

## CLIMADE AFRICA WORKING GROUP MEETING MINUTES – MEETING 4 (April)

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**Host:** Centre for Epidemic Response and Innovation (CERI)

**Date:** April 30, 2024

**Time:** 12:00 – 13:00 p.m. (SAST)

**Facilitators:** Dr Houriiyah Tegally and Dr Monika Moir

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**Attendance/ No. of Participants: 45**

**Start time:** 12:00 p.m. (SAST)

### **Purpose of the meeting**

The Epidemiology of Dengue Virus in Ethiopia.

### Agenda Items

1. Welcome
2. Presentation Adugna Abera on The Epidemiology of Dengue Virus in Ethiopia.
3. Discussion and feedback

### **Presentation Overview**

- Welcome by Dr Houriiyah Tegally
- Adugna Abera, a Researcher at the Ethiopian Public Health Institute and PhD student at Addis Ababa University discussed the epidemiology of Dengue in Ethiopia.
- Background on Dengue in the Region
  - o The dengue (DENV) virus causes Dengue Fever and is transmitted through the *Aedes mosquito* species.
  - o DENV genome is ~ 11,000 bp.
  - o Caused by four closely related serotypes.
- Epidemiology of Dengue in the WHO African Region.
  - o 15 countries have reported cases/outbreaks.
  - o All four serotypes circulate in Africa.

- Dengue Fever in Ethiopia
  - o First reported in Dire Dawa city and affected 9, 441 individuals.
  - o The second outbreak occurred in Somale Godey Town and Afar Region in 2014 and 2015
  - o Since 2015, there has been an increase in febrile illnesses.
  - o Serological evidence in each region
- Recent Outbreaks (2023 – 2024)
  - o A total of 26,512 cases and 21 deaths in all 5 regions from 2 -24 April 2024.
  - o 68% of cases were reported in Dire Dawa and 33.75% from the Afar Region.
- Genomic Characterization
- Study sites and patient recruitment.
- Results
  - o Two new co-circulating serotypes (DENV1 and DENV3) were isolated from Dire Dawa.
  - o Previous outbreaks (2013) in Dire Dawa were due to serotype 2.
  - o Only serotype 3 was isolated from the Afar Region.
- Sequencing progress
  - o 55 samples were sequenced (20 from Afar and 35 from Dire Dawa)
  - o Successfully sequenced 33 near whole genomes (5 DENV1 III\_A from Dire Dawa and 28 DENV3 III\_B from Afar Region)
  - o 18 genomes were submitted to GISAID.
  - o Phylogenetic analysis

### **Questions and discussion points**

Molalengne Bitew – The strains and genotypes are coming from Italy or Asia, how valid are the results since Ethiopia does not do routine surveillance?

Rob – Why did low CT values not produce high-coverage genomes? This was likely due to improper storage conditions. The difference between storage conditions in Afar and Dire Dawa regions affected the integrity of the samples as Dire Dawa samples were storage at -20 C.

Dr Monika Moir –What is the distribution of cases between males and females? Is there a behavioral influence?

Francine Berlangue – Was there an association between pathogeneses?

Gambiella – Do you plan to expand sequencing soon?

Rosemary – There was confusion between clinical symptoms from the current outbreak and the 2013 outbreak, are there plans to create new guidelines for Dengue?

Girma – How did you collect serum during sample collection?

Gaspar – Are there intervention practices in Ethiopia during high transmission seasons?

### **Adjournment and Closing points.**

1. Acknowledgment to Dr Houriiyah Tegally and Lucious for sequencing and analysing the DENV samples from Ethiopia.
2. The meeting was adjourned at 13.04 p.m. (SAST).
3. Climate meeting will be held every last Tuesday of the month.

### **Next Meeting**

Will be confirmed via email for June 4, 2024, at 12.00 p.m. (SAST).

**Submitted by:** Yajna Ramphal

**Approved By:** Monika Moir