CLIMATE CHANGE & EPIDEMICS 2023
Synthesis Report for COP28

Summary for Policymakers

A Report of the Climate Amplified Diseases and Epidemics (CLIMADE) consortium

CLIMATE CHANGE & EPIDEMICS 2023

CLIMADE Consortium Report

Summary for Policymakers COP28

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Cover photo reference

Alexis Huguet / AFP via Getty Images

The following abbreviations have been used:

BMRI   Biomedical Research Institute
CERI   Centre for Epidemic Response and Innovation
CFR   Case Fatality rate
CLIMADE   Climate Amplified Diseases and Epidemics
ENSO   El Nino Southern Oscillation
FIOCRUZ   Fundação Oswaldo Cruz
IDMC   Internal Displacement Monitoring Centre
ILRI   International Livestock Research Institute
IRESSEF   Institut de Recherche en Santé, de Surveillance Épidémiologique et de Formations
KRISP   KwaZulu Research Innovation Sequencing Platform
PAHO   Pan American Health Organization
SARS-CoV-2 severe acute respiratory syndrome coronavirus 2
UKZN   University of KwaZulu-Natal
WNV   West Nile Virus

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Summary for Policymakers

Introduction:

As the world endeavours to recover from the COVID-19 pandemic, it is crucial to recognize that another crisis, unfolding at an alarming pace, demands our immediate attention. **Climate change has assumed a dominant role our lives, causing unprecedented levels of distress**. Populations across the globe are grappling with the devastating consequences of extreme climatic events, necessitating efforts to control wildfires, rebuild infrastructure damaged by floods, and adapt to a progressively hotter and more perilous environment. Regrettably, amidst these challenges, there is a looming threat that is being overlooked—the intricate interaction between climate change and infectious diseases. A review has revealed that climate change has the potential to **aggravate over 50% of known human pathogens[1]**. This distressing phenomenon is not a distant projection but a stark reality currently unfolding before us[2].

Emergence of new pathogens

Within the short span of less than two years since the last major wave of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), exemplified by the emergence of the Omicron variant, a concerning array of pathogens have surfaced. Some are not well-known, such as mpox (formerly known as monkeypox) and chikungunya virus, while others, such as *Vibrio cholerae* (which causes cholera) and *Plasmodia* parasites (responsible for malaria) have been recognized for centuries. Furthermore, there exists the ominous possibility that pathogens frozen in the permafrost, to which our immunity is presently unaccustomed, may be released as the climate continues to warm. While some might think that climate change and epidemics are either exaggerated or transient, there is overwhelming evidence linking climate change to the surge of disease outbreaks and epidemics[3]. It is no longer a question of "if", but "when: the next epidemic will be set off by these events[2].

Mechanisms of disease aggravation

The exacerbation of infectious diseases due to climate hazards can be attributed to both direct and indirect factors. The three main factors include:

1. Gradual temperature rise: The slow but relentless increase in global temperatures creates a conducive environment for disease vectors such as mosquitoes, rodents, and ticks. The rising temperatures facilitate their proliferation and extends their geographical range, intensifying the transmission of diseases, including in previously unaffected areas[4,5]. Dispersal of disease vectors is also enhanced through altered rainfall patterns that can create breeding grounds for mosquitoes, thereby increasing the incidence of vector-borne diseases.

2. Extreme events: Sudden and more frequent occurrences of extreme events, such as floods, further compound the problem. These events contaminate drinking-water sources, causing outbreaks of diseases[6,7,8], and trigger the displacement of humans and animals.

[1] Mora C, McKenzie T, Gaw IM, *et al.* Over half of known human pathogenic diseases can be aggravated by climate change. *Nat Clim Chang* 2022; **12**: 869–75.

[2] de Oliveira T, Tegally H. Will climate change amplify epidemics and give rise to pandemics?. *Science*, 2023; **381**, 6660, DOI: 10.1126/science.adk450

[3] Milman O. 'Potentially devastating': Climate crisis may fuel future pandemics. The Guardian. 2022; published online April 28. https://www.theguardian.com/environment/2022/apr/28/climate-crisis-future-pandemics-zoonotic-spillover (accessed Oct 2, 2023).

[4] Kraemer MUG, Reiner RC, Brady OJ, *et al.* Past and future spread of the arbovirus vectors Aedes aegypti and Aedes albopictus. *Nat Microbiol* 2019; **4**: 854–63.

[5] Nakase T, Giovanetti M, Obolski U, *et al.* Global transmission suitability maps for dengue virus transmitted by Aedes aegypti from 1981 to 2019. *Sci Data* 2023; **10**: 275.

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[8] Rieckmann A, Tamason CC, Gurley ES, *et al.* Exploring Droughts and Floods and Their Association with Cholera Outbreaks in Sub-Saharan Africa: A Register-Based Ecological Study from 1990 to 2010. *Am J Trop Med Hyg* 2018; **98**: 1269–74.

3. Climate Migration: Changes in temperature and precipitation patterns can also impact food and water availability and impact livelihoods. Droughts and crop failures can lead to food scarcity, prompting migration in search of sustenance and new economic opportunities. Animal migrations can also contribute to the transmission of pathogens.

While countries in the global south contribute less than 10 percent of greenhouse gas emissions, they are likely to suffer the largest health impacts from climate change. Not only are developing countries more at risk of climate disasters and harm, but they also have less adaptive capacity and preparedness to respond to these threats, making developing countries highly vulnerable (low preparedness vs climate risk).

The urgency of addressing the nexus between climate change and infectious diseases cannot be overstated. The response to climate change should be used as an opportunity to build capacity to protect and support health, especially in underserved and underrepresented communities. As responsible policymakers, it is imperative that we acknowledge this reality and take swift, decisive action to mitigate the impending public health crisis.

We urge governments, academic institutions, scientists, public health officials, private sector industries and health organizations to collectively address the urgent and interconnected challenges of climate-amplified diseases and epidemics through their diverse expertise, resources, and influence by:

1. **Reporting outbreaks timeously** - Immediate and transparent reporting of infectious disease outbreaks is paramount. Governments and health organizations should commit to reporting outbreaks promptly and openly, sharing crucial data with relevant stakeholders. This transparency is essential for global preparedness and response efforts.

2. **Strengthen Genomic Surveillance** - Governments, academic institutions, and health organizations must invest in and expand genomic surveillance capabilities to monitor the spread and evolution of infectious diseases. This will enable early detection and response to emerging threats, allowing us to prevent outbreaks before they escalate.

3. **Prioritizing Vulnerable Populations** - The most vulnerable communities are disproportionately affected by the intersection of climate change and infectious diseases. Governments and private sector industries must prioritize these populations by investing in resilient healthcare systems, infrastructure, and disaster preparedness measures.

4. **Promoting Climate Resilience** - Academic institutions and private sector industries should collaborate to develop innovative solutions that enhance climate resilience within healthcare systems. This includes designing infrastructure to withstand extreme weather events and ensuring the availability of essential medical supplies during crises.

5. **Committing Sustainable Funding** - Governments, private sector industries, and health organizations must commit to sustainable funding dedicated to the fight against climate change-related infectious diseases. This funding should support research, capacity-building, and community engagement to create a robust defense against these converging threats.

A. Observed Slow Rise in Temperature and Increased Risk of Epidemics

A.1 The increase in temperature gradually alters the likelihood of disease transmission as environmental conditions become more favourable for certain disease vectors. An increase in viruses and parasites causing outbreaks has been noticed around the world. In 2023, the largest outbreaks of chikungunya and dengue ever recorded occurred in South Asia and South America and many of the outbreaks are in areas previously unaffected, such as Paraguay and Uruguay. There are also increasing rates of transmission of malaria, dengue, chikungunya and West Nile Virus in Europe and North America with many countries and states identifying the first local transmission of these pathogens. In Africa, arboviral outbreaks are increasingly being detected, with Senegal having concurrent outbreaks of dengue and chikungunya and countries having more frequent yellow fever virus outbreaks.

A.1.1 **Dengue** outbreaks in South Asia have been the highest on record. For example, in 2022, Vietnam went through one of its worst dengue outbreaks, with more than 360,000 reported cases and 140 deaths. By comparison, Vietnam recorded 72,880 cases and 27 deaths in 2021[9].

A.1.2 This year, there was a surprising and large outbreak of **chikungunya in Paraguay** with over 120,000 confirmed cases[10]. This is the largest outbreak of chikungunya in Paraguay ever and coincided with the highest average temperatures in the country's history (Figure 1). Paraguay has never experienced a fatality from this virus before, but this outbreak killed 46 individuals, including neonates, and caused major health disruption in the country as the virus spread to all provinces.

A.1.3 The tiger mosquito (*Aedes albopicus*) is increasing in frequency in the south of Europe and fuelling new viral outbreaks. Last year, a British woman was infected with mosquito-borne **dengue** virus while traveling in France[11]. In 2023, there were reports of outbreaks of dengue virus in France[12] and multiple cases of local transmission detected in the Lombardy and Lazio regions of Italy. Most of southern Europe is now susceptible to outbreaks of arboviruses.

> "Extreme temperatures, droughts, floods and cyclones cause death directly and indirectly through outbreaks of diseases such as cholera and dengue fever that are being witnessed in 16 and 7 African countries respectively. Climate Amplified Diseases and Epidemics (CLIMADE) consortium of global scientists is acting now by developing surveillance tools, knowledge and adequate interventions in order to address climate hazards."
>
> **Nicksy Gumede-Moeletsi**
> World Health Organization Regional Office for Africa, November 2023

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9 Vietnam: Elevated dengue fever activity reported in Hanoi in early September. Crisis 24. 2023; published online Sept 5. https://crisis24.garda.com/alerts/2023/09/vietnam-elevated-dengue-fever-activity-reported-in-hanoi-in-early-september-update-1. (accessed Nov 20, 2023).

10 Giovanetti M, Vazquez C, Lima M, *et al.* Rapid Epidemic Expansion of Chikungunya Virus East/Central/South African Lineage, Paraguay. *Emerg Infect Dis* 2023; **29**: 1859–63.

11 Noyce E. British woman infected with dengue fever on holiday to France. Independent. https://www.independent.co.uk/news/health/dengue-france-british-woman-cases-b2319050.html (accessed Nov 18, 2023).

12 Head M. Dengue in France: tropical diseases in Europe may not be that rare for much longer. *The Conversation* 2022. https://theconversation.com/dengue-in-france-tropical-diseases-in-europe-may-not-be-that-rare-for-much-longer-191033 (accessed Oct 2, 2023).

A.1.4   Increasing temperatures in southern Europe have also been linked to a **chikungunya** epidemic in Italy in 2017[13] that spread in the Lazio region and caused a secondary outbreak in the Calabrian village of Guardavalle in 2023.

A1.5   With global climate change, more areas—even those away from the equator or at relatively high elevations—are becoming susceptible to mosquitoes. The first ever local cases of **malaria** were detected in the USA, including in Texas, Florida, Maryland and Arkansas this year[14, 15].

A.1.6   This year, Colorado, in the USA, is experiencing the worst **West Nile Virus** (WNV) outbreak so far. And it's been one of the deadliest WNV seasons in Colorado since the mosquito-borne illness arrived in the U.S. back in 1999. By Sept. 1, 2023, 11 people had died in Colorado due to WNV[16].

A1.7   As of 2023, 34 countries in Africa and 13 countries in Central and South America are either endemic for, or have regions that are endemic for, **yellow fever virus[17]**. In 2022, 12 countries in the WHO African Region reported confirmed cases of yellow fever (Cameroon, the Central African Republic, Chad, Côte d'Ivoire, the Democratic Republic of the Congo, Ghana, Kenya, Niger, Nigeria, the Republic of the Congo, Sierra Leone and Uganda) (WHO AFRO). Eight of these countries are experiencing a continuation of transmission from 2021 (Cameroon, the Central African Republic, Chad, Côte d'Ivoire, the Democratic Republic of the Congo, Ghana, Nigeria, and the Republic of the Congo) and four countries are newly reporting confirmed cases (Kenya, Niger, Sierra Leone and Uganda).

> "Climate change has caused a lot of outbreaks of arboviruses in the highlands and midlands of Ethiopia which were not present in the country previously. Now chikungunya and dengue fever viruses are becoming common outbreaks in the eastern part of our country."
>
> Molalegne Bitew
> Bio and Emerging Technology Institute, Ethiopia, October 2023

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[17] World Health Organization. Yellow Fever. Geneva, Switzerland: World Health Organization, 2023 https://www.who.int/news-room/fact-sheets/detail/yellow-fever#:~:text=As%20of%202023%2C%2034%20countries,to%20grant%20life%2Dlong%20protection. (accessed Nov 2, 2023).
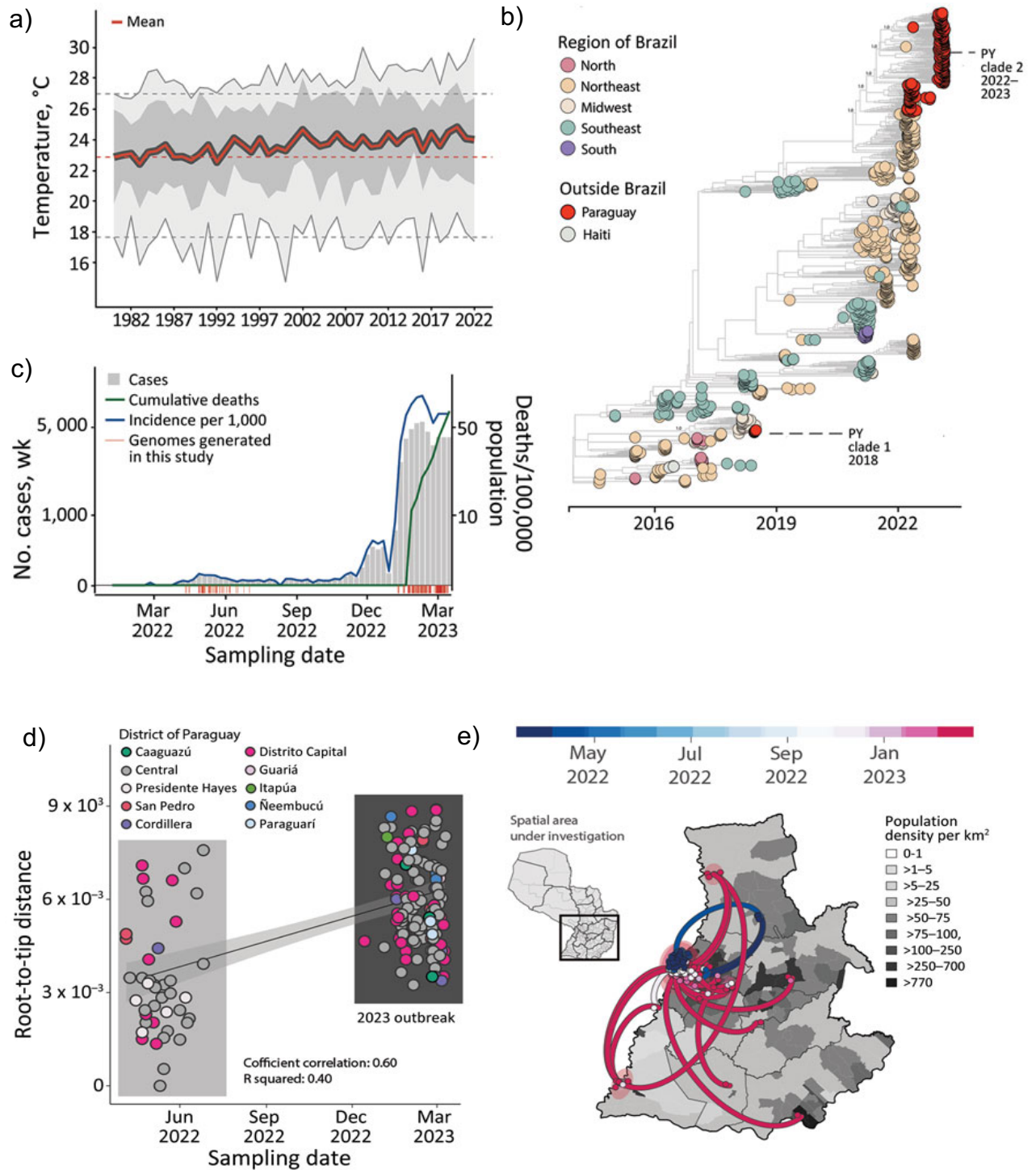
Figure 1. Spatial and temporal distribution of cases of chikungunya in Paraguay. A) Temperature trends during 1981–2022. Yearly mean (red line), yearly minimum and maximum (light gray shading), yearly 50% quantiles (dark gray shading), minimum and maximum temperatures in 1981 (dashed gray lines) and mean temperature in 1981 (dashed red line) are shown. B) Number of chikungunya virus genome sequences in Paraguay compared with Brazil (by region) and Haiti. Size of circles indicates number of new genomes generated in this study. C) Weekly reported chikungunya cases (gray area), incidence normalized per 100,000 persons (blue line), and cumulative deaths (green line -or other color if you need to change this line color) during 2022–2023 (through epidemiologic week 11). Red bars indicate dates of sample collection of genomes generated in this study. D) Expansion of the chikungunya East/Central/South/African lineage epidemic in Paraguay. Regression of root-to-tip genetic distances and sampling dates estimated by using TempEst version 1.5.3, (http://tree.bio.ed.ac.uk/software/tempest), buffers (shaded area) representing 90% CIs. Colors indicate geographic location of sampling. E) Spatiotemporal reconstruction of the spread of CHIKV ECSA in Paraguay. Circles represent nodes of the maximum clade credibility phylogeny, colored according to their inferred time of occurrence (scale shown). Shaded areas represent 80% highest posterior density interval and depict uncertainty of the phylogeographic estimates for each node. Solid curved lines indicate links between nodes and directionality of movement. Differences in population density are shown on a gray-white scale.

Figure adapted from Giovanetti (2023) et al. Emerg Infect Dis 2023; 29: 1859–63.

B. Extreme climate events are driving the rise in epidemics.

B.1   Extreme climate events and disasters are also contributing to a surge in epidemics, often unfolding within a matter of days or weeks, catching regions and countries off guard with limited time for preparation. The aftermath of such disasters can be further compounded by the rapid spread of infectious diseases. Extreme cholera epidemics were detected in south Asia and Africa in 2022 and 2023. Contamination of water with e coli after floods has been detected in multiple regions of the world. Floods have amplified the likelihood of mosquitoes breeding, subsequently leading to an increase in malaria and dengue transmission across many parts of the world, especially in Southeast Asia.

B.1.1   Infectious disease outbreaks following extreme weather events occur as **microbes**, **vectors**, and **reservoir animal hosts** take advantage of the disrupted social and environmental conditions resulting from such weather extremes.

B.1.2   According to the World Health Organization (WHO), the world is currently in the midst of an acute upsurge of the 7th **cholera** pandemic since mid-2021. This pandemic has been characterized by the number, size and concurrence of multiple outbreaks, the spread to areas free of cholera for decades and alarming high mortality rates.

B.1.3   In 2022 and 2023, the world witnessed two devastating **cholera** epidemics that demanded global attention. The first occurred in Pakistan following a period of extreme flooding, resulting in hundreds of thousands of infections. The strain responsible for the outbreak in Pakistan was also associated with the deadliest cholera epidemic in Malawi's history. Although Malawi usually registers a few hundred cholera cases per year, there were over 57,000 confirmed cases and 1,733 deaths during the 2022 to 2023 outbreak (Figure 2)[18]. This outbreak, characterised by an unusually high mortality rate of approximately 3% shocked the international medical community, as reported by a Médicins Sans Frontières team responding to the crisis in Malawi.

B.1.4   Rising temperatures and increased rainfall patterns attributed to the El Nino Southern Oscillation (ENSO) have heightened the risks of **dengue** transmission in Peru[19].

B.1.5   Floods in Pakistan in 2020 were linked to an upsurge in **dengue** cases with 733 cases being reported from the Sindh province in the first 8 months of the year[20].

B1.6   Furthermore, floods, often associated with extreme weather events, have amplified the likelihood of mosquitoes breeding, subsequently leading to an increase in **malaria** transmission across many parts of the world, especially in Southeast Asia. In Pakistan, malaria cases increased four-fold to 1.6 million following the devastating floods in 2022 that left a third of the country under water[21].

[18] Chabuka L, Choga WT, Mavian CN, *et al.* Genomic epidemiology of the cholera outbreak in Malawi 2022-2023. Public and Global Health, *MedRxiv* 2023 DOI:10.1101/2023.08.22.23294324.

[19] Dostal T, Meisner J, Munayco C, *et al.* The effect of weather and climate on dengue outbreak risk in Peru, 2000-2018: A time-series analysis. *PLoS Negl Trop Dis* 2022; **16**: e0010479.

[20] News Report. Waterborne diseases, dengue surge in Karachi after urban flooding. The News. 2020; published online Sept 4. https://www.thenews.com.pk/print/709977-waterborne-diseases-dengue-surge-in-karachi-after-urban-flooding (accessed Nov 20, 2023).

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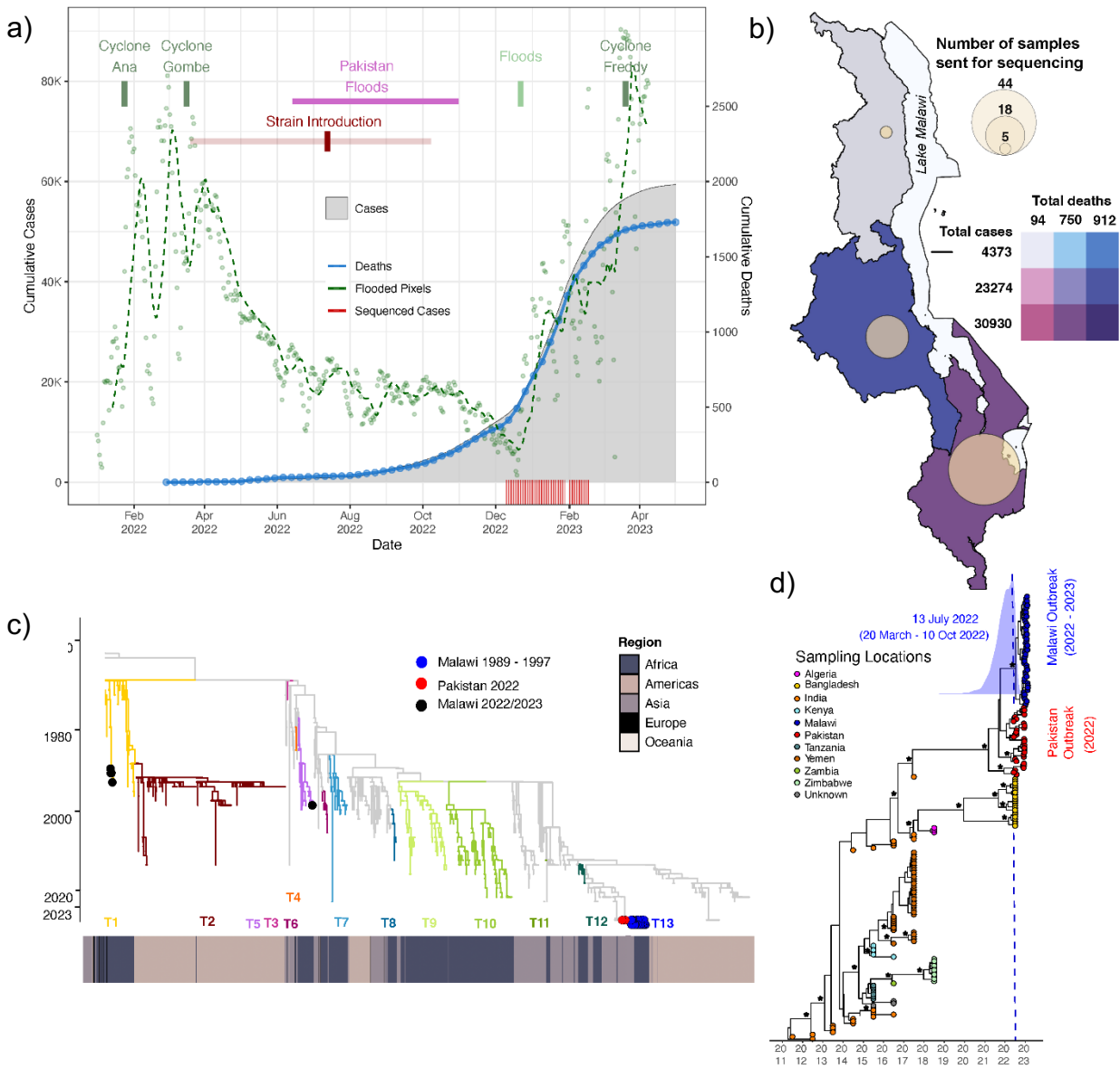
Figure 2: Epidemiological trends of the recent cholera outbreak in Malawi. A) Cumulative number of confirmed cholera cases and deaths are depicted on the y-axes from February 2022 to April 2023. Green dots portray the daily number of pixels demonstrating flooding conditions across Malawi as detected from remotely sensed satellite imagery with the moving average shown as the dashed green line. Inferred time of introduction of a Pakistan strain into Malawi is annotated on the plot as well as the timing of cyclones and flooding events affecting Malawi. Temporal distribution of cases sequenced by this study are displayed as the red rug plot. B) Map showing the total number of cases and deaths for the northern, central, and southern regions of Malawi. Overlayed circles represent the number of samples per region sequenced from the recent outbreak. C) Time-scaled maximum likelihood global phylogeny of all publicly available cholera genomes. Genomes sampled from the 2022 – 2023 Malawi outbreak are displayed as blue circles while genomes sampled from Malawi prior to this outbreak are depicted as black circles. Red circled tips were sampled from Pakistan in 2022. Clade branches are coloured by the previous 12 introduction events involving Africa (T1 – T12) as per Weill et al. (2017). We denote the 2022 – 2023 Malawi genomes as the 13th introduction (T13). Heat map below the tree is coloured by continental region of sample origin. D) Zoom in of the time-resolved phylogeny depicting the clade containing genomes from the 2022 – 2023 outbreak in Malawi in blue (n= 49, sampled between 10 December 2022 and 17 February 2023) with a basal clade of genomes sequenced from Pakistan in 2022 in red. Time to the most common recent ancestor (TMRCA) is estimated at 13 July 2022 (HPD 95%: 20 March – 10 October 2022). The posterior distribution of the TMRCA is shown as the blue curve. Bootstrap support values >0.9 are displayed with asterisks. Figure adapted from Chabuka et al. https://www.medrxiv.org/content/10.1101/2023.08.22.23294324v1.

C. Climate Migrants and Epidemics

C.1 Notably, in an increasingly globalized world, the movement of people, animals, and cargo can further compound the challenges of climate change and epidemics. As demonstrated by the rapid spread of SARS-CoV-2 variants, highly transmissible pathogens can easily cross borders despite severe travel restrictions. This means that pathogens can arrive undetected and cause epidemics if the conditions for transmission are appropriate. Scientists anticipate that 2024 will be an even warmer year because of the El Niño event (a climate pattern that results in the warming of surface waters in the eastern Pacific Ocean). This will likely produce severe drought in some regions of the world, potentially spurring mass temporary and permanent migrations.

C.1.1 The 2017 outbreak of **chikungunya** virus in Italy was traced to index cases from India. Climate change can also drive populations to migrate, causing more interactions with wildlife and increasing the risk of spillover of pathogens.

C.1.2 Migrations following extreme weather events have caused outbreaks of **cholera** in Haiti and Bangladesh[22,23].

C.1.3 **Hepatitis E virus** (HEV) outbreaks have occurred in displaced persons camps linked to unclean water supply, low hygiene, and sanitation standards. Severe droughts in the Horn of Africa in 2011 aggravated socio-economic issues in the region, including increased food-insecurity[24]. This led to population displacements into overcrowded refugee camps in Kenya and Ethiopia, where devastating outbreaks of **cholera**, **shigellosis**, and acute **HEV** have followed[25,26].

C.1.4 Risk of importation modelling of **dengue** in Africa shows increased risks of epidemics in African countries following dengue introductions from South Asia (Figure 3a). The results show that most introductions from Brazil are likely to fall within cold-spots in Africa (Figure 3b), whereas the introductions from South Asia are likely to fall in hot-spots and potentially cause large outbreaks.

C.1.5. Climate extreme events in 2022 caused >100,000 people to be displaced internally according to reports from the Internal Displacement Monitoring Centre (Figure 4)

C.1.6 During the SARS-CoV-2 pandemic, shifts in global mobility patterns impacted on the synchrony of epidemic waves on different continents, suggesting the potential of global outbreaks fuelled by human movements[27]. Advanced phylogeographic mapping of variants global dispersal dynamics revealed that global dispersal of pathogens happens along well-connected travel hubs and along air traffic networks, providing support to the simultaneous movement of pathogens along with human mobility[28].

C.1.7 Human migration resulting from climate pressures has been linked to changes in the geographical distribution of disease vectors as they are introduced to new ecological areas[29]. For example, during the **yellow fever virus** (YFV) epidemic in Brazil, frequent movements to rural and forested areas have been shown to be associated with an increased risk of acquiring

[22] Reiner RC, King AA, Emch M, *et al.* Highly localized sensitivity to climate forcing drives endemic cholera in a megacity. *Proc Natl Acad Sci USA* 2012; **109**: 2033–6.

[23] Rinaldo A, Bertuzzo E, Mari L, *et al.* Reassessment of the 2010–2011 Haiti cholera outbreak and rainfall-driven multiseason projections. *Proc Natl Acad Sci USA* 2012; **109**: 6602–7.

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29 Wilder-Smith A, Gubler DJ. Geographic expansion of dengue: the impact of international travel. *Med. Clin. North Am*. 2008; **92**: 1377–90.

YVF from the sylvatic cycle (the transmission of virus between non-human primates and forest-canopy mosquitoes)[30]

C.1.8   Factors such as overcrowding and poor sanitation associated with climate disasters and human migrations may lead to outbreaks of mosquito-borne disease (e.g., **malaria** and **dengue**) and water-borne diseases (e.g., **cholera**, **hepatitis A**) in the destination location of the displaced population [31,32,33].

C.1.9   Close proximity to vectors and animal populations near temporary shelters may further exacerbate the risk of zoonotic spillovers. For example, it was shown by Thompson et al (2002) [34] that there was an elevated risk of visceral leishmaniasis near water supplies in northeastern Brazil, where sand fly vectors are prevalent because of an increase in human settlements driven by drought events.

C.1.10   The increased urbanisation and population density as a result of long-term migration events has been shown to impact infectious disease transmission dynamics[35,36,37,38].
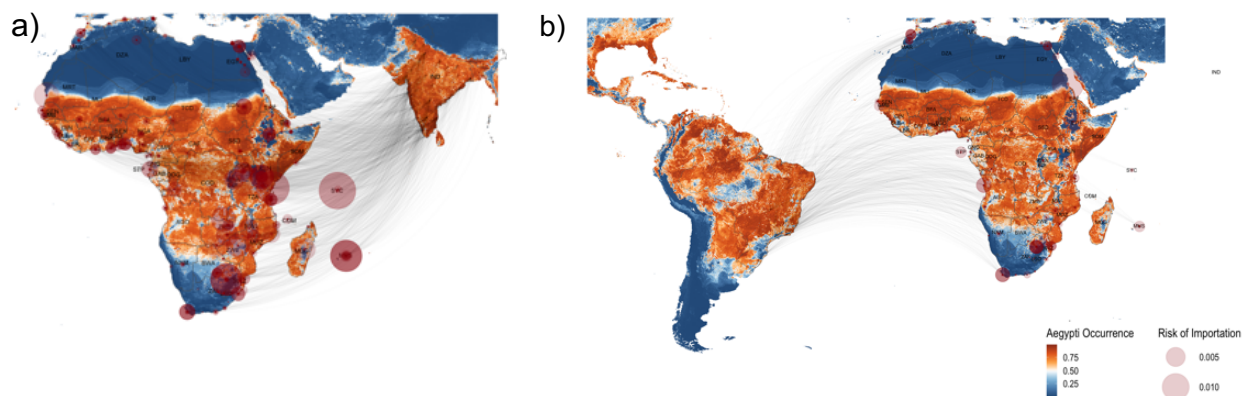

Figure 3: Risk of importation of dengue in Africa shows increased risks of epidemics in African countries following dengue introductions from A) South Asia compared to B) Brazil where introductions from dengue are likely to fall within low-risk areas in Africa

30 Faria NR, *et al*. Genomic and epidemiological monitoring of yellow fever virus transmission potential. *Science* 2018; **361**: 894–9.

[31] Chaparro P, Padilla J, Vallejo AF, *et al*. Characterization of a malaria outbreak in Colombia in 2010. *Malar. J.* 2013; **12**: 330.

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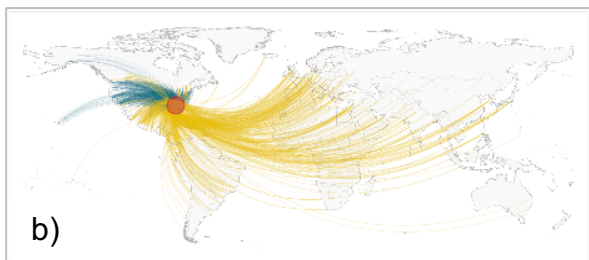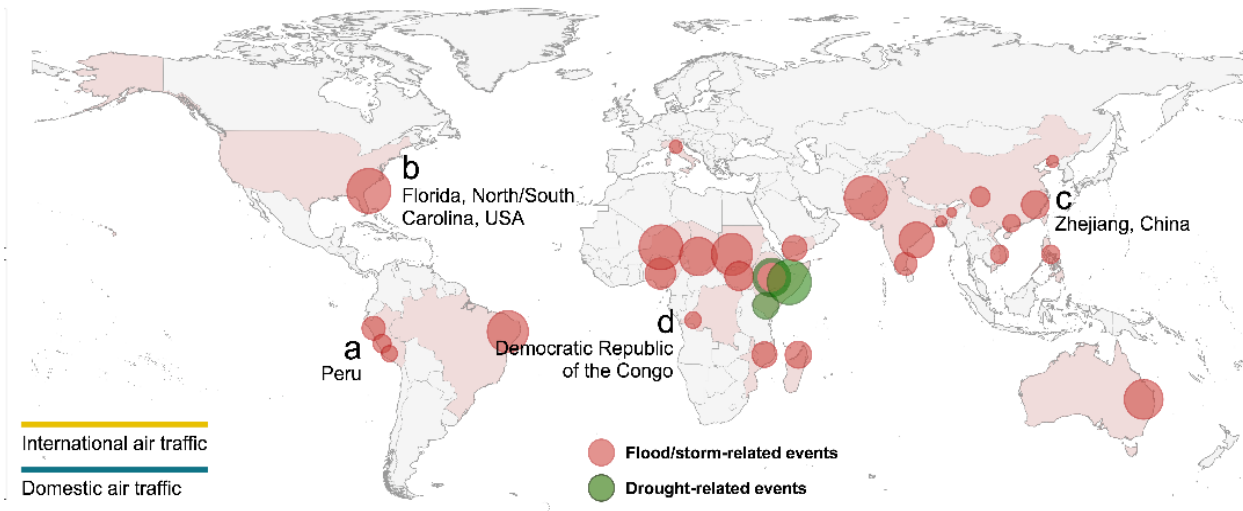
Figure 4: Climate extreme events in 2022 that caused >100,000 people to be displaced internally according to reports from the Internal Displacement Monitoring Centre (IDMC) [https://www.internal-displacement.org/database/displacement-data]. Red and green circles indicate regions affected by flood or storm-related and drought-related events, respectively. Maps a-d show air travel from regions affected to airports globally. Green lines show travel within a country and yellow lines show air travel to airports internationally.

D. Creating of a Global Consortium on Climate Amplified Epidemics and Diseases (CLIMADE)

D.1 The CLIMADE (Climate Amplified Diseases & Epidemics) consortium brings together leading global scientists focused on bridging knowledge gaps, improving surveillance tools and expanding adequate interventions to decrease the impact of diseases and epidemics amplified by climate change. The overarching long-term goal of CLIMADE is to predict, track and control diseases and epidemics that are amplified by human-caused climate change in the most affected countries in the world.

D.1.1 The mission of CLIMADE is to use the medical, scientific, and public health experience of epidemics in the global south to help the world create a robust surveillance system to quickly identify pathogens and track their evolution and spread to control outbreaks before they become epidemics and epidemics before they become pandemics.

D.1.2 The CLIMADE consortium brings together partners from around the globe that have long-term experience with pathogen genomics and epidemics that are amplified by climate change (Figure 5). Partners include public health agencies, academic organizations, and industry. The CLIMADE consortium is led by Professor Tulio de Oliveira, from the CERI in South Africa, Professor Luiz Carlos Alcantara, from the Fundação Oswaldo Cruz (FIOCRUZ) in Brazil, and Professor Edward C Holmes, from the University of Sydney in Australia. Together, with key public health agencies such as the Africa CDC and the WHO/PAHO, they bring decades of experience in genomics surveillance and epidemic response and have assembled a leading team of academic and industrial experts to start developing the global CLIMADE network.

D.1.3 The long-term goal of CLIMADE is to develop tools to predict, track and control diseases and epidemics in the most affected countries in the world and to use this data to prevent new epidemics and pandemics that can be amplified by climate change.
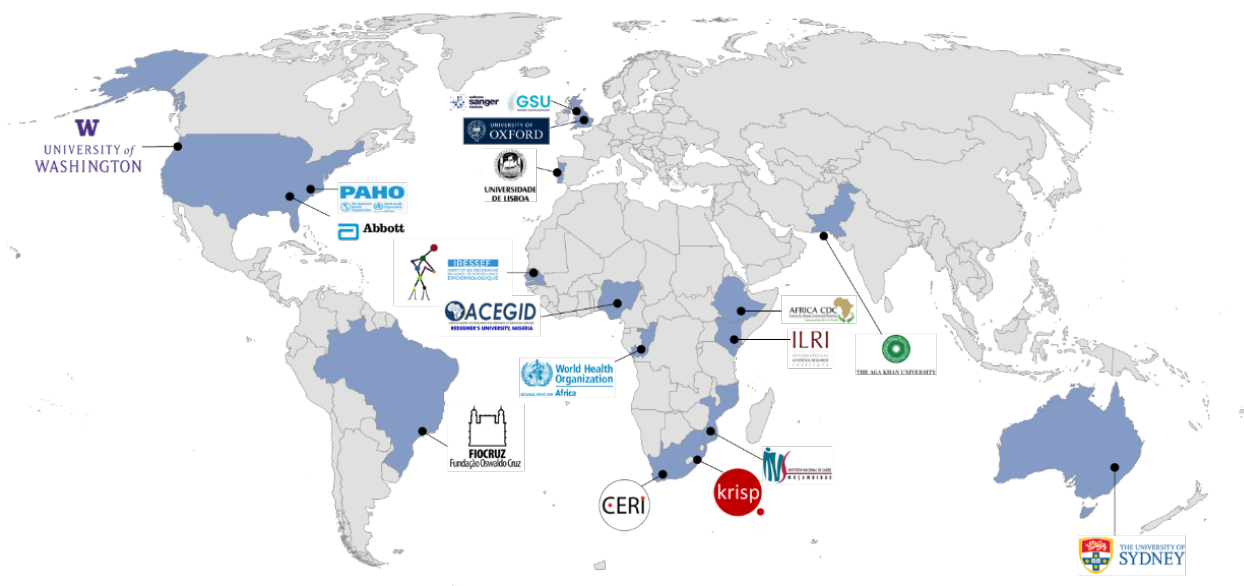

Figure 5: Founding members of CLIMADE Consortium

E.   CLIMADE current activities

E.1   CLIMADE will generate knowledge, develop localized tools, and inform public health action for early warning and timely/targeted response to pathogens amplified by climate change. The current activities include: 1) Building a pan-African coalition to assess vector-borne pathogen susceptibility and transmission hotspots in Africa that will inform context-specific modelling, 2) Accelerating the representation of vector-borne pathogen genomes from Africa, and 3) Establishing sustainable capacity and processes for pathogen genomics in African countries. The CLIMADE activities are already making important impacts in Africa and South America by rapidly responding to outbreaks of cholera, chikungunya and dengue.

E1.1   In the aftermath of three large tropical storms (Figure 6) in 2022 and 2023, Malawi experienced the **largest outbreak of cholera** in the country's history. The outbreak started in March 2022 and was declared a public health emergency on December 5, 2022. Between May 2022 and April 2023, a total of 58,171 confirmed cases and 1,743 deaths were reported with an overall case fatality ratio (CFR) of 3.0%. The higher than usual CFR associated with the recent cholera outbreaks is of particular concern. The CLIMADE team assisted in responding to the cholera outbreak in Malawi by sending personnel to Malawi (Figure 6), along with the required reagents, to sequence the Vibrio cholerae isolates from confirmed cholera cases. The analysis of the sequences indicates that the outbreak in Malawi resulted from a new introduction of cholera in Africa, likely from Pakistan. These new cholera sequences provide important clues about the introduction and spread of cholera in Africa and emphasize the need for coordinated global action on cholera, and the importance of early outbreak detection and response.

> "CLIMADE is helping with capacity building on the African continent by training young scientists in molecular approaches for detection and sequencing pathogens. By doing this, scientists in these countries can get first-hand data on the impact of climate changes on the health of their countries"
>
> *Michael Owusu*
> *Kwame Nkrumah University of Science and Technology, Ghana, November 2023*

E1.2   In Brazil, the CLIMADE team worked with the Paraguayan Ministry of Health to track the real-time evolution and spatial spread of **chikungunya from an unusually large outbreak** in Paraguay in March 2023. This outbreak resulted in over 120,000 cases, including 3,510 hospitalized case-patients and 46 deaths. Although chikungunya has been detected in Paraguay since 2015, this outbreak was much larger than prior outbreaks and coincided with the highest mean temperatures reported in Paraguay. The phylogeography analysis shows that the virus transmission dynamics roughly followed patterns of population density, moving most often between the most populous urban localities.

E1.3   CLIMADE has also contributed to enhancing the surveillance of **dengue** and **chikungunya** in West Africa by providing training, reagents and protocols. The training received from CLIMADE enabled the establishment of whole genome sequencing technologies at IRESSEF laboratory in Senegal. With support from the CLIMADE team, IRESSEF sequenced 85 dengue samples from Burkina Faso and Senegal. This initial sequencing effort resulted in the doubling of available whole genomes of dengue from Burkina-Faso. Prior to this sequencing effort, there were just 42 whole genomes (collected between 1980 – 2019) in publicly accessible databases. The team at IRESSEF also sequenced 31 chikungunya samples from an ongoing outbreak in the country. The results revealed a novel strain of the West African chikungunya genotype, phylogenetically distinct from strains circulating in previous outbreaks, which suggests a likely new spillover from sylvatic cycles in rural Senegal[39].

E1.4   A full list of projects and activities associated with CLIMADE is available in the **appendix**

Figure 6: (above) Photo of the aftermath of the flooding in Malawi, 2023, Left: Mr Lucious Chabuka from the Public Health Institute of Malawi received training at the Centre for Epidemic Response and Innovation (CERI) at Stellenbosch University and conducted the cholera sequencing in Malawi

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F. Call for Action: Join the CLIMADE Consortium in Combating Climate-Amplified Diseases and Epidemics

F.1   Climate change and infectious diseases have emerged as intertwined challenges that demand our immediate attention. The impacts of climate change on health and disease are undeniable, and the **governments, academic institutions, private sector industries, and health organizations** must unite to combat this threat. It is imperative that we address this intersection of climate change and infectious diseases, prioritizing the most vulnerable populations and fostering health equity.

While countries in the global south contribute less than 10 percent of greenhouse gas emissions, they are likely to suffer the largest health impacts from climate change because of proximity to hotspots of disease emergence (biodiversity), an already high burden of infectious diseases in these countries, geographical association with the tropics where temperatures are high year-round, and critically, because of its large vulnerable populations, which typically have inadequate access to functional health systems.

Not only are developing countries more at risk of climate disasters and harm, but they also have less adaptive capacity and preparedness to respond to these threats, making developing countries highly vulnerable (low preparedness vs climate risk) (Figure 7). The response to climate change should be used as an opportunity to build capacity to protect and support health, especially in underserved and underrepresented communities.

The time to act is now! The intersection of climate change and infectious diseases poses a formidable challenge to global health, and we cannot afford to delay our response. By taking these actions, we can work collectively to mitigate the impending public health crisis and build a more resilient, equitable world for all.
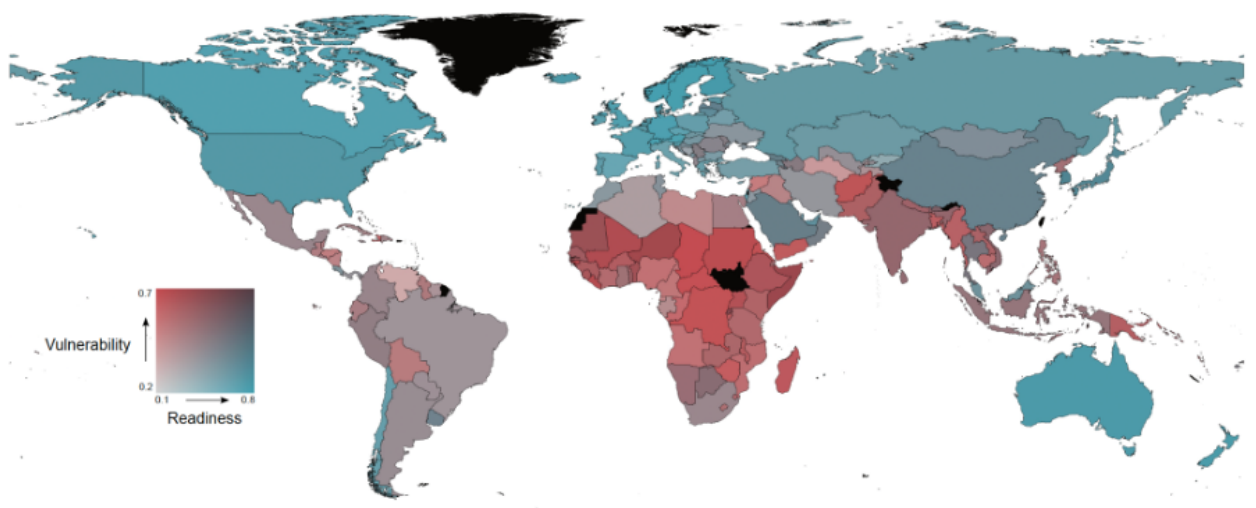
Figure 7: Geographical inequalities of disease burden and vulnerability to projected climate change. Map shows the climate vulnerability and readiness index for 2020 (data retrieved from https://gain.nd.edu/our-work/country-index). Notre Dame Global Adaptive INitiative (ND-GAIN) highlighting that sub-Saharan Africa and parts of South and Southeast Asia are at the dangerous intersection of high vulnerability and low readiness. Index values are not available for countries/regions shaded in black.

Call for Action:

We call on governments, academic institutions, scientists, public health officials, private sector industries and health organizations to collectively address the urgent and interconnected challenges of climate-amplified diseases and epidemics through their diverse expertise, resources, and influence by:

1. Report Outbreaks Timely	2. Strengthen Genomic Surveillance	3. Prioritize Vulnerable Populations	4. Promote Climate Resilience	5. Commit Sustainable Funding

Call to Action 1:
Report Outbreaks timeously
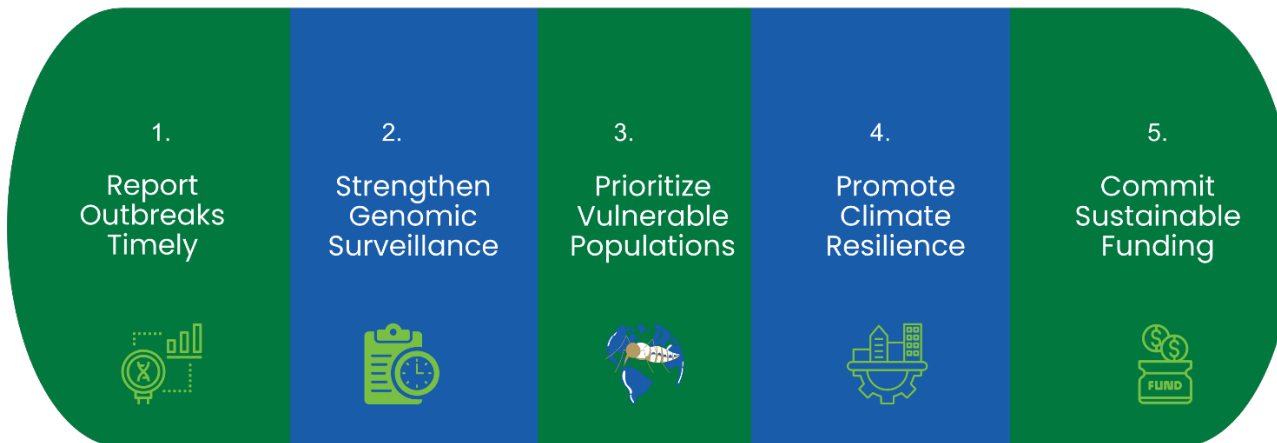
> *Early detection of an outbreak can help to guide the response and reduce the spread of diseases*
>
> **James Ayei Maror**
> National Public Health Laboratory, South Sudan

Immediate and transparent reporting of infectious disease outbreaks is paramount. **Governments and health organizations** should commit to reporting outbreaks promptly and openly, sharing crucial data with relevant stakeholders. This transparency is essential for global preparedness and response efforts.

CLIMADE

Call to Action 2:
Strengthen Genomic Surveillance

> *The monitoring of pathogenic agents through research and the study of their behaviour in the face of climate change will make it possible to anticipate actions to prevent epidemics or their rapid response in the event of an outbreak.*
>
> **Nkuurunziza Jerome**
> National Institute of Public Health, Burundi

Governments, academic institutions, and health organizations must invest in and expand genomic surveillance capabilities to monitor the spread and evolution of infectious diseases. This will enable early detection and response to emerging threats, allowing us to prevent outbreaks before they escalate.

CLIMADE

> *Climate change, infectious diseases and outbreaks/ epidemics in Uganda are closely intertwined and can result in long-lasting socio-economic effects such as a weakened and less productive workforce in addition to increased healthcare costs on already stretched system*

Aloysious Ssemaganda
Uganda - National Health Laboratories and Diagnostic Services

Call to Action 3:
Prioritize Vulnerable Populations

The most vulnerable communities are disproportionately affected by the intersection of climate change and infectious diseases. **Governments and private sector industries** must prioritize these populations by investing in resilient healthcare systems, infrastructure, and disaster preparedness measures.

CLIMADE

> *Climate resilience helps combat disease outbreaks by enhancing a community's ability to adapt and respond to changing environmental conditions. Resilient systems can withstand and recover from climate-related challenges, reducing vulnerabilities that could otherwise facilitate disease transmission.*

Yameen Badrodien
University of Cape Town, South Africa

Call to Action 4:
Promote Climate Resilience

Academic institutions and private sector industries should collaborate to develop innovative solutions that enhance climate resilience within healthcare systems. This includes designing infrastructure to withstand extreme weather events and ensuring the availability of essential medical supplies during crises.

CLIMADE

> *The biggest challenge is the high technical and financial costs of genomic surveillance, need to train bioinformaticians in Africa, need to develop more user-friendly pipeline for genomic data analysis*

Joseph Fokam
Cameroon

Call to Action 5:
Commit Sustainable Funding

Governments, private sector industries, and health organizations must commit to sustainable funding dedicated to the fight against climate change-related infectious diseases. This funding should support research, capacity-building, and community engagement to create a robust defense against these converging threats.

CLIMADE

Acknowledgements

For more information about CLIMADE:

CLIMADE Secretariat, Centre for Epidemic Response and Innovation (CERI), Level 3, Biomedical Research Institute (BMRI) Building, Tygerberg Medical School Campus, Stellenbosch University, Francie Van Zijl Dr, Tygerberg, Cape Town, 7505

ceri@sun.ac.za   https://climade.health/   https://twitter.com/climade_health

Appendix – List of ongoing projects and activities of CLIMADE

CLIMADE Africa

Weekly CLIMADE-Africa working group meetings

Monika Moir (South Africa), Tulio de Oliveira (South Africa), Houriiyah Tegally (South Africa), John Juma (Kenya)

Regular online seminars and training sessions hosted with CLIMADE Africa Consortium and contributions from CLIMADE Europe and CLIMADE Latin America. Topic covered thus far in the meetings include:

- Introduction to CLIMADE
- The landscape of prevalence and surveillance of climate sensitive vector-borne diseases in Africa
- Accelerating genomics in Africa (list of labs to facilitate sequencing, set up MTA, showcasing github page with protocols, advertising training opportunities)
- Genomic monitoring of arboviruses in South America
- Details for drawing up a Material Transfer Agreement with the regional laboratories in Africa (CERI, ACEGID, and ILRI)
- Preliminary phylogenetics and transmission dynamics for arboviruses in Africa
- Progress report on the prevalence and surveillance of climate sensitive vector-borne diseases in Africa,
- Genomic classification for Rift Valley Fever Virus
- Cholera introduction and spread across the African continent
- Tutorial on the use of Rift Valley Fever Virus typing tools on web-based Genome Detective and command line based Nextflow language
- Adapting the protocol for Cholera whole genome sequencing during the Malawi epidemic
- Pipelines for viruses: Bioinformatic analysis and viral typing tools
- Workflow for Genomic Analysis of Vibrio Cholera: Application for recent outbreak
- Second Quarter CLIMADE progress report
- The contribution of climate to the global transmission potential of the dengue virus
- Assessing the current and future gaps of dengue genomic surveillance in Africa
- Dengue transmission risk areas and enhancing surveillance data systems from climate-sensitive diseases in Africa
- Continued discussion of dengue transmission risk areas and enhancing surveillance data systems from climate-sensitive diseases in Africa - with a focus on data sources
- Understanding the persistence vs introductions of dengue in Africa
- Third Quarter CLIMADE progress report
- Master protocols and preparedness through pivoting of integrated genomic surveillance for public health response
- Translation of modelling outputs for maximum impact of the public health response
- Integrated data analytics for arbovirus risk assessment
- Implementing an integrated system to enhance the surveillance of emerging and reemerging viral threats across the Americas

Genomic and Ecological characterization of Dengue circulation in West Africa

Souleymane Mboup (Senegal), Abdou Padane (Senegal), Tulio de Oliveira (South Africa), Houriiyah Tegally (South Africa), Monika Moir (South Africa), Jenicca Poongavanan (South Africa), Graeme Dor (South Africa)

Unlike other parts of Africa which seem to suffer from Dengue outbreaks following regular re-introductions from Asia, it is clear that circulation of Dengue in West Africa may rather be maintained endemically. During the first half of 2023, we engaged with public health offices in various countries who stressed the need for serological and genomic characterization of non-malaria febrile cases in West Africa. Genomic information on the circulation of Dengue had so far been limited, often emanating from testing of returning travelers to Europe. CLIMADE therefore organized and mobilised reagents for the sequencing of 300 Dengue positive cases sampled from 2017 to 2022. Preliminary results indicate the co-circulation of 3 Dengue serotypes in West Africa (DENV1,2,3), with viral movement between densely populated urban areas of the region over several years. Preliminary evidence suggests that large outbreaks in 2017 and 2019 were caused by explosive growth of the DENV2 serotype after cryptic low level circulation for decades, while other serotypes remained stable. Further sampling, sequencing and analysis are ongoing to confirm these conclusions.

Genomic characterization of Chikungunya outbreaks in Coastal Kenya

Sam Oyola (Kenya), John Juma (Kenya), Tulio de Oliveira (South Africa), Houriiyah Tegally (South Africa), Yajna Ramphal (South Africa), Marta Giovanetti (Brazil), Jose Lourenco (Portugal), Luiz Alcantara (Brazil)

Outbreaks of chikungunya virus have been recorded in Kenya since the 1970s with perhaps the most devastating occurring on the coastal island of Lamu in 2004. Chikungunya virus is considered as endemic in coastal Kenya with a 0.7% prevalence in asymptomatic children and common recurrent infections. Under this project, 43 serum samples were retrieved from patients suspected of suffering arboviral infections. These specimens were sequenced with the generation of 28 complete chikungunya viral genomes. These genomes, in context with all other publicly available genomes from Africa, are analysed within a phylogenetic and phylogeographic framework to understand the evolution, direction of spread, and speed of spread of chikungunya across the African continent.

Assessing the current and future gaps in Dengue genomic surveillance in Africa in the face of climate change and human mobility

Houriiyah Tegally (South Africa), Jenicca Poongavanan (South Africa), Monika Moir (South Africa), Moritz U.G. Kraemer (Oxford), Tulio de Oliveira (South Africa)

This project will contribute to risk assessment for Dengue circulation and outbreaks in Africa by developing a conceptual and methodological framework to integrate climatic, mobility and population covariates within genomic epidemiology with the following goals: 1) Research towards arboviruses (e.g. Dengue) in Africa are limited and when they exist, are restricted to small local outbreak investigations. This project aims to take a continental approach to investigate risks of importations of Dengue from Asia and Latin-America, cross-border transmission in Africa and uncover patterns linked to climate events and human mobility; 2) Rather than analyzing genomic, epidemiological or climatic data in silos, like is often the case in infectious disease research, this proposal aims to employ integrative data analysis approaches with genomic epidemiology, phylodynamics and climatic modeling approaches; 3) Assess the likelihood of endemic circulation vs re-introductions of Dengue in Africa and consequently pinpoint the current and future gaps in genomic surveillance to guide upcoming efforts to scale up sequencing.

Genomic characterization of deadly Cholera in Malawi following severe flooding events
Lucious Chabuka (Malawi), Tulio de Oliveira (South Africa)
Since early 2022, in the aftermath of two extreme weather events, Malawi experienced its largest ever cholera outbreak, with over 58,000 reported cases and 1,761 deaths as of May 2023. We generated 49 high-quality, near-complete Vibrio cholerae genomes in Malawi from isolates collected between December 2022 and March 2023 from all three regions of Malawi. Using phylogenetic methods with 2159 publicly available genomes, we present evidence suggesting that the Malawi outbreak strains originated from the Pakistan outbreak, the estimated most recent ancestor of this lineage, named T15, was during the Pakistan floods, and once introduced into Malawi was exacerbated by major floods between June and October 2022. The extreme weather events and humanitarian crises in Malawi provided the environment for the spread of Vibrio cholerae, and the subsequent movement of large numbers of people may have facilitated its spread to susceptible populations in areas relatively unaffected by cholera for over a decade.

Expert Voices Column in Science Magazine - "Will climate change amplify epidemics and give rise to pandemics?"
Houriiyah Tegally (South Africa), Tulio de Oliveira (South Africa)
We were invited to participate in this new monthly column in Science Magazine. We decided to write and publish a short piece as a call for action towards the dangers of climate change and epidemics. Engagement on the piece has been very large showing the interest that the general community holds towards this pressing issue. The aim of this exercise was to raise awareness, which is as important an activity to engage in as research for scientists.

Climate change and infectious diseases module development for 28th VEME (Viral Evolution and Molecular Epidemiology workshop) 2024
Houriiyah Tegally (South Africa), Jenicca Poongavanan (South Africa)
Researchers in the CLIMADE consortium have spent years, and even decades, training the next generation of virus genomic epidemiologists, many of whom have been critical in our collective response to the pandemic and during other viral epidemics. As the world now faces increasing threats of the intersection between climate change and epidemics, it is critical to equip upcoming scientists with the necessary skills to research this topic. As such, we are developing a short course of advanced analysis of climate change and infectious disease dynamics for the VEME workshop for 2024, which will be a first for this workshop. This short module will involve extracting and visualizing environmental raster files, spatiotemporal regressions of large climatic and epidemiological datasets, and integration of environmental parameters into phylodynamic analyses. This new short module will complement perfectly the other workshop streams at VEME, focused on genomic, phylogenetics and epidemiological analysis of viral pathogens.

Continent-wide survey to assess the landscape of prevalence and surveillance of arboviruses in Africa
Monika Moir (South Africa)
A detailed questionnaire was designed to understand what arboviral outbreaks are occurring in Africa, where they are occurring, what genomic surveillance programs have been conducted during these outbreaks and the extent of surveillance capacity currently available in Africa. We received responses from 64 individuals representing public health laboratories, academic institutions and non-profit research centres from 34 African countries. The results of this study will allow us to identify geographical hotspots for arboviral outbreaks and capacity cold spots for genomic surveillance of these neglected diseases. Through this survey we are understanding the barriers faced by institutions in sequencing these viruses, which likely extends to many other pathogens, but also the successes from their regional programs fighting these diseases.

CLIMADE Europe
The ecological backgrounds of historical West Nile virus transmission in Portugal
Martim Geraldes (Portugal), Mónica Vieira Cunha (Portugal), José Lourenço (Portugal)
There is historical evidence for West Nile virus (WNV) transmission since 1979 in Portugal. However, to date, only four human infections and sporadic infections in equids have been detected. WNV is now endemic in most of the Mediterranean Basin with yearly epidemic activity in humans and equids. Informed by a large number of ecological and climate variables, machine learning approaches are being developed to unravel and characterize the ecological backgrounds matching historical evidence of WNV transmission in Portugal.

Estimating suitable ecological backgrounds for West Nile virus on the island of São Tomé
Martim Geraldes (Portugal), Mónica Vieira Cunha (Portugal), José Lourenço (Portugal)
There is no evidence for West Nile virus (WNV) transmission on the island of São Tomé, although it is generally accepted that local ecological conditions are favourable. Transferring knowledge generated from another activity in the context of Portugal, machine learning approaches are being used to identify the ecological backgrounds (areas) of the island likely suitable for WNV

transmission. The overarching goal is to identify where and when targeted surveillance of mosquitos, birds and humans should be deployed to demonstrate presence or absence of WNV on the island.

Historical climate-stress on dengue virus transmission potential across the globe
Taishi Nakase (USA), Uri Obolski (Israel), Marta Giovanetti (Italy), José Lourenço (Portugal), Túlio Oliveira (South Africa)
Recently we generated and made available a large dataset holding climate-driven estimations of dengue virus (DENV) transmission potential for the period 1979 to 2019 across the globe with high spatial resolution. Resorting to several statistical, time series approaches, we are now quantifying how much DENV transmission potential has decreased or increased due to climate-change trends between 1979 to 2019. Areas of the globe where climate has stressed transmission potential will be identified.

Historical climate-stress on West Nile virus transmission potential in Portugal
Martim Geraldes (Portugal), Mónica Vieira Cunha (Portugal), Uri Obolski (Israel), José Lourenço (Portugal)
Transferring knowledge from another activity where the suitable ecological backgrounds for West Nile virus (WNV) in Portugal have been identified and characterized, we are retrospectively (and prospectively) assessing what the contribution of climate change has been (and will be) in decreasing or increasing WNV transmission potential in Portugal.

Natural climate variation predicts Aedes aegypti population dynamics
Tarek Alrefae (UK), Uri Obolski (Israel), José Lourenço (Portugal)
Over the last 5 years we have been successful at developing modelling tools that can predict the spatio-temporal transmission activity of a variety of mosquito-borne pathogens. So far, we have neglected local mosquito population dynamics, with open questions still standing on how natural climate variation dictates spatio-temporal abundance and presence of key mosquito species. We are developing new tools, informed by climate, that accurately predict mosquito population dynamics of Aedes aegypti, the main vector for dengue and Zika viruses.

CLIMADE Africa/Europe Collaboration
Impact of climate related human migrations on the establishment of arboviral disease transmission in Africa through 2100
Houriiyah Tegally & Monika Moir, Stellenbosch, South Africa & Moritz Kraemer, Oxford, UK
Climate change will continue to cause major disruptions to human society, including large-scale human migration. Infectious diseases are also predicted to increase in frequency and intensity over the next century. Whereas the link between climate and infectious diseases has been explored in detail, the intersecting crises of climate induced human migration and health remains understudied. Diseases most affected by climate change in Africa are predicted to be arboviruses (Dengue, Chikungunya, and Zika). We propose to develop a transdisciplinary framework that links climate, extreme weather events, and human migration into prediction studies of future changes in climate sensitive arboviral diseases across Sub-Saharan Africa. First, we will explore how climate contributes to the risk of arboviruses to cause epidemics in a larger geographical range, and how this is influenced by behavioural factors in areas most affected by climate migrations. Secondly, we will explore the impact of migrations related to climate hazards and their impact on bringing people closer together in environments where pathogen transmission can be accelerated (urbanization). Our work will be done across multiple public health and research institutions in South Africa, Kenya and clinical research sites in West and Central Africa, making our outputs directly relevant to decision makers.

Robust and scalable computational pipelines for the joint analysis and sharing of genomic, epidemiological, and spatial data
Houriiyah Tegally & San James, Stellenbosch, South Africa & Moritz Kraemer, John Brittain, Joseph Tsui, Oxford, UK
GRAPEVNE (https://grapevne.readthedocs.io/en/latest/) is an interactive environment for building and validating data processing workflows built around Snakemake. The grapevine is a symbol of growth, development, and productivity, highlighting the software's ability to help users grow and develop their analytical pipelines. It was originally focussed on solving phylogenetic problems, but has developed to support a broad range of use-cases. This software will aid the CLIMADE consortium in standardizing and disseminating analytical workflows seamlessly especially when it concerns large epidemiological, genomic and environmental datasets.

Impacts of climate change-induced human migration on infectious diseases
Houriiyah Tegally, Stellenbosch, South Africa & Moritz Kraemer, Oxford, UK
Health consequences arising from climate change are threatening to offset advances made to reduce the burden of infectious diseases. The impact resulting from weather events and long-term gradual changes vary by region and the resilience of the local health system. In this review, we discuss the impact of climate on societal transformations, particularly human migration, as a response to extreme weather events and longer-term climate changes. Climate change-induced migrations and infectious disease burden are linked through various processes such as the expansion of pathogens into non-endemic areas, overcrowding in new informal settlements, the closer proximity of disease vectors and susceptible human populations, and encroachment into wildlife habitats. Countries that are predicted to have the highest burden of infectious diseases as a result of climate-related human migrations are the ones that made little contribution to climate change. Further studies are needed to generate robust evidence on the potential consequences of climate-induced human movements and migration, as well as identify effective short- and long-term interventions.

CLIMADE Americas
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

The spread of Chikungunya virus (CHIKV) is a significant public health concern in the Americas, with over 120,000 cases and 51 deaths in 2023, of which 46 occurred in Paraguay. Using a suite of genomic, phylodynamic, and epidemiological techniques, we characterized the ongoing large CHIKV epidemic in Paraguay.

Retrospective spatio-temporal dynamics of Dengue virus 1, 2 and 4 in Paraguay

Cynthia Vazquez, Luiz Carlos Junior Alcantara, Vagner Fonseca, Mauricio Lima, Joilson Xavier, Talita Adelino, Hegger Fritsch, Emerson Castro, Carla de Oliveira, Gabriel Schuab, Alex Ranieri Jerônimo Lima, Shirley Villalba, Andrea Gomez de la Fuente, Analia Rojas, Cesar Cantero, Fatima Fleitas, Carolina Aquino, Andrea Ojeda, Guillermo Sequera, Juan Torales, Julio Barrios, Maria Carolina Elias, Felipe C. M. Iani, Maria Jose Ortega, Maria Liz Gamarra, Romeo Montoya, Evandra Strazza Rodrigues, Simone Kashima, Sandra Coccuzzo Sampaio, Norma Coluchi, Juliana Leite, Lionel Gresh, Leticia Franco, José Lourenço[11], Jairo Mendez Rico, Ana Maria Bispo de Filippis, Marta Giovanetti

Dengue virus (DENV) has been a major public health concern in Paraguay, with frequent outbreaks occurring since early 1988. Although control measures have been implemented, dengue remains a significant health threat in the country, and continued efforts are required for prevention and control. In response to that, in collaboration with the Central Public Health Laboratory in Asunción we conducted a portable whole-genome sequencing and phylodynamic analysis to investigate DENV viral strains circulating in Paraguay over the past epidemics. Our genomic surveillance activities revealed the co-circulation of multiple DENV serotypes: DENV-1 genotype V, the emerging DENV-2 genotype III, BR4-L2 clade, and DENV-4 genotype II. Results additionally highlight the possible role of Brazil as a source for the international dispersion of different viral strains to other countries in the Americas emphasizing the need for increased surveillance across the borders, for the early detection and response to outbreaks. This, in turn, emphasizes the critical role of genomic surveillance in monitoring and understanding arbovirus transmission and persistence locally and over long distances.

Unveiling Paraguay's Monkeypox Epidemic: Genomic Insights and Response Strategies

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In recent months, Paraguay faces a concerning Monkeypox outbreak, straining its healthcare system. To understand transmission and response, here we obtained the first 30 whole genome sequences of the virus using a genomic surveillance approach and provide initial insights into transmission and response activities in this public health issue.

Genomics-based timely detection of Dengue Virus type I genotypes I and V in Uruguay

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We report the first whole-genome sequences of Dengue Virus type I genotypes I and V from Uruguay, including the first cases ever reported in the country. Through timely genomic analysis, identification of these genotypes was possible, aiding in timely public health responses and intervention strategies to mitigate the impact of dengue outbreaks.

Genomic and eco-epidemiological investigations in Uruguay reveal local Chikungunya virus transmission dynamics during its expansion across the Americas in 2023.

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Uruguay experienced its first Chikungunya virus outbreak in 2023, resulting in a significant burden to its healthcare system. We conducted analysis based on real-time genomic surveillance (30 novel whole genomes) to offer timely insights into recent local transmission dynamics and eco-epidemiological factors behind its emergence and spread in the country.

Increased interregional virus exchange and nucleotide diversity outline the expansion of chikungunya virus in Brazil

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The emergence and reemergence of mosquito-borne diseases in Brazil such as yellow fever, zika, chikungunya, and dengue have had serious impacts on public health. Concerns have been raised due to the rapid dissemination of the chikungunya virus across the country since its first detection in 2014 in Northeast Brazil. In this work, we carried out on-site training activities in genomic surveillance in partnership with the National Network of Public Health Laboratories that have led to the generation of 422 chikungunya virus genomes from 12 Brazilian states over the past two years (2021–2022), a period that has seen more than 312 thousand chikungunya fever cases reported in the country. These genomes increased the amount of available data and allowed a more comprehensive characterization of the dispersal dynamics of the chikungunya virus East-Central-South-African lineage in Brazil. Tree branching patterns revealed the emergence and expansion of two distinct subclades. Phylogeographic analysis indicated that the northeast region has been the leading hub of virus spread towards other regions. Increased frequency of C > T transitions among the new genomes suggested that host restriction factors from the immune system such as ADAR and AID/APOBEC deaminases might be driving the genetic diversity of the chikungunya virus in Brazil.

Unveiling the Impact of the Omicron Variant: Insights from Genomic Surveillance in Mato Grosso do Sul, Midwest Brazil

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Genomic surveillance has emerged as a crucial tool in monitoring and understanding the dynamics of viral variants during the COVID-19 pandemic. In the Midwest region of Brazil, Mato Grosso do Sul has faced a significant burden from the SARS-CoV-2 epidemic, with a total of 613,000 confirmed cases as of June 2023. In collaboration with the Central Public Health Laboratory in the capital city of Campo Grande, we conducted a portable whole-genome sequencing and phylodynamic analysis to investigate the circulation of the Omicron variant in the region. The study aimed to uncover the genomic landscape and provide valuable insights into the prevalence and transmission patterns of this highly transmissible variant. Our findings revealed an increase in the number of cases within the region during 2022, followed by a gradual decline because of the successful impact of the vaccination program together with the capacity of this unpredictable and very transmissible variant to quickly affect the proportion of susceptible population. Genomic data indicated multiple introduction events, suggesting that human mobility played a differential role in the variant's dispersion dynamics throughout the state. These findings emphasize the significance of implementing public health interventions to mitigate further spread and highlight the powerful role of genomic monitoring in promptly tracking and uncovering the circulation of viral strains. Together those results underscore the importance of proactive surveillance, rapid genomic sequencing, and data sharing to facilitate timely public health responses.

Dengue Fever Surveillance in Mato Grosso do Sul: insights from genomic analysis and implications for Public Health Strategies

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Since its discovery in early 1916, dengue fever, a common vector-borne illness in Brazil, has resulted in extensive urban outbreaks and poses a serious threat to the public's health. Understanding the dynamics of Dengue Virus (DENV) serotypes circulating in different regions of Brazil is essential for implementing effective disease control and prevention measures. In response to this urgent need, we conducted an on-site training program in genomic surveillance in collaboration with the Central Laboratory of Health and the Secretary of Health of the Mato Grosso do Sul state. This initiative resulted in the generation of 177 DENV genome sequences collected between May 2021 and May 2022, a period during which over 11,391 dengue fever cases were reported in the state. Through this approach, we were able to identify the co-circulation of two different dengue serotypes (DENV1 and DENV2) as well as the existence of diverse viral lineages within each genotype, suggesting that multiple introduction events of different viral strains occurred in the region. By integrating epidemiological data, our findings unveiled temporal fluctuations in the relative abundance of different serotypes throughout various epidemic seasons, highlighting the complex and changing dynamics of DENV transmission throughout time. These findings demonstrate the value of ongoing surveillance activities in tracking viral transmission patterns, monitoring viral evolution, and informing public health actions.

NAVIO (NAVEGAÇÃO AMPLIADA PARA VIGILÂNCIA INTENSIVA E OTIMIZADA - Expanded Navigation for Intensive and Optimized Surveillance (From the Consortium CLIMADE: http://climade.health).

Luiz Carlos Alcantara, Marta Giovanetti, Crhistinne Cavalheiro, Maymone Gonçalves, Tulio de Oliveira, Edward Holmes, Jose Lourenco

Viral infectious diseases represent a major global public health problem, with spread and emergence associated with several factors, among which environmental and climate change have been increasingly correlated. To mitigate the possible impacts of these changes on the emergence of new outbreaks and to respond actively and rapidly, it becomes crucial to expand active pathogen surveillance from a mobile and multidisciplinary (human-environment-animals) approach. In the Pantanal, many riverside communities live under the effects of environmental imbalance caused by biome degradation, reduced biodiversity, and increased fires, which favours the circulation of pathogenic organisms in populations in situations of environmental vulnerability. However, few studies are reported about the introduction, prevalence and spread of viral infectious agents in this region. Therefore, the project aims to monitor viral pathogens in Pantanal riverine communities in the states of Mato Grosso and Mato Grosso do Sul and to determine the previous exposure of resident individuals to these pathogens. For the realization of this project, trips will be made by boat (Figure 8) to five regions of the Pantanal, where biological samples (blood, oropharyngeal secretion,

and faces) will be collected from riverine populations that voluntarily seek the health service during the term of the project, mosquito vectors, faces of domestic animals and waters. With these samples, serology and molecular diagnosis of viral pathogens will be performed, in which positive samples will be followed by sequencing of the complete pathogen-specific genome and other subsequent analyses. With this, the data generated about eco-epidemiology, genomics and seroprevalence, combined with bioinformatics and modelling tools will allow the identification and characterization of viral pathogens circulating in these communities and a better understanding of the impacts caused by these viruses in the scope of public and environmental health.

Figure 8: The NAVIO boat project that includes teams from FIOCRUZ, CERI and University of Sydney who will be sequencing pathogens in the Pantanal

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