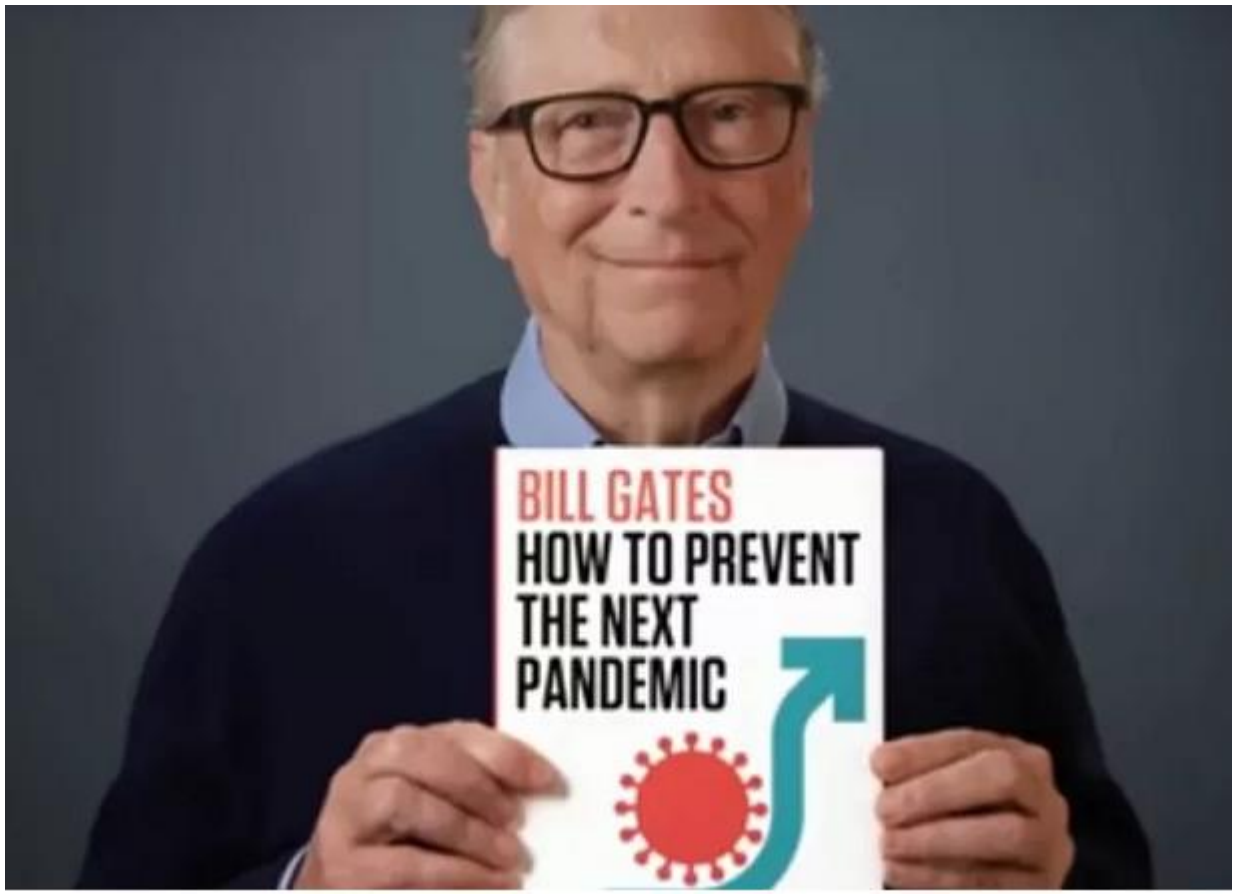
Some conclusions - mitigation

- Evolving epidemiology of old and new foes
- Prone social and environmental conditions for transmission
- Socio political crisis, everywhere
- Migration, including forced one, refugees, going North, South, and beyond, including Europe and abroad
- More cocirculation and coinfections, not just differential diagnoses
- Need for enhanced surveillance (including entomological), lab diagnosis improvements (available molecular tools), appropriate response and preparedness

Conclusions

- *Question is not if we will have more pandemics!*
- *Question is, when?*
- We should be more prepared
- Systems, HCW, society
- We may control it



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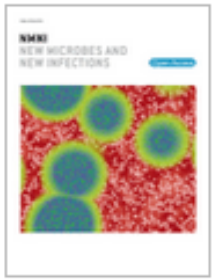

Editorial

The next pandemic catastrophe: can we avert the inevitable?

Maryam Shafaati, Hitesh Chopra, Priyanka, Rekha Khandia, Om Prakash Choudhary, Alfonso J. Rodriguez-Morales

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Gate’s proposals

- **1. Improve Health systems in the world.**
- **2. A global pathogen surveillance system.**
- **3. Improve, innovation at detection, treatment and prevention.**

More vaccines!!!

- This chapter can be summarized in two key points.
- **First**, as horrible as the COVID-19 pandemic is, the world is fortunate to have been able to create vaccines at the speed that has been made.
- **Second,** we've only scratched the surface of how good vaccines can be. Since we can't assume we'll be so lucky next time (and because they also give us the great opportunity to save lives even when there's no pandemic threat), the world should set an **ambitious plan to make vaccines even better**.

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Perspective

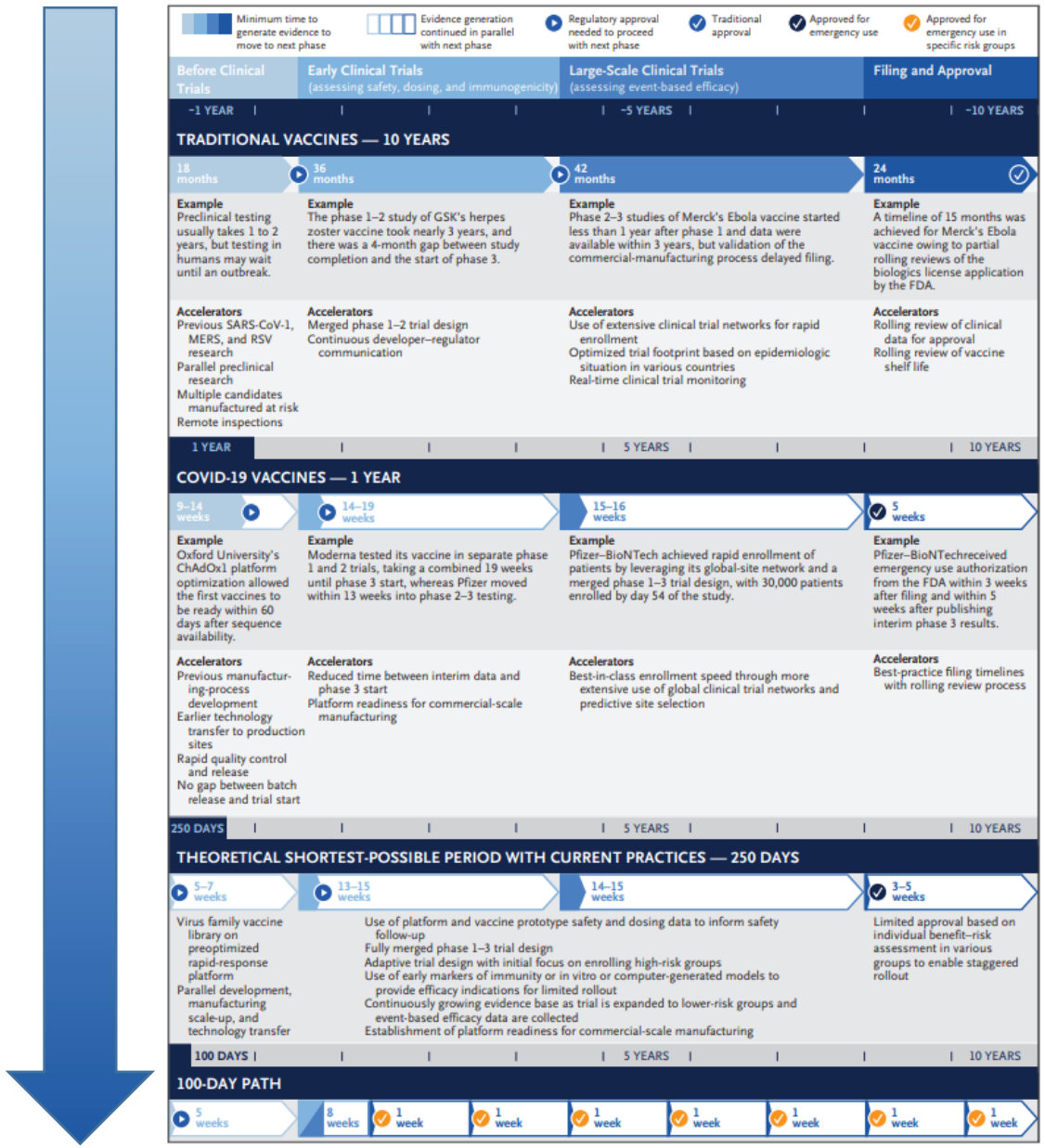
JULY 14, 2022

Delivering Pandemic Vaccines in 100 Days — What Will It Take?

Melanie Saville, M.B., B.S., Jakob P. Cramer, M.D., Matthew Downham, Ph.D., Adam Hacker, Ph.D., Nicole Lurie, M.D., M.S.P.H., Lieven Van der Veken, M.D., Mike Whelan, Ph.D., and Richard Hatchett, M.D.

The development of SARS-CoV-2 vaccines in less than 1 year was a scientific triumph. Yet, during the 326 days between the viral sequence becoming available in January 2020 and emergency

gens and development technologies, supporting innovation in the vaccine-development process, using advanced analytics to inform development and manufacturing



Strategies for Achieving Faster Vaccine Development.

Shown are critical activities on the path to condensing vaccine-development timelines and further changes that would be needed to reach the 100-day goal. MERS denotes Middle East respiratory syndrome, RSV respiratory syncytial virus, GSK GlaxoSmithKline, and FDA Food and Drug Administration.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Aquí en tu ciudad
de lo más pequeño...
Hacemos lo más grande!
Bolivar Desnudo
Pereira, Risaralda, Colombia
Thank you!
Por siempre las Américas
Luciano García Gómez
"In Pereira there are no foreigners, we are all Pereirans"