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Genomic surveillance of Dengue virus in Central Côte d’Ivoire: Insight from the 2024 outbreak

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Dengue virus (DENV) is a significant public health concern in Côte d’Ivoire, reflecting broader trends across West Africa. Despite the clear public health burden, the true extent and diversity of DENV strains circulating in Côte d’Ivoire remain poorly characterized due to insufficient diagnostic capacity and a lack of genomic data. Understanding the genomic diversity of Dengue virus is crucial for public health interventions and epidemic preparedness.

As part of the Public Health Actions for Côte d’Ivoire (PAcCI) project, operating at the Centre Hospitalier Universitaire (CHU) de Bouaké in the center of the country, we investigate the genetic diversity of circulating Dengue virus strains in Central Côte d’Ivoire with the aim of tracing introductions and identifying mutations potentially associated with transmission or pathogenicity.

Between May and August 2024, blood samples were collected from 172 individuals with suspected dengue infection residing in Bouaké and its surrounding areas. Real time PCR screening identified 40 positives cases. Whole-genome sequencing of 37 positive samples was performed using an amplicon-based approach with a pan-serotype primer scheme, implemented on the Oxford Nanopores Technology Minion Mk1b platform. Sequencing libraries were prepared using a native barcoding ligation kit. Basecalling and demultiplexing were performed using the Dorado software. Genome reconstruction was conducted using a customized Nextflow workflow incorporating the ARTIC pipeline. Laboratory analyses were conducted directly at the CHU Bouaké’ s laboratory. Phylogenetic analyses were conducted to characterize serotypes, genotypes and viral lineages.

Among sequenced samples, Dengue virus serotype 3 (DENV1) was detected in 50%, DENV2 in 25% and DENV1 in 25 % of cases. There was no detection of Dengue virus serotype 4 (DENV4). A total of 32 samples yielded eight DENV1, eight DENV2 and sixteen DENV3 partial genomes (genome coverage ranging 57-98%). Further analyses including multiple sequence alignment and phylogenetic inference are currently underway to assess genotype distribution, determine the phylogenetic placement of Ivorian strains within the context of global DENV diversity, and investigate evidence for new introductions, local evolution, as well as the presence of unique or rare mutations.

This pilot study is the first of its kind to set up a sequencing workflow for whole genome amplification of dengue virus in an Ivorian laboratory. The preliminary findings underscore a multi-serotype circulation of Dengue virus during the 2024 outbreak in Central Côte d’Ivoire. This study provides a critical foundation for the implementation and continuous genomic surveillance in Côte d’Ivoire to track dengue virus circulation dynamics for an efficient epidemic preparedness and response.

Keywords

DENV diversity, Genomic surveillance, Côte d’Ivoire.

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No, I am not a Junior Scientist.

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