

CLIMADE AFRICA WORKING GROUP MEETING MINUTES – WEEK 26

Host: Centre for Epidemic Response and Innovation (CERI)

Date: October 17, 2023

Time: 12:00 – 13:00 p.m. (SAST)

Facilitators: Dr Monika Moir and Dr Houriiyah Tegally

Attendance/ No. of Participants: 63

Start time: 12:03p.m. (SAST)

Purpose of the meeting

Implementing an Integrated System to Enhance the Surveillance of Emerging and Reemerging Viral Threats.

Agenda Items

1. Welcome
2. Presentation by Dr. Marta Giovanetti from Fundação Oswaldo Cruz, Brazil on 'Implementing an Integrated System to Enhance the Surveillance of Emerging and Reemerging Viral Threats Across the Americas'.
3. Discussion and feedback

Discussion points and questions

- Welcome by Dr Monika Moir
- Request to fill in the google form for participation in the COP28 report, links were shared in the meeting chat (google form: <https://forms.gle/vDuwQdmykLmmAw2q9> and link to the CLIMADE health COP28 report: <https://climade.health/2023/09/29/cop28-climate-amplified-diseases-and-epidemics-report/>)
-
- Dr. Marta Giovanetti from Fundação Oswaldo Cruz, Brazil presented and provided insight into Implementing an Integrated System to Enhance the Surveillance of Emerging and Reemerging Viral Threats Across the Americas

- The presentation highlighted the following topics and research:
- Mosquito Habitat- current and projected. The projected habitats are based on the worst-case climate change scenario.
- Responding to emerging and reemerging outbreaks and circulating pathogens
- Responding with science in real-time
 - o Sample Collection
 - o Molecular Screening
 - o Whole genome sequencing
 - o Phylogenetic inference
 - o Mutational pattern profile
 - o Epidemiological Modeling
- Sequencing protocols
 - o Targeted sequencing – Multiplex tiling PCR
 - o Untargeted sequencing – RNA metagenomics
- 54 Zika virus genomes obtained in Northeastern Brazil (road trip)
- Genomic and epidemiological surveillance of Zika virus in Amazon region
- The use of phylogenetic to describe the spread and transmission dynamics of Zika.
- The spread of Zika in the Midwest of Brazil
- Genetic characterization of Zika in different bodily fluids of a newborn with severe congenital syndrome
- Dengue Virus (DENV) Monitoring
- The replacement of different DENV serotypes over time across different Brazilian regions
- Portable sequencing in the field and classroom: a retrospective examination of circulating DENV1 and DENV2 in Brazil
- Reconstructing the transmission dynamics of DENV
- Emergence of DENV serotype 2 cosmopolitan genotypes in Brazil
- Whole genome sequencing (WGS) of DENV cosmopolitan genotype in Brazil, Paraguay, Uruguay, and Peru.
- Understanding the different genotypes and monitoring
- DENV1 -V and DENV 2 – III more than 1000 genomes generated.
- Chikungunya Monitoring
- Increased interregional virus exchange and nucleotide diversity outlined the expansion of CHIKV ECSA lineage in Brazil.

- 2 Clades with lineage specific mutations
 - Increased C > T substitutions
- Yellow Fever Monitoring
- Genomic epidemiology sheds light on the recent spatio-temporal dynamics of Yellow Fever Virus and spatial corridor that fueled its ongoing emergence in Brazil.
 - Cases in non-human primates
 - The presences of 3 different clades
 - Likely source of the outbreak
- Enhancing the monitoring across borders
- Sharing expertise and whole genome sequence
- Chikungunya in Paraguay in early 2023
 - Using genomic and epidemiological data to understand the outbreak.
 - >175 genomes generated.
 - ECSA genotype
 - Detection of 2 synonymous mutations within novel strain in NSP3 and NSP4 gene.
- Retrospective spatio-temporal dynamics of DENV 1, 2 and 4 in Paraguay
- Identifying BR-4 in Paraguay
- The first CHIKV genomes in Uruguay and Argentina
- Tracing CHIKV evolution in Argentina: shifting from Asian to ECSA using whole genome sequencing.
- Unlocking the Dominican Republic's viral Universe: expanding Genomic Surveillance Beyond SARS-CoV-2
 - 29 DENV 2 and 56 DENV 3 -III whole genomes
 - Transmission was associated with regions with high viral suitability.
- Strengthening of surveillance all across Americas and over borders.
- Integrated training
 - Data sharing
 - Real-time sequencing
 - Sample handling
 - Phylogenetics
 - BEAST
 - Case study of sequencing
 - Lab-in-suitcase
 - Nexstrain

- Concluding points
 - o Half of known pathogen outbreaks are expected to increase due to global warming.
 - o Brazil and Latin America was hit by multiple, concurrent viral epidemics.
 - o Need to increase surveillance across borders for early detection and respond to outbreaks and epidemics.
- Cross country collaboration
 - o Involved in on-site genomic surveillance.
 - o Strengthen local infrastructure.
 - o Lab-in-suitcase approach
- Consequences of climate change and main viruses of concern
- DENV 3 – III and CHIKV co-infection – rare sporadic cases

Adjournment and Closing points.

1. Dr Monika Moir thanked Dr Marth and Prof Luiz Alantara for sharing the arbovirus sequencing protocols. The meeting was adjourned at 12:54 p.m. (SAST).

Next Meeting

To be confirmed by email.

Submitted by: Yajna Ramphal

Approved By: Monika Moir