Release of Complete CHIKV Coding Sequence from Réunion Island 2024 (GenBank: PV035814)

We are pleased to announce the public release of one complete coding sequence (CDS) representative of the virus lineage associated with the re-emergence of chikungunya virus (CHIKV) on Réunion Island since 2024, now available under GenBank accession number PV035814. This sequence was obtained from one of the first confirmed cases in September 2024.

Following the major 2005–2006 outbreak, which affected 38% of the island's population, CHIKV circulation remained undetected for years. In 2024, CHIKV reemerged and is currently causing a new epidemic on the island.

Sequencing was performed using the Oxford Nanopore MinION platform, with an in-house amplicon protocol previously developed for dengue virus (Frumence et al., 2024). Phylogenetic analysis indicated that the CHIKV strain detected belongs to a previously described clade of the East-Central South African (ECSA) genotype, which includes sequences from the Central African region, as well as a strain from the 2017 autochthonous chikungunya outbreak in France.

Key molecular findings:

- **E1-A226V** mutation: associated with enhanced transmission by *Aedes albopictus*
- **E2-L210Q** and **E2-I211T** substitutions: linked to increased infectivity in *Ae. albopictus*
- Closest related strain: **Cameroon 2018 (MT666073)**, showing >99.67% nucleotide identity, 37 SNPs, and 9 amino acid differences (8 in the non-structural polyprotein, 1 in the structural polyprotein)

Genomic surveillance is ongoing at the associated Arbovirus National Reference Center (NRC) of Réunion University Hospital, showing that the same virus lineage continues to circulate locally.

GenBank accession: PV035814
Sequence type: Complete viral coding sequence (CDS)
Collection location: Réunion Island
Collection date: September 2024
Sequencing platform: Oxford Nanopore MinION
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