CLIMADE AFRICA WORKING GROUP MEETING MINUTES – WEEK 10

Host: Centre for Epidemic Response and Innovation (CERI)

Date: May 2, 2023

Time: 12:00 – 13:00 p.m. (SAST)

Facilitators: Prof Tulio de Oliveira, Dr Eduan Wilkinson, Dr Houriiyah Tegally,

Attendance/ No. of Participants: 65

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

Purpose of the meeting

Rift Valley Fever virus (RVFV) typing tools.

Agenda Items

1. Welcome and update by Dr Houriiyah Tegally and Prof Tulio de Oliveira.
2. Dr John Juma – Tutorial on how to use RVFV typing tools on web-based Genome Detective and Command line based Nextflow language.

Discussion points and questions

1. Dr John Juma facilitated and explained the step-by-step process on how to use RVFV typing tools on Genome Detective and NextFlow using the S, M and L segments of the RVFV**.**
2. Tutorial and documentations can be found: https://github.com/ajodeh-juma/rvfv-typing-tutorial/tree/master
3. Genome Detective uses phylogenetic lineage assignment with a bootstrap support value of >70.
4. Most assignment uses the M segment as this region is most commonly sequenced.
5. RVFV has a stable genome.
6. The method was validated with a dataset comprising of 234 samples using both partial and whole genome sequences, some lineages only have one sequence.

7. Publication on the RVFV typing tools:
   https://bmcgenomics.biomedcentral.com/articles/10.1186/s12864-022-08764-6

Adjournment and Closing points.

1. The development of tools such as the RVFV typing tool by African scientists are important steps in accelerating epidemic response and genomics in the continent.
2. Dr Houriiyah Tegally and Prof Tulio de Oliveira adjourned the meeting at 13:02 p.m. (SAST).

Next Meeting

Tuesday, May 9, 2023, at 12:00 – 13:00 p.m. (SAST)

Submitted by: Yajna Ramphal

Approved By: Monika Moir