

Genomic characterization of dengue circulation in Togo, 2024

Issaka Maman

mamanissaka@yahoo.fr

Institut National d'Hygiène <https://orcid.org/0000-0002-6465-5116>

Afiwa Halatoko

Institut National d'Hygiène

Carla Mavian

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa; Emerging Pathogens Institute, Department of Pa

Monika Moir

Stellenbosch University <https://orcid.org/0000-0003-1095-1910>

Eduan Wilkinson

Stellenbosch University <https://orcid.org/0000-0002-2503-9441>

Lavanya Singh

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa

Graeme Dor

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa <https://orcid.org/0000-0001-9036-9933>

Jenicca Poongavanan

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa

Yajna Ramphal

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking, Stellenbosch University, Stellenbosch, South Africa

Eninam Kouma

Institut National d'Hygiène, Lomé, Togo

Christelle Nikiema

Division de la surveillance intégrée des urgences et réponse, Ministère de la Santé et de l'Hygiène publique, Lomé, Togo

Ali Napo

Ministère de l'environnement et des ressources forestières, Lomé, Togo

TJ Sanko

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Bertha Baye

(7) KwaZulu-Natal Research Innovation and Sequencing Platform (KRISP), Nelson R Mandela School of
Medicine, University of KwaZulu-Natal, Durban, South Africa

Lucious Chabuka

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Tebogo Ramakutoane

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Velda Wentzel

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Nondumiso Zakwe

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Cheryl Baxter

Centre for Epidemic Response and Innovation (CERI), Stellenbosch University <https://orcid.org/0000-0002-6033-7655>

Tulio De Oliveira

KwaZulu-Natal Research Innovation and Sequencing Platform, Nelson R Mandela School of Medicine,
University of KwaZulu-Natal <https://orcid.org/0000-0002-3027-5254>

Houriyyah Tegally

Stellenbosch University

Derek Tshiabuila

Centre for Epidemic Response and Innovation (CERI), School of Data Science and Computational
Thinking, Stellenbosch University

Stepfan De Villiers

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Kerwin Liedeman

Centre for Epidemic Response and Innovation, School for Data Science and Computational Thinking,
Stellenbosch University, Stellenbosch, South Africa

Richard Lessells

University of KwaZulu-Natal (UKZN) <https://orcid.org/0000-0003-0926-710X>

Fortune A. Salah

Institut National d'Hygiène, national public health laboratory, WHO National Influenza Reference Center,
26 QAD, Rue Nangbeto, 1BP1396, Lomé, Togo

Maleki Assih

Institut National d'Hygiène, national public health laboratory, WHO National Influenza Reference Center,
26 QAD, Rue Nangbeto, 1BP1396, Lomé, Togo

Micheline H. Tettekpoe

Institut National d'Hygiène, national public health laboratory, WHO National Influenza Reference Center,
26 QAD, Rue Nangbeto, 1BP1396, Lomé, Togo

Tchao G. Gnama

Institut National d'Hygiène, national public health laboratory, WHO National Influenza Reference Center,
26 QAD, Rue Nangbeto, 1BP1396, Lomé, Togo

Zoulkarneiri Issa

Institut National d'Hygiène, national public health laboratory, WHO National Influenza Reference Center,
26 QAD, Rue Nangbeto, 1BP1396, Lomé, Togo

Yahaya Sylla

Institut Pasteur de Côte d'Ivoire

Ahou Melissa Koffi

Institut Pasteur de Côte d'Ivoire

Koffi M. Ahadji-Dabla

University of Lomé, 1BP: 1515, Lomé1, Togo

Tchadjobo Tchacondo

University of Lomé, 1BP: 1515, Lomé1, Togo

Article**Keywords:**

Posted Date: September 14th, 2026

DOI: <https://doi.org/10.21203/rs.3.rs-10559267/v1>

License:  This work is licensed under a Creative Commons Attribution 4.0 International License.

[Read Full License](#)

Additional Declarations: There is **NO** Competing Interest.

Abstract

Togo experienced its first nationally reported dengue outbreak in 2024 amid a broader resurgence of dengue across Africa. Data on serotype distribution, genomic diversity, and transmission dynamics in the region were limited. Here, we integrated epidemiological, genomic, and environmental analyses to characterize the origins and spread of dengue transmission in Togo. Of 475 samples tested, 213 (44.8%) were dengue virus (DENV) positive by PCR. Of these, 190 samples ($Ct < 35$) were serotyped and 159 of those successfully serotyped underwent whole-genome sequencing. Sequencing generated one DENV-3 genome and 129 DENV-1 genomes, predominantly of genotype III lineage A.2. Our phylogenetic results suggest importation of this lineage from Tanzania into West Africa and Togo, linked to a large Tanzanian outbreak in 2019. Time-scaled phylogenies indicated the timing of introduction likely goes back early 2020, with cryptic circulation preceding the detected outbreak. Bayesian phylogeographic reconstruction support the inference of one common introduction into Togo/West-Africa and identified short- and long-range viral movements nationally and regionally. We conclude that 2024 dengue epidemic in Togo resulted from a single introduction followed by extensive local and regional spread facilitated by favourable environmental conditions and human mobility. In addition, this study doubles the number of available West African DENV-1-III A.2 genomes and highlights significant gaps in regional genomic surveillance that present challenges in understanding transmission pathways. Integrated, high-resolution genomic and epidemiological monitoring for dengue is essential for national and regional preparedness, readiness and response.

Introduction

Dengue fever is one of the most widespread arboviral diseases globally, predominantly affecting tropical and subtropical regions. According to the WHO, in 2024, approximately 13 million dengue cases were reported worldwide, including 42,000 severe cases and more than 8,700 deaths, with active transmission documented in 90 countries (1). In December 2023, the WHO assigned the highest emergency level (grade 3) to the global rise in dengue cases, and in June 2024, classified dengue orthoflavivirus as a priority pathogen in all six WHO regions (1).

In Africa, dengue is increasingly expanding, although frequently underestimated due to underreporting and limited access to specific diagnostic tests. In the first four months of 2024, 13 countries in the WHO African region reported a total of 32,925 dengue cases (14,095 confirmed) and 57 deaths (case fatality rate: 0.11%). Burkina Faso with 17,098 cases (73% of all cases), Mauritius with 7,177 cases, and Mali with 3,231 cases, were among the most affected (2, 3). These outbreaks illustrate growing active regional transmission.

In Togo, the Ministry of Health (MoH) officially declared the country's first reported dengue fever outbreak on 27 June 2024. Sporadic dengue cases were reported between January and April, followed by a steady increase that peaked at 273 weekly cases in early July. As of July 2024, 823 cases had been reported nationwide with 395 confirmed and 428 suspected (unpublished MoH data in Togo) (4).

Despite the large number of suspected and confirmed dengue cases during this outbreak, data on circulating serotypes and viral genomic diversity were limited in Togo. Through the Climate Amplified Diseases and Epidemics (CLIMADE) consortium collaboration between the Institut National d'Hygiène, the WHO National Influenza Reference Center in Togo, and the Centre for Epidemic Response and Innovation (CERI) in South Africa, we generated whole genome sequences from 190 febrile samples, representing strains circulating in five regions and eight districts in Togo between May and August 2024. This is the first genomic epidemiology characterization of DENV circulation in the country. We also conducted phylogenetic analysis to reconstruct the spatial and temporal patterns of dengue transmission in the country.

Materials and methods

Sampling and Data Collection

Through routine public health surveillance of diseases with epidemic potential in Togo, samples from individuals with suspected or probable dengue (5) are sent for testing to the INH together with a standardized disease notification form. This form includes the patient's sociodemographic information, clinical signs and symptoms, type of samples collected and laboratory results. The patient notification form is completed by the surveillance focal points in each district and then sent together with the sample to the reference national public health laboratory at the Institut national d'Hygiène (INH). For this study, we retrieved all samples with collection date between May and September 2024. Samples were obtained from all health districts nationwide. At the Institut National d'Hygiène (National public health laboratory), serum or plasma was separated by centrifugation and subsequently processed for laboratory testing.

This study is part of the surveillance of diseases with epidemic potential in Togo. Therefore, it was not necessary to obtain authorization from the ethics committee. However, the national public health laboratory approved this study and authorized the use of data collected.

RNA extraction and PCR testing

Viral RNA was extracted from all serum or plasma samples using the QIAmp Viral RNA Kit (Qiagen) following the manufacturer's instructions. All RNA extracts collected were stored at -80°C. The Novaplex™ Tropical fever virus Assay, a real-time PCR assay, was used for pathogen detection. A sample was considered positive for DENV if it presented with an amplification curve with a cycle threshold (Ct) value below 35. Following initial PCR testing, 190 dengue-positives samples with a Ct < 35, were selected for serotyping and genome sequencing. These included 190 febrile samples collected between May and September 2024 from four regions (Kara, Grand Lomé, Plateaux, Savanes).

Serotyping and sequencing were carried out with the technical support from CERI at Stellenbosch University in South Africa, through the CLIMADE consortium (climade.health).

Dengue Serotyping

We tested all DENV PCR positive samples for the four dengue serotypes (DENV-1, DENV-2, DENV-3, DENV-4). A multiplex RT-qPCR was performed by using the genesig® advanced kit with primers and fluorescent probes. A sample was considered positive for any dengue serotype with a Ct < 35.

Dengue Sequencing

RNA from samples with confirmed serotypes and a Ct < 30 on the serotype-specific PCR was treated with DNase (ezDNase, Invitrogen) to remove residual genomic DNA. RNA reverse transcription and cDNA synthesis were performed with simultaneous target enrichment using two primer pools (Pool 1 and Pool 2). An initial quality control was performed on Pools 1 and 2 of each sample using the Qubit to verify successful amplification. Pools 1 and 2 were then combined, and the resulting double-stranded cDNA was enzymatically fragmented (EBLTS) and converted into Illumina-compatible dual-indexed libraries using the Covid-Seq kit. A second quality control step was performed using the Qubit and the D1000 ScreenTape with the TapeStation 4150 (Agilent Technologies, USA). Libraries were subsequently pooled, and the final library concentration was measured by Qubit or qPCR with the Takara Library Quantification kit (third quality control). The libraries were normalized to 4 nM to ensure balanced loading during sequencing. Following dilution and denaturation according to the "Denature and Dilute Libraries for the MiSeq system" protocol, the final library was sequenced on the Illumina MiSeq platform (2 × 150 cycles).

Bioinformatic analysis

Fastq files were obtained from the sequencer, which were then analyzed with Chan Zuckerberg ID (CZ ID, <https://czid.org/>) to carry out the quality control and to obtain the FASTA consensus sequence files. Genotype, clades and lineages were determined using Nextclade (6)

Epidemiological analysis (Rt estimation)

The time-varying effective reproduction number (Rt) was estimated using confirmed case counts, aggregated weekly and at the national level, using the estimate_R_agg function implemented in the EpiEstim R Package (v.2.4) (7). A parametric serial interval distribution with a mean of 17 days and a standard deviation of 8 days was specified based on published estimates for dengue virus transmission (8, 9). The full set of model outputs, including Rt trajectories and uncertainty intervals, is provided in the Supplementary information (Figure S1-S5).

Transmission potential

We obtained monthly spatiotemporal estimates of dengue transmission suitability (the P index) for 2023 from a published study (10). The P index reflects the potential number of human infections generated by

a single adult female mosquito over its lifetime in a fully susceptible population, integrating climate-driven effects on mosquito infectiousness and reproduction. It is derived from local temperature and humidity time series at a $0.25^\circ \times 0.25^\circ$ spatial resolution. P values greater than one indicates conditions that favour epidemic growth.

Phylogenetic analysis

We retrieved DENV reference sequence datasets from the GISAID Epi-Arbo database corresponding to the DENV1 genotype III lineage A. We subjected the retrieved sequences to initial quality control by removing unverified sequences and incomplete records (i.e., geographic location and sampling dates). The final dataset used for phylogenetic analyses consisted of 90 sequences generated from Togo (1 of the 91 near-whole-genomes did not have a precise date of sampling) as well as 985 publicly available sequences of DENV1 genotype III major lineage A, for a total dataset of 1075 sequences. We aligned the DENV1 datasets from this study with the DENV1 serotype reference genome (GenBank accession no. NC_001477.1) by using the Nextalign version 1.3.0 alignment tool (11).

We generated a maximum-likelihood trees by using IQ-TREE version 2.2.2.2 and 1,000 bootstraps (12). Using ModelFinder in IQ-TREE, we selected the best nucleotide substitution model according to Bayesian information criterion. We evaluated the molecular clock signal using TempEst v1.5.3 (13) and removed potential outliers ($n = 32$) that violated the molecular clock assumption before inferring a time-scaled tree using TreeTime version 0.10.0 (14). We used a molecular clock rate of 7.22×10^{-4} nucleotide substitutions per site per year, determined by the clock function in TreeTime.

Bayesian Phylogeography

A time-calibrated Bayesian phylogenetic tree was constructed for DENV1 genotype III lineage A.2 and the associated effective population size was estimated using public DENV1 sequences available for West Africa, Tanzania and China ($n = 483$). Prior to this, temporal signal and molecular clock analysis was performed using Tempest (15). BEAST X was used along with the BEAGLE library v3.2.0 to improve computational speed (16). A relaxed clock model was applied for all analyses along with the HKY + G+I nucleotide substitution model. A skygrid (17) coalescent growth model with 28 grid points over 6.5 years prior to the most recent sampling date was used for effective population size calculations. We then performed a continuous phylogeography with relaxed random walk with the biggest local clade of the A.2 lineage in Togo to estimate the spatiotemporal dispersal within the country. All analyses were performed in two independent runs of 400 million iterations each. For the continuous phylogeography analysis, we ran the MCMC chain for 1 billion iterations. Convergence of MCMC chains was checked using Tracer v.1.7 (12) (ESS values for all estimated parameters > 200) and 10% of initial chains was discarded as burn-in. Post-burn in samples were pooled to summarize parameter estimates using LogCombiner and TreeAnnotator (18), including posterior probability of each parameter and maximum clade credibility (MCC) trees.

Results and Discussions

The 2024 dengue epidemic in Togo unfolded against a backdrop of widespread regional transmission across West Africa, with Togo reporting one of the highest burdens on the continent (Fig. 1A). As of September 2024, dengue transmission was recorded in Burkina Faso (53,756 cases; 68 deaths), Mali (5,944; 7), and Togo (2,827; 3) (20) (Fig. 1A). National epidemic trends showed a rapid rise in confirmed dengue cases beginning in early May 2024, peaking in mid-June, followed by a gradual decline through October. Correspondingly, national $R(t)$ estimates exceeded 4 during the early expansion phase before falling below 1 as transmission slowed (Fig. 1B, S1). A regional breakdown of daily incidence revealed pronounced spatial heterogeneity, with Grand Lomé and Maritime, the most densely populated regions in the south of the country, experiencing the earliest and largest surge, while Kara and Savanes in the north showed later but distinct peaks (**Figure S2**). Regional $R(t)$ analyses further highlighted these differences: in Grand Lomé, $R(t)$ rose above 6 at the start of the epidemic before rapidly decreasing (**Figure S3**); in Savanes, transmission intensified later, with $R(t)$ approaching 10 in August before subsiding (**Figure S4**); and in Kara, a moderate early peak was followed by a second period of elevated transmission in late October (**Figure S5**).

The outbreak was concentrated in the Grand Lomé region, which accounted for 773 (27,3%) of 2827 suspected cases (Fig. 1) detected nationwide. Three deaths occurred among confirmed cases, all within Grand Lomé. From May to September 2024, 213 of 475 RT-qPCR tests (44.8%) were positive for DENV. Among confirmed cases, 67.4% occurred in individuals aged 15–44 years, with a male-to-female sex ratio of 1.33 (Figure S6). The 190 DENV-positive samples with Ct values < 35 selected for serotyping were collected from four regions and eight districts of Togo with minimum Ct value of 14.9. Of these, 158 (83.1%) samples were serotyped as DENV-1, one (0.5%) as DENV-3, and 31 (16.3%) were negative on the serotype-specific PCR. We proceeded to sequence all 159 typeable samples and obtained 129 DENV-1 genomes, 91 (70.5%) of which had coverage > 70%. Of the DENV-1 genomes, 125 genomes were successfully genotyped as lineage III_A.2. One genome corresponded to DENV-3 genotype III_B.2. Twenty samples failed genome assembly due to insufficient reads, all associated with higher Ct values.

In Togo, Lomé area had the highest cases from which we obtained a total of 99 specimens sampled for sequencing collected between May 16 and August 26, 2024, corresponding with the peak of the outbreak that occurred in this area between June and September 2024 (Fig. 1B). District-level curves revealed substantial spatial heterogeneity, with Grand Lomé experiencing the earliest and largest surge, followed by more modest waves in Kara, Plateaux, and Savane (Fig. 1C). We sampled 73 specimens from the region of Kara for sequencing and four from Plateau where the outbreak peaked between July and August 2024 (Fig. 1C). Lastly, we obtained nine genomes from the region of Savanes which experienced the peak of the outbreak later as compared to the rest of Togo, during the month of September 2024 (Fig. 1C). Specimen sampling covered all major affected districts and captured the full temporal range of the epidemic, with the highest density of sequences originating from Lomé, the area reporting the most cases (Fig. 1D).

The estimated average transmission potential for DENV in 2023 in Togo ranges between 1.2 and 2.2, with the highest year mean estimated in the north of the country in the regions of Savanes, Kara Maritime and Grand Lomé (Fig. 1E). These environmental modelling estimates showed that transmission potential was consistently elevated throughout 2024, with seasonal peaks aligned with the onset of the epidemic reaching maximum values between May and October, thus corresponding to the peak of the epidemic in 2024, and sustained suitability across densely populated southern districts (Fig. 1F). Monthly maps from 2023 also revealed that high transmission suitability emerged months before the first detected cases, and transmission potential shifts spatially during the year, suggesting that ecological conditions were primed for rapid amplification nationwide once the virus was introduced (Fig. 1F). These observations are consistent with data from a study conducted in Togo in 2022–2023 (21), which showed that the larval density of the dengue vector followed a marked seasonal pattern, with a peak during the rainy season between May and July and a minimum density during the dry season (20). This explains the increased risk of dengue virus transmission during the rainy season.

Our samples cluster with Tanzanian genomes from 2017–2019 within DENV-1 (genotype III, lineage A.2), with all newly generated genomes from Togo forming a single, well-supported A.2 subclade with basal Tanzanian genomes (Fig. 2A). Although the timed maximum likelihood tree demonstrates a topology suggesting multiple introductions into Togo, the nodes separating the Togo clustering are not well supported with bootstrap values on those nodes being as low as 7 (**Supplementary Figure S9**). The phylogeographic time-scaled MCC tree indicates that the lineage circulating in Togo belongs to a distinct subclade of lineage A.2 (Fig. 2B) and that the 2024 outbreak resulted from a single introduction into Togo, with high posterior support at the relevant nodes branching from the Tanzania cluster to Togo ((**Supplementary Figure S10**). Given sparse sampling in certain West African countries, the inferred introduction from Tanzania is likely better interpreted as a common introduction into the whole region of West Africa, rather than directly into Togo, although the available evidence points to Togo given the extensive dataset of the current study. The introduction is inferred to have occurred as early as February 2020 (95% HPD: February–October 2020). Following this initial introduction into West Africa, the virus diversified into four independent clades. Clade A emerged in April 2021 (95% HPD: July 2020–February 2022) and clade D in November 2020 (95% HPD: March 2020–August 2021), both likely stemming from this first introduction (Fig. 2B). Clade C, related to the circulation of DENV-1 circulating in Burkina Faso emerged in June 2022 (95% HPD: August 2021–March 2023), followed by the emergence of clade B in February 2023 (95% HPD: April 2022–October 2023), linked to strains circulating in Benin (Fig. 2B). This clade evolved along a strong molecular clock (**Supplementary Figure S8**).

Given the topology of the MCC tree, where clades A and D form monophyletic groups with relatively deep internal branches, we cannot exclude the possibility that these clades represent additional re-introductions into Togo from unsampled locations in the region. This interpretation remains tentative, as the observed clustering could also arise from limited sampling density or incomplete geographic coverage, underscoring the need for broader and more systematic genomic surveillance across the region

Our analysis also highlighted the origin of the contemporaneous outbreak in Côte d'Ivoire (Fig. 2B). Most of the sampled outbreak forms a large monophyletic cluster which appears to be linked to an introduction from Togo, and one sequence shows a likely connection to Tanzania directly. Population-dynamic inference showed a rapid increase in the effective viral population size of the lineage A.2 beginning in late 2022 and accelerating through 2024, consistent with the observed epidemiological surge (Fig. 2C). Phylogeographic reconstruction revealed early viral movements across Togo prior to the main epidemic period, followed by markedly more extensive dispersal during peak transmission (Fig. 2D). Although dispersal events are concentrated in the most populous regions, geocoding limitations cause the plotted positions of these events to appear slightly displaced from their actual locations.

Conclusion

Our analyses provide fine-scale resolution of the temporal and spatial heterogeneity underlying the nationwide dengue epidemic in Togo, demonstrating that local outbreak dynamics were asynchronous across the country. Genomic sampling for this DENV outbreak in Togo was comprehensive, covering the full epidemic peak across all districts. Lomé, one of the most affected areas, contributed the highest number of cases and genome sequences, reflecting its central role in national transmission. This sequencing effort doubles the number of genomes available for this lineage and helps close important surveillance gaps in Africa. Although substantial gaps remain in West Africa, limiting our ability to fully resolve introduction routes and transmission dynamics, our findings indicate that the population size of this lineage is continuing to grow across the region. The Togo A.2 subclade is closely related to sequences from Tanzania and neighbouring West African countries, indicating a recent introduction into Togo followed by rapid local expansion. This suggests inter-regional spread within the continent from East Africa to West Africa, and then regional circulation and expansion within West Africa. This has been previously documented (REF). However, limited genomic sampling across West Africa during the Benin and Burkina Faso outbreaks of 2022–2023, combined with the five-year gap since the 2017 Tanzanian outbreak, makes it highly probable that intermediate locations, where the virus circulated undetected, remain unsampled. The strong temporal signal and increasing effective population size observed for lineage A.2 further support ongoing cryptic circulation in the region prior to its detection in Togo.

Environmental modelling showed that transmission suitability across Togo remained high throughout 2023–2024, suggesting that ecological conditions were primed for establishment once the virus arrived. Phylogeographic analyses identified multiple short- and long-range dispersal events within Togo, with viral movements concentrated along high-density coastal and central transport corridors, linking Lomé to northern districts. These routes overlap with areas of elevated population mobility and favourable climatic conditions for *Aedes* vectors, providing a plausible mechanism for rapid geographic spread. Together, these results reveal a pattern of recent introduction, rapid diversification, and structured spatial dissemination of DENV-1 across Togo, facilitated by both environmental suitability and human mobility networks. Our integrated epidemiological and genomic dataset underscores the importance of

sustained, high-resolution surveillance to detect early introductions and interrupt emerging transmission chains in West Africa.

Declarations

The study protocol was clearly explained to the participants. All patients provided their consent and the participation was voluntary. For children, informed consent was obtained from a parent or legal guardian.

Authors contribution

Conceptualization: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally

Methodology: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally, Eduan Wilkinson, Carla Mavian, Monika Moir, Graeme Dor, TJ Sanko, Bertha C. Baye, Derek Tshiabuila, Lucious Chabuka, Stepfan De Villiers, Tebogo Ramakutoane, Velda Wentzel, Kerwin Liedeman, Nondumiso Sihlobile Zakwe

Investigation: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally, Eduan Wilkinson, Carla Mavian, Monika Moir, Graeme Dor

Formal Analysis: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally, Eduan Wilkinson, Carla Mavian, Monika Moir, Graeme Dor

Resources: Issaka Maman, Ahadji-Dabla, Tchadjobo Tchacondo, Tulio de Oliveira, Cheryl Baxter

Data Curation: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally, Eduan Wilkinson, Carla Mavian, Monika Moir, Graeme Dor, Lucious Chabuka³, Stepfan De Villiers³, Tebogo Ramakutoane³, Velda Wentzel³, Kerwin Liedeman³, Nondumiso Sihlobile Zakwe³,

Writing – Original Draft: Carla Mavian, Graeme Dor, Monika Moir

Writing – Review & Editing: All authors.

Visualization: Houriiyah Tegally, Monika Moir, Graeme Dor

Supervision: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally, Eduan Wilkinson, Carla Mavian, Monika Moir

Project Administration and Funding: Issaka Maman, Afiwa W. Halatoko, Houriiyah Tegally, Eduan Wilkinson, Carla Mavian, Monika Moir, Cheryl Baxter, Tulio de Oliveira.

Data and code availability statement

All DENV near-whole-genomes (>70% coverage) generated and presented in this study are publicly accessible through the GISAID platform (<https://www.gisaid.org/>) at GISAID EPI_SET_260728zs, <https://doi.org/10.55876/gis8.260728zs>. The reference genomes analyzed in this study are also

accessible on GISAID at EPI_SET_260728ak (<https://doi.org/10.55876/gis8.260728ak>). Raw sequencing reads have been deposited on NCBI's Sequence Read Archive (SRA), with the following biorepository ID: PRJNA1231728. Other data for this study are provided in our online repository: https://github.com/CERI-KRISP/DENV_Togo_2024. R code to reproduce the analyses and figures presented in this paper are available at https://github.com/CERI-KRISP/DENV_Togo_2024.

Acknowledgements

We gratefully acknowledge the authors, originating and submitting laboratories of the sequences deposited in GISAID and NCBI databases, which were used in the phylogenetic analyses of this study. We acknowledge that this work is an initiative of the CLIMADE consortium. We thank the Director of the INH for authorizing this study and the collaboration with CERI.

Our gratitude goes to all the focal points for surveillance of diseases with epidemic potential in Togo and to the Togolese population from whom the blood samples were obtained.

Funding statement

This work is an initiative of the Climate Amplified Diseases and Epidemics (CLIMADE) consortium. The Centre for Epidemic Response and Innovation (CERI) is supported in part by grants from the Rockefeller Foundation (HTH 017), the Abbott Pandemic Defense Coalition (APDC), the SAMRC South African mRNA Vaccine Consortium (SAMVAC), the UK's Medical Research Foundation (MRF-RG-ICCH-2022-100069), the Wellcome Trust for the Global.health project (228186/Z/23/Z) and H.T.'s Career Development Award (335374/Z/25/Z), the Novo Nordisk Foundation (NNF24OC0094346), and student support from the SAMRC through its Division of Research Capacity Development under the SAMRC Clinician Researcher Development Programme, funded by the South African National Department of Health (G.D.). Reagents and whole-genome sequencing training were supported by the Health Emergency Preparedness and Response Umbrella Program (HEPR Program) managed by the World Bank Group (TF0B8412). The content and findings reported herein are the sole deduction, view and responsibility of the researcher/s and do not reflect the official position and sentiments of the funding agencies.

References

1. Pan American Health Organization, World Health Organization. Dengue Multi-Country Grade 3 Outbreak [Internet]. [cited 2025 Dec 12]. Available from: <https://www.paho.org/en/topics/dengue/dengue-multi-country-grade-3-outbreak>
2. Patrick GEROME. (2024). *Evolution des épidémies de dengue en Afrique depuis le début novembre 2024 | MesVaccins*.<https://www.mesvaccins.net/web/news/22570-evolution-des-epidemies-de-dengue-en-afrique-depuis-le-debut-novembre-2024>.
3. World Health Organization. Weekly Bulletin on Outbreak and other Emergencies: April 2024. [https://www.who.int/emergencies/disease-outbreak-news/item/2024-DON518#:~:text=Burkina%20Faso%20reported%2072%25%20of,deaths%20\(67%25\)%20in%202024](https://www.who.int/emergencies/disease-outbreak-news/item/2024-DON518#:~:text=Burkina%20Faso%20reported%2072%25%20of,deaths%20(67%25)%20in%202024)

4. World Health Organization. Regional Office for Africa. Weekly Bulletin on Outbreak and other Emergencies: Week 29: 15 - 21 July 2024. . World Health Organization. Regional Office for Africa; 2024.
5. World Health Organization. (2009a). *Dengue guidelines for diagnosis, treatment, prevention and control: New edition*. WHO/HTM/NTD/DEN/2009.1. <https://iris.who.int/handle/10665/44188>
6. Aksamentov I, Roemer C, Hodcroft E, Neher R. Nextclade: clade assignment, mutation calling and quality control for viral genomes. JOSS. 2021 Nov 30;6(67):3773.
7. ash RK, Bhatt S, Cori A, Nouvellet P. Estimating the epidemic reproduction number from temporally aggregated incidence data: A statistical modelling approach and software tool. PLoS Comput Biol. 2023 Aug 28;19(8):e1011439.
8. Aldstadt J, Yoon IK, Tannitisupawong D, Jarman RG, Thomas SJ, Gibbons RV, Uppapong A, Iamsirithaworn S, Rothman AL, Scott TW, Endy T. Space-time analysis of hospitalised dengue patients in rural Thailand reveals important temporal intervals in the pattern of dengue virus transmission. Trop Med Int Health. 2012 Sep;17(9):1076-85. doi: 10.1111/j.1365-3156.2012.03040.x. Epub 2012 Jul 19. PMID: 22808917; PMCID: PMC4099473.
9. Codeço CT, Villela DAM, Coelho FC. Estimating the effective reproduction number of dengue considering temperature-dependent generation intervals. Epidemics. 2018 Dec;25:101-111. doi: 10.1016/j.epidem.2018.05.011. Epub 2018 May 31. PMID: 29945778.
10. Nakase T, Giovanetti M, Obolski U, Lourenço J. Global transmission suitability maps for dengue virus transmitted by *Aedes aegypti* from 1981 to 2019. Sci Data. 2023 May 12;10(1):275.
11. Aksamentov I, Roemer C, Hodcroft EB, Neher RA. Nextclade: clade assignment, mutation calling and quality control for viral genomes. J Open Source Softw. 2021;6:3773.
12. Nguyen LT, Schmidt HA, von Haeseler A, Minh BQ. IQ-TREE: a fast and effective stochastic algorithm for estimating maximum-likelihood phylogenies. Mol Biol Evol. 2015;32:268–74.
13. Rambaut A, Lam TT, Max Carvalho L, Pybus OG. Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). Virus Evol. 2016;2:vew007
14. Sagulenko P, Puller V, Neher RA. TreeTime: Maximum-likelihood phylodynamic analysis. Virus Evol. 2018;4:vex042.*
15. Rambaut A, Lam TT, Max Carvalho L, Pybus OG. Exploring the temporal structure of heterochronous sequences using TempEst (formerly Path-O-Gen). Virus Evol. 2016 Jan;2(1):vew007.
16. Baele G, Ji X, Hassler GW, McCrone JT, Shao Y, Zhang Z, et al. BEAST X for Bayesian phylogenetic, phylogeographic and phylodynamic inference. Nat Methods. 2025 Aug;22(8):1653–6.
17. Gill MS, Lemey P, Faria NR, Rambaut A, Shapiro B, Suchard MA. *Improving Bayesian population dynamics inference: a coalescent-based model for multiple loci*. Molecular Biology and Evolution, 2013;30 (3):713–724.
18. Rambaut A, Drummond AJ, Xie D, Baele G, Suchard MA. Posterior summarization in Bayesian phylogenetics using Tracer 1.7. Syst Biol. 2018 Sep 1;67(5):901–4.

19. Suchard MA, Lemey P, Baele G, Ayres DL, Drummond AJ, Rambaut A. Bayesian phylogenetic and phylodynamic data integration using BEAST 1.10. *Virus Evol.* 2018 Jan;4(1):vey016.
20. Gerome P. Dengue in Africa: Summary of reported cases in September 2024 [Internet]. 2025 [cited 2025 Dec 12]. Available from: [https://www.mesvaccins.net/web/news/22376-la-dengue-en-afrique-bilan-des-signalements-faits-en-septembre-2024#:~:text=Depuis%20le%20d%C3%A9but%20de%20l,d'Ivoire%20\(39%20%3B%20](https://www.mesvaccins.net/web/news/22376-la-dengue-en-afrique-bilan-des-signalements-faits-en-septembre-2024#:~:text=Depuis%20le%20d%C3%A9but%20de%20l,d'Ivoire%20(39%20%3B%20)
21. Akagankou, K. I., Ahadji-Dabla, K. M., Romero-Alvarez, D., Navarro, J.-C., Ortega-López, L. D., Villanueva-Sarmiento, M., N'Tsoukpoe, K. G. J., Koffi, E., Kondo, Y., Amekudi, A. A., Apetogbo, Y., Lenhart, A., & Ketoh, G. K. (2025). Widespread distribution of *Aedes aegypti* larvae, a potential risk of arbovirus transmission in the Grand Lomé health region, Togo, West Africa. *Parasites & Vectors*, 18(1), 241. <https://doi.org/10.1186/s13071-025-06835-7>

Figures

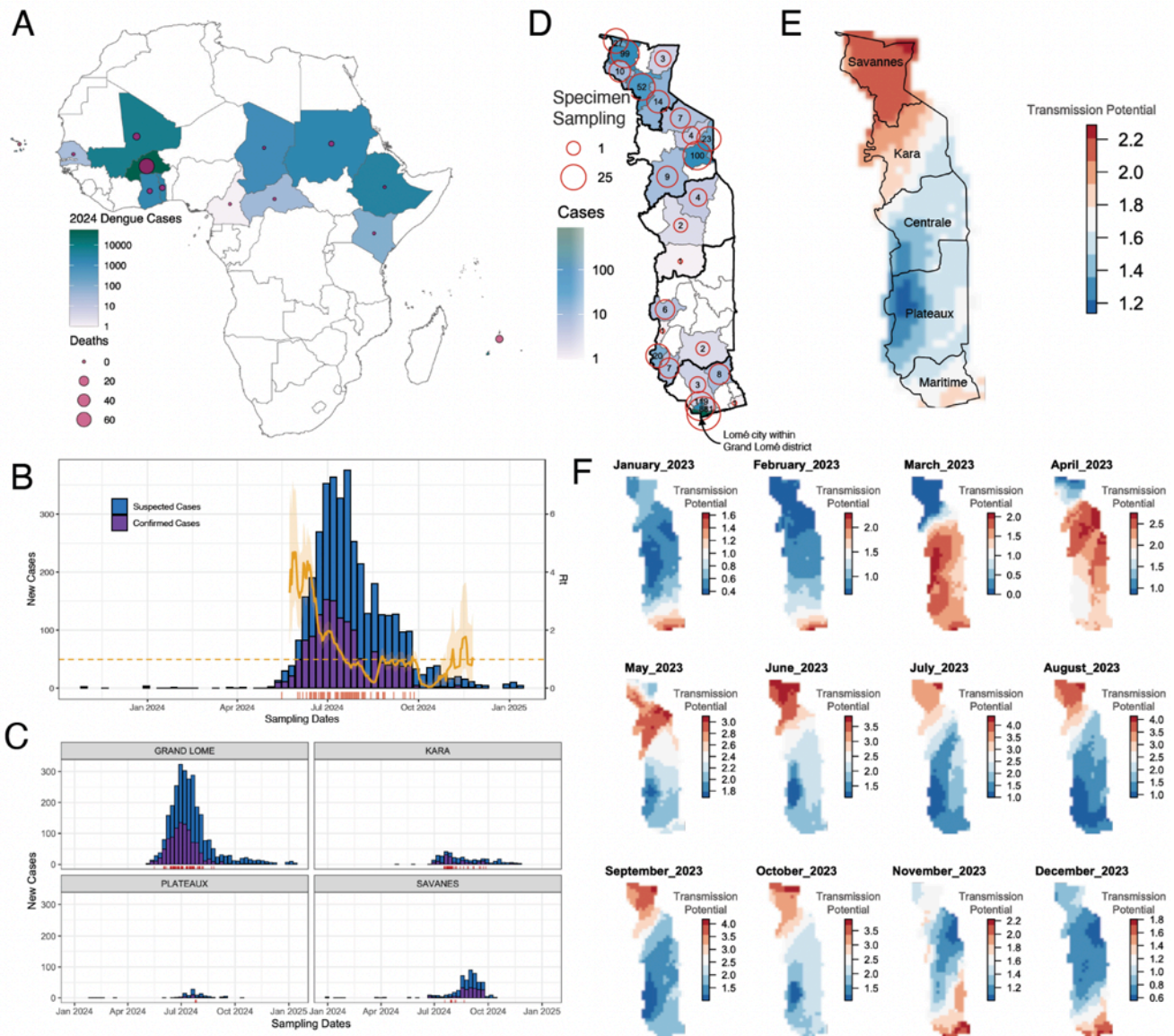


Figure 1

Epidemiological and environmental dynamics of the 2024 DENV outbreak in Togo. (A) Geographic distribution of dengue activity across Africa in 2024, showing reported cases and deaths. (B) National epidemic curve displaying weekly suspected and confirmed dengue cases in Togo, with the estimated effective reproduction number (R_t) overlaid in yellow. Rug plot displays the collection dates of genomes generated (sequencing intensity) in red. (C) District-level epidemic curves for Grand Lomé, Kara, Plateaux, and Savanes, illustrating heterogeneity in outbreak timing and magnitude. (D) Spatial distribution of specimen sampling across Togo, with circles scaled by the number of sequenced samples and the background colour ramp displays the number of reported cases. (E) Mean estimated transmission potential across Togo for 2024, highlighting spatial variation in environmental suitability for dengue transmission. (F) Mean monthly transmission-potential maps for 2023, showing seasonality and geographic shifts in environmental suitability in the year preceding the outbreak.

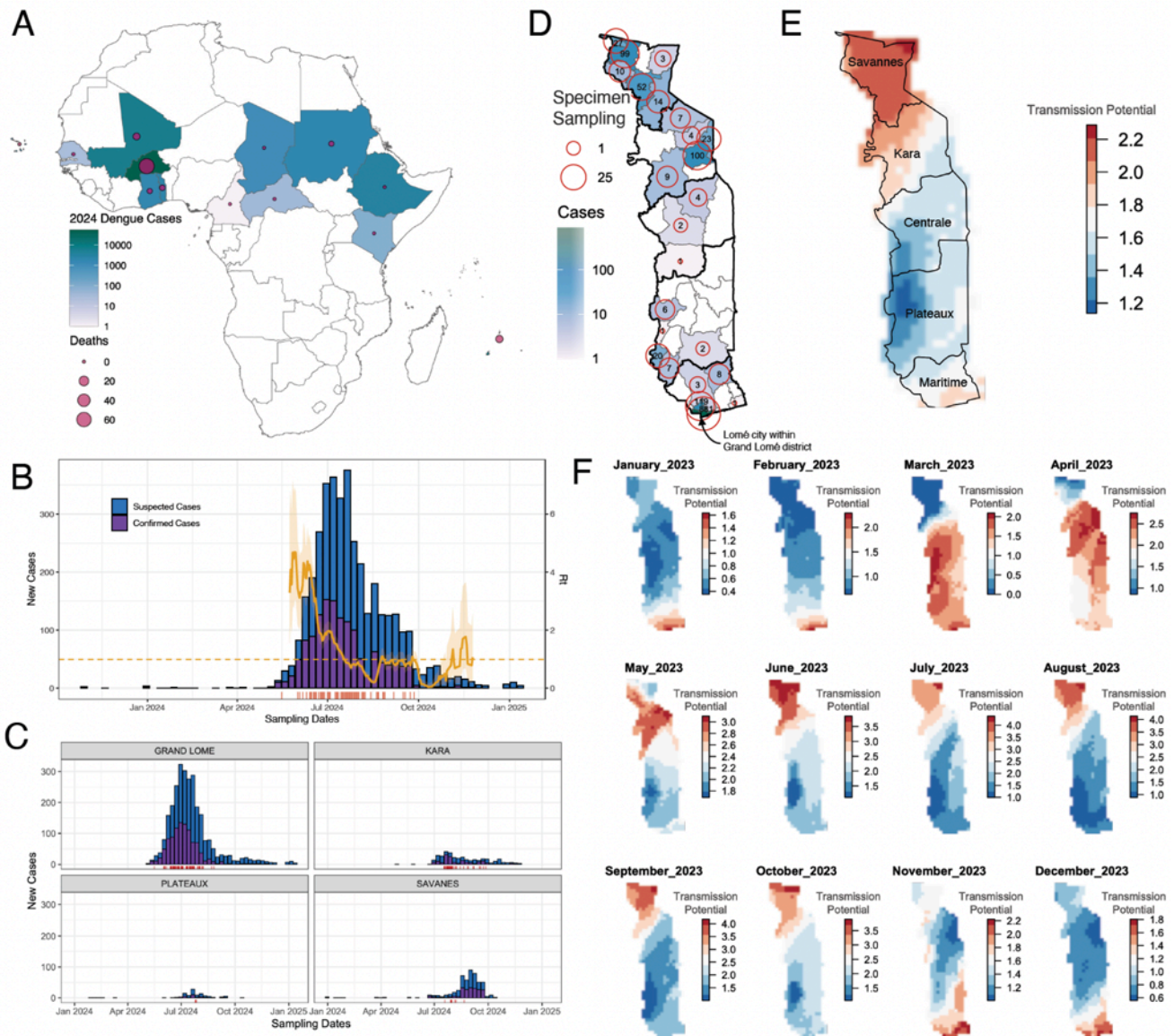


Figure 1

Epidemiological and environmental dynamics of the 2024 DENV outbreak in Togo. (A) Geographic distribution of dengue activity across Africa in 2024, showing reported cases and deaths. (B) National epidemic curve displaying weekly suspected and confirmed dengue cases in Togo, with the estimated effective reproduction number (R_t) overlaid in yellow. Rug plot displays the collection dates of genomes generated (sequencing intensity) in red. (C) District-level epidemic curves for Grand Lomé, Kara, Plateaux, and Savanes, illustrating heterogeneity in outbreak timing and magnitude. (D) Spatial distribution of specimen sampling across Togo, with circles scaled by the number of sequenced samples and the background colour ramp displays the number of reported cases. (E) Mean estimated transmission potential across Togo for 2024, highlighting spatial variation in environmental suitability for dengue transmission. (F) Mean monthly transmission-potential maps for 2023, showing seasonality and geographic shifts in environmental suitability in the year preceding the outbreak.

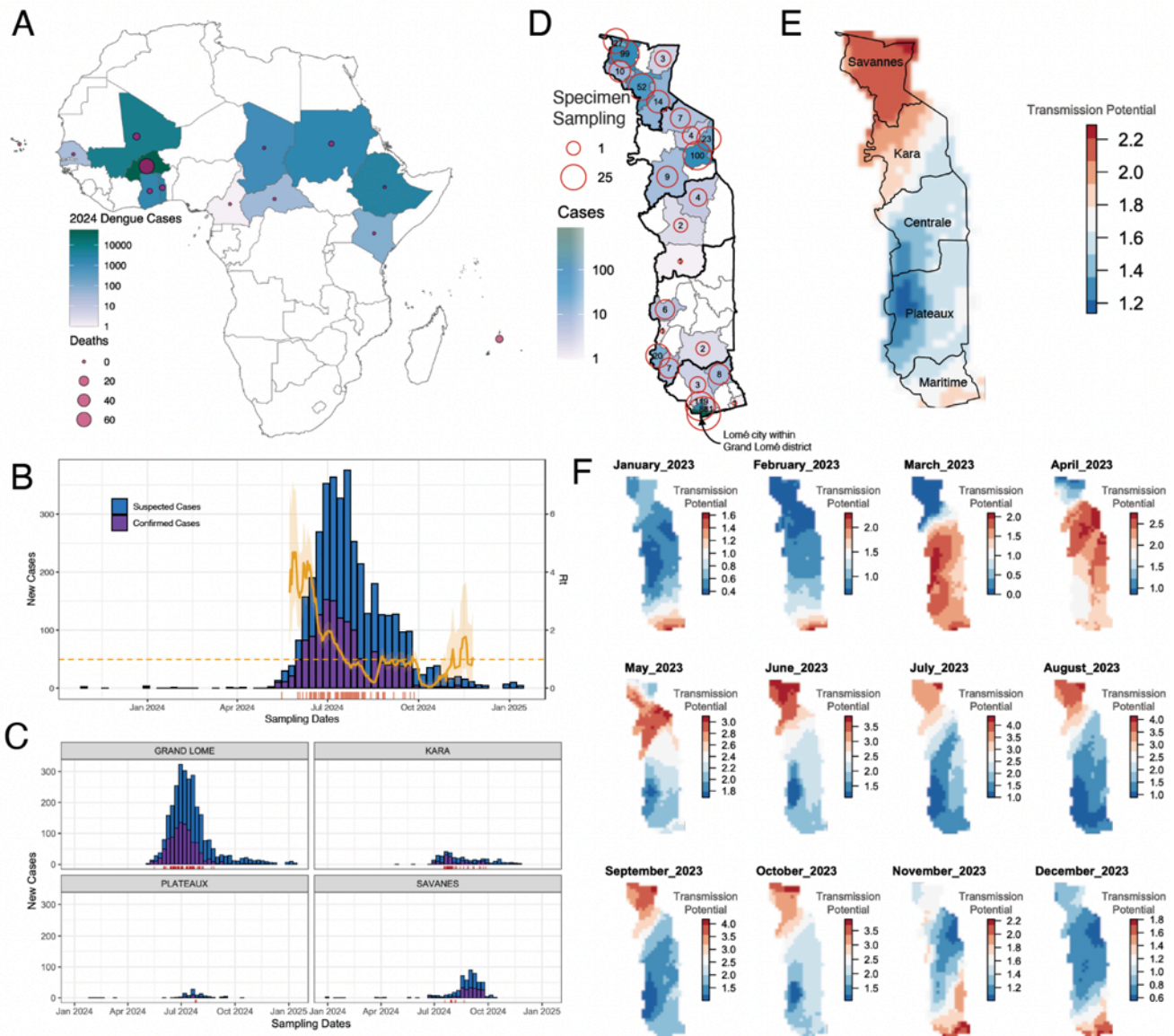


Figure 1

Epidemiological and environmental dynamics of the 2024 DENV outbreak in Togo. (A) Geographic distribution of dengue activity across Africa in 2024, showing reported cases and deaths. (B) National epidemic curve displaying weekly suspected and confirmed dengue cases in Togo, with the estimated effective reproduction number (R_t) overlaid in yellow. Rug plot displays the collection dates of genomes generated (sequencing intensity) in red. (C) District-level epidemic curves for Grand Lomé, Kara, Plateaux, and Savanes, illustrating heterogeneity in outbreak timing and magnitude. (D) Spatial distribution of specimen sampling across Togo, with circles scaled by the number of sequenced samples and the background colour ramp displays the number of reported cases. (E) Mean estimated transmission potential across Togo for 2024, highlighting spatial variation in environmental suitability for dengue transmission. (F) Mean monthly transmission-potential maps for 2023, showing seasonality and geographic shifts in environmental suitability in the year preceding the outbreak.

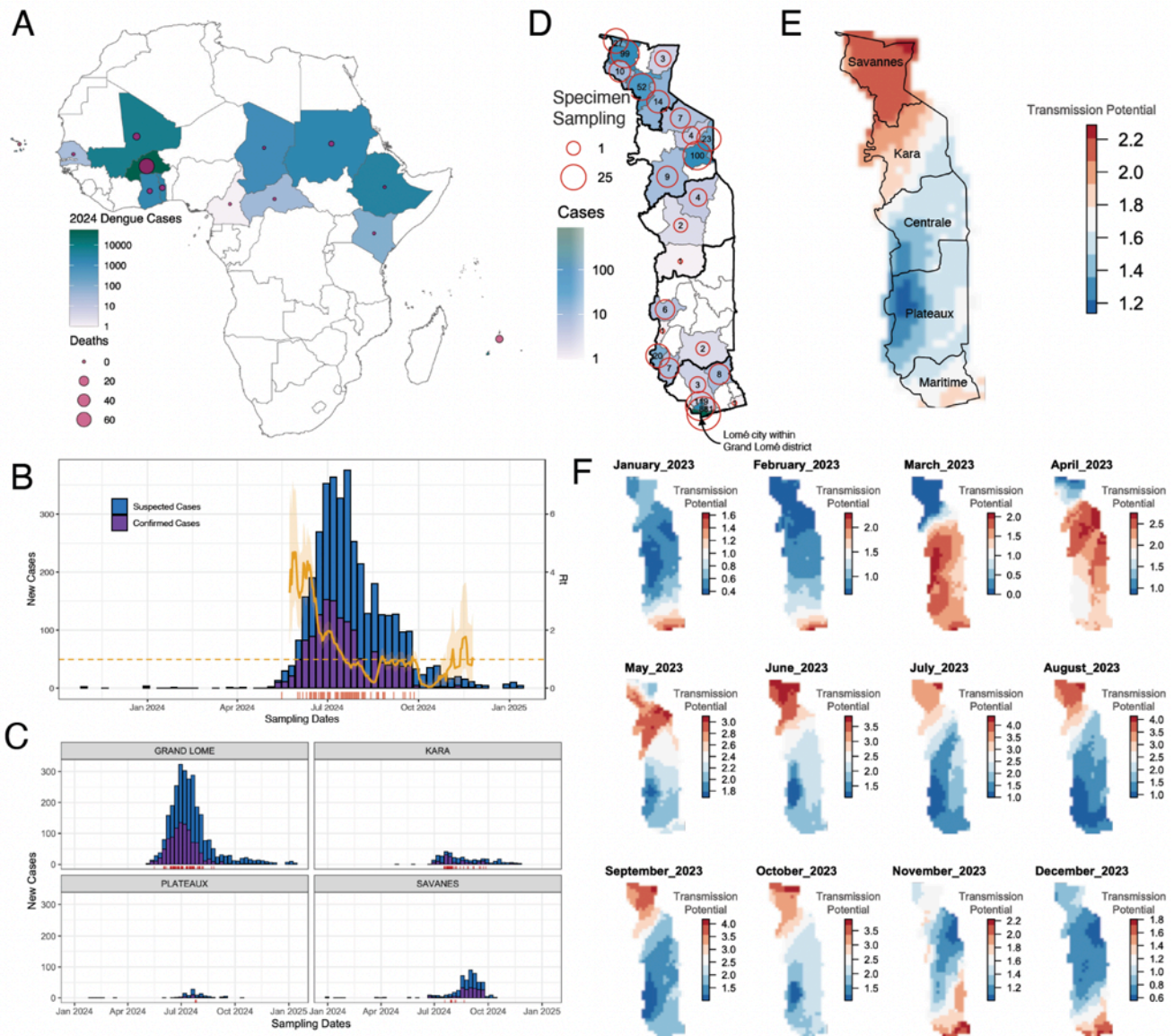


Figure 1

Epidemiological and environmental dynamics of the 2024 DENV outbreak in Togo. (A) Geographic distribution of dengue activity across Africa in 2024, showing reported cases and deaths. (B) National epidemic curve displaying weekly suspected and confirmed dengue cases in Togo, with the estimated effective reproduction number (R_t) overlaid in yellow. Rug plot displays the collection dates of genomes generated (sequencing intensity) in red. (C) District-level epidemic curves for Grand Lomé, Kara, Plateaux, and Savanes, illustrating heterogeneity in outbreak timing and magnitude. (D) Spatial distribution of specimen sampling across Togo, with circles scaled by the number of sequenced samples and the background colour ramp displays the number of reported cases. (E) Mean estimated transmission potential across Togo for 2024, highlighting spatial variation in environmental suitability for dengue transmission. (F) Mean monthly transmission-potential maps for 2023, showing seasonality and geographic shifts in environmental suitability in the year preceding the outbreak.

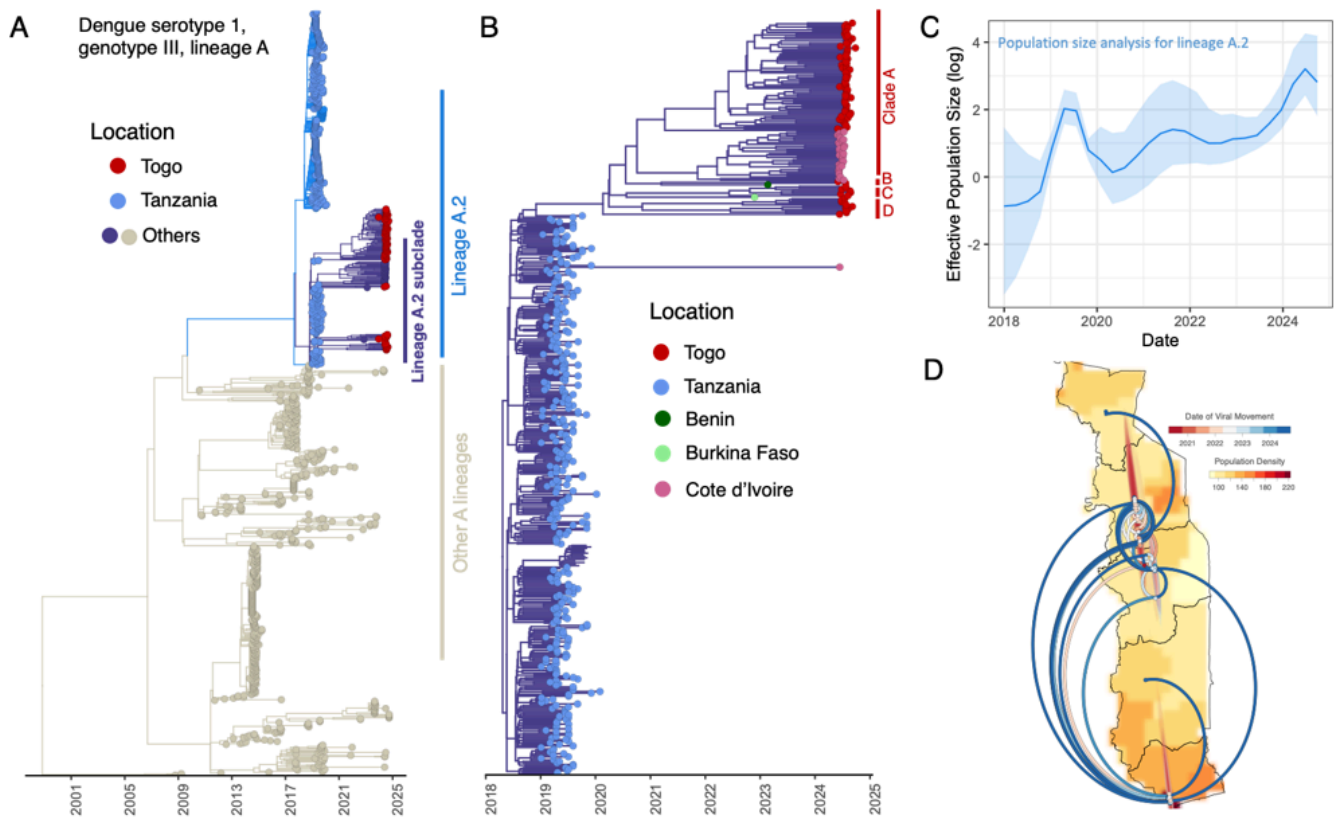


Figure 2

Phylogenetic and phylogeographic reconstruction of the DENV-1 (genotype III, lineage A) epidemic in Togo. (A) Time-scaled maximum likelihood phylogeny of DENV-1 lineage A showing the placement of Togo sequences (red) relative to genomes from Tanzania (blue) and other countries (grey). (B) Maximum clade credibility tree of the A.2 lineage, highlighting the geographic origins of closely related sequences from Togo, Tanzania, Benin, Burkina Faso, and Côte d'Ivoire, and showing the formation of clades A–D during the regional diversification of this lineage. (C) Bayesian Skygrid estimates of the effective population size for lineage A.2 (log scale) from 2018–2024, illustrating a marked increase in viral population size leading up to and during the 2024 epidemic in Togo. (D) Spatial reconstruction of viral movements within Togo, with arrows representing inferred dispersal events between districts and their timing (colored by inferred year of movement). Directionality of movement is anti-clockwise along the curve. Circles represent nodes of the maximum clade credibility phylogeny, coloured by the inferred time of occurrence. The underlying map shows population density, indicating that viral spread occurred primarily through densely populated corridors and coastal regions.

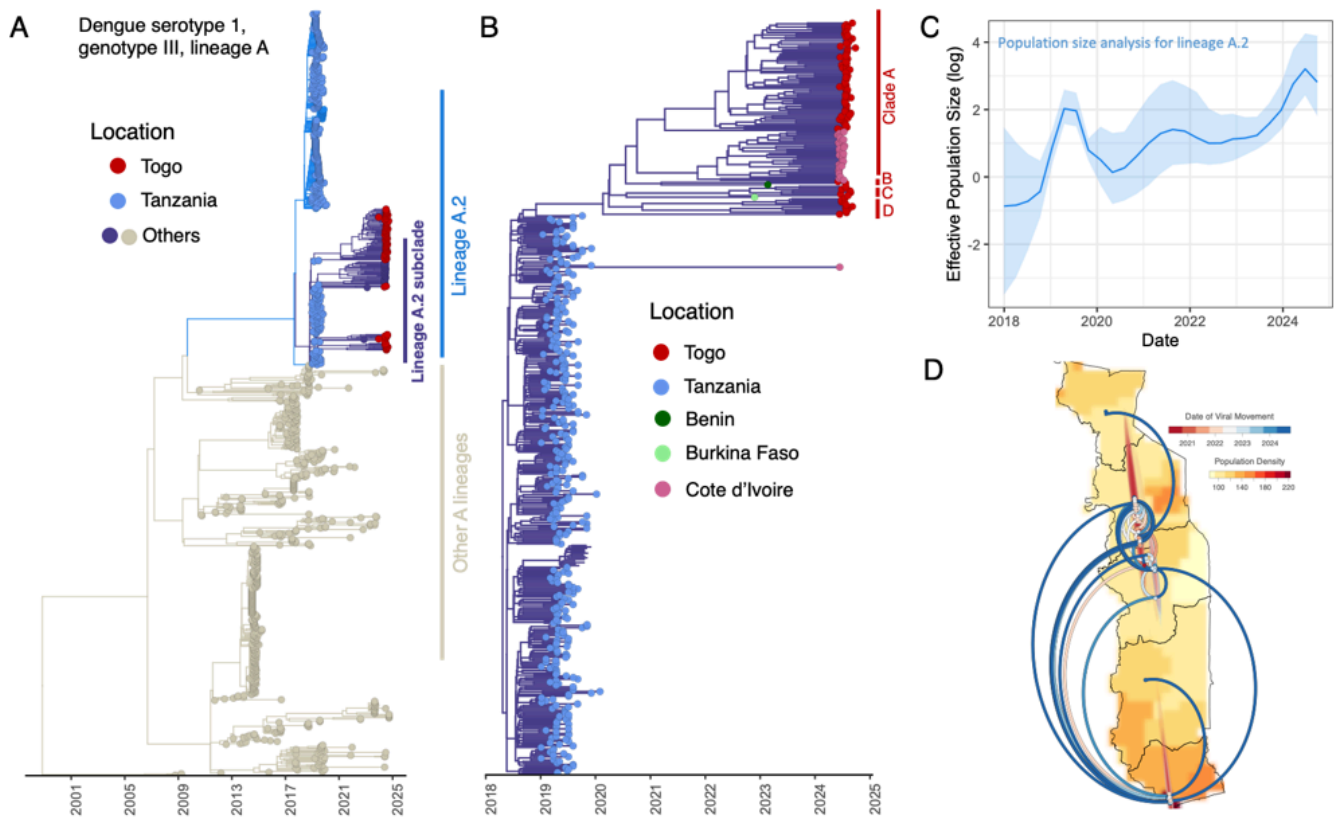


Figure 2

Phylogenetic and phylogeographic reconstruction of the DENV-1 (genotype III, lineage A) epidemic in Togo. (A) Time-scaled maximum likelihood phylogeny of DENV-1 lineage A showing the placement of Togo sequences (red) relative to genomes from Tanzania (blue) and other countries (grey). (B) Maximum clade credibility tree of the A.2 lineage, highlighting the geographic origins of closely related sequences from Togo, Tanzania, Benin, Burkina Faso, and Côte d'Ivoire, and showing the formation of clades A–D during the regional diversification of this lineage. (C) Bayesian Skygrid estimates of the effective population size for lineage A.2 (log scale) from 2018–2024, illustrating a marked increase in viral population size leading up to and during the 2024 epidemic in Togo. (D) Spatial reconstruction of viral movements within Togo, with arrows representing inferred dispersal events between districts and their timing (colored by inferred year of movement). Directionality of movement is anti-clockwise along the curve. Circles represent nodes of the maximum clade credibility phylogeny, coloured by the inferred time of occurrence. The underlying map shows population density, indicating that viral spread occurred primarily through densely populated corridors and coastal regions.

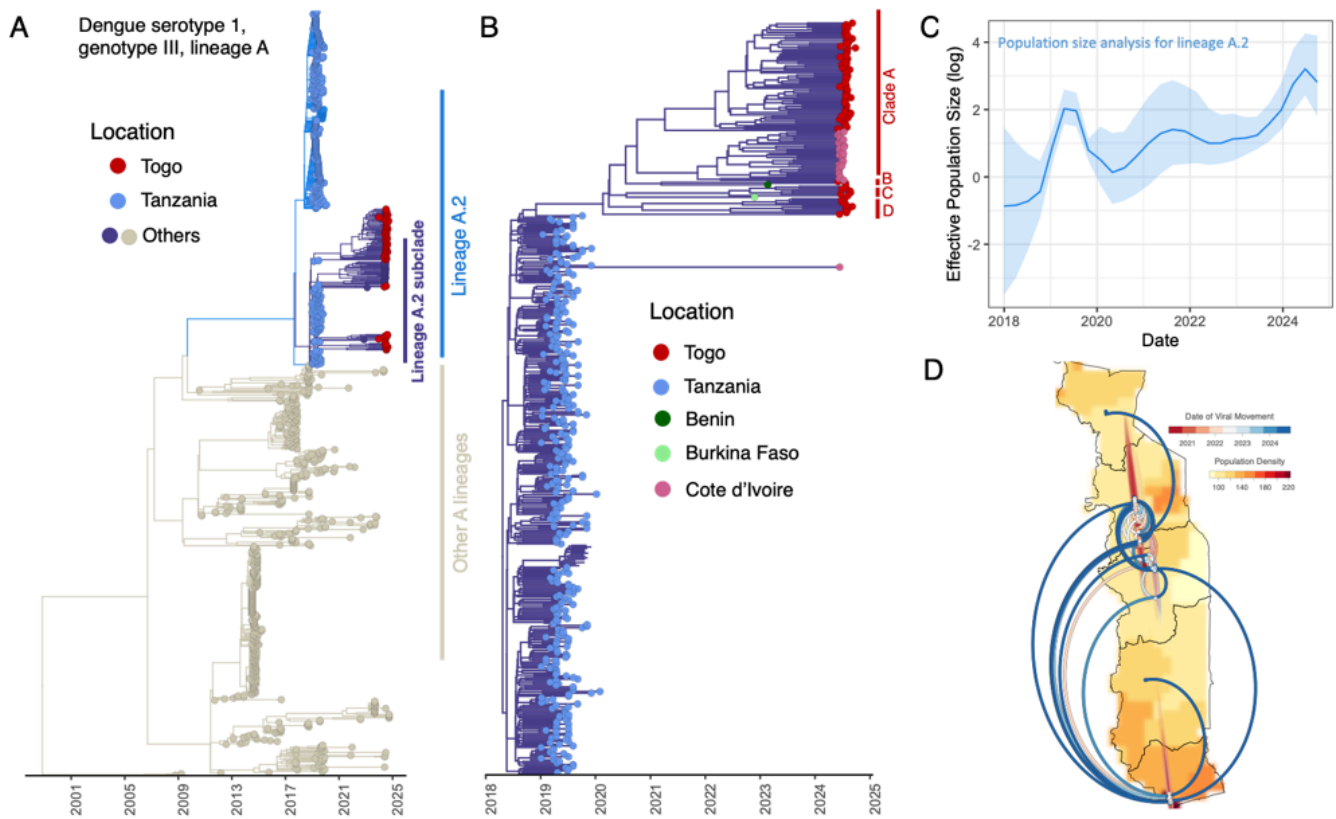


Figure 2

Phylogenetic and phylogeographic reconstruction of the DENV-1 (genotype III, lineage A) epidemic in Togo. (A) Time-scaled maximum likelihood phylogeny of DENV-1 lineage A showing the placement of Togo sequences (red) relative to genomes from Tanzania (blue) and other countries (grey). (B) Maximum clade credibility tree of the A.2 lineage, highlighting the geographic origins of closely related sequences from Togo, Tanzania, Benin, Burkina Faso, and Côte d'Ivoire, and showing the formation of clades A–D during the regional diversification of this lineage. (C) Bayesian Skygrid estimates of the effective population size for lineage A.2 (log scale) from 2018–2024, illustrating a marked increase in viral population size leading up to and during the 2024 epidemic in Togo. (D) Spatial reconstruction of viral movements within Togo, with arrows representing inferred dispersal events between districts and their timing (colored by inferred year of movement). Directionality of movement is anti-clockwise along the curve. Circles represent nodes of the maximum clade credibility phylogeny, coloured by the inferred time of occurrence. The underlying map shows population density, indicating that viral spread occurred primarily through densely populated corridors and coastal regions.

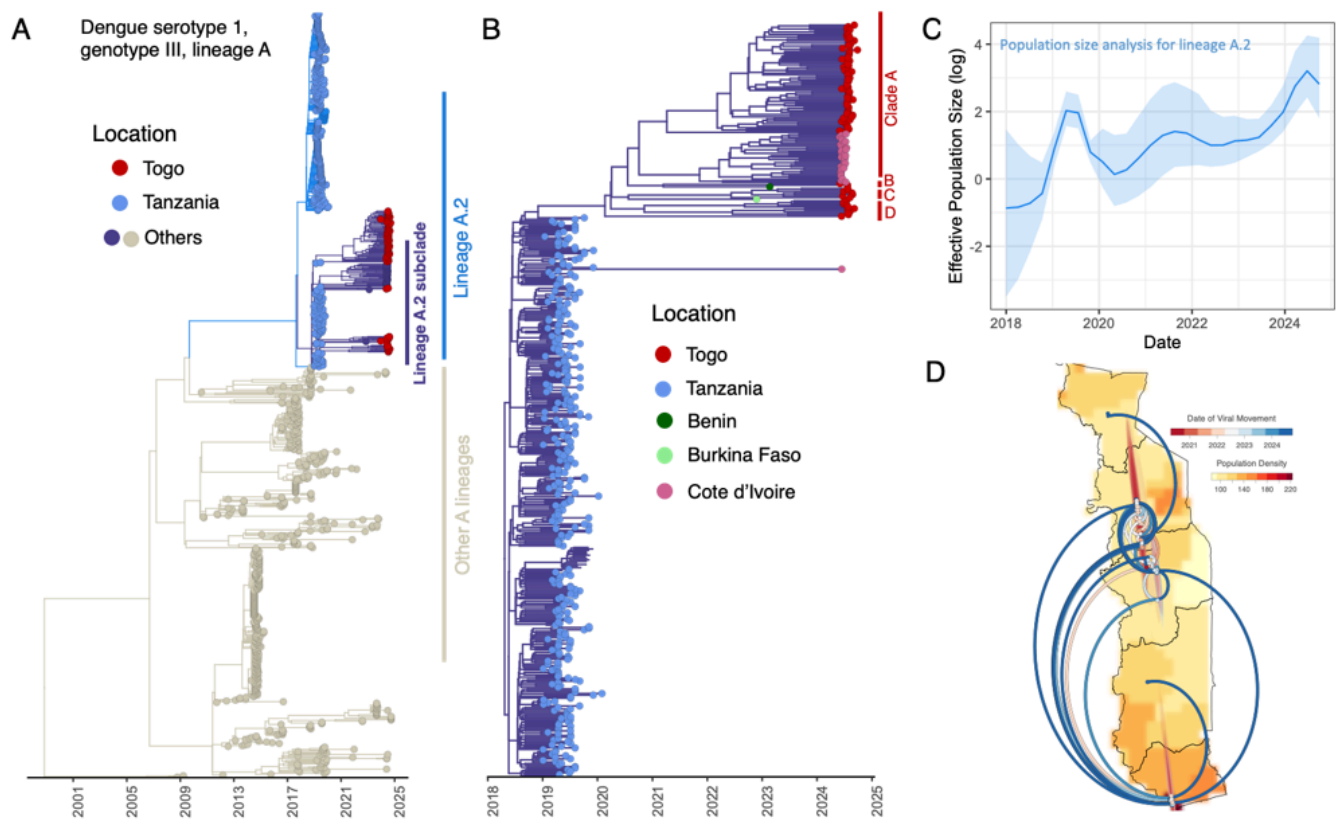


Figure 2

Phylogenetic and phylogeographic reconstruction of the DENV-1 (genotype III, lineage A) epidemic in Togo. (A) Time-scaled maximum likelihood phylogeny of DENV-1 lineage A showing the placement of Togo sequences (red) relative to genomes from Tanzania (blue) and other countries (grey). (B) Maximum clade credibility tree of the A.2 lineage, highlighting the geographic origins of closely related sequences from Togo, Tanzania, Benin, Burkina Faso, and Côte d'Ivoire, and showing the formation of clades A–D during the regional diversification of this lineage. (C) Bayesian Skygrid estimates of the effective population size for lineage A.2 (log scale) from 2018–2024, illustrating a marked increase in viral population size leading up to and during the 2024 epidemic in Togo. (D) Spatial reconstruction of viral movements within Togo, with arrows representing inferred dispersal events between districts and their timing (colored by inferred year of movement). Directionality of movement is anti-clockwise along the curve. Circles represent nodes of the maximum clade credibility phylogeny, coloured by the inferred time of occurrence. The underlying map shows population density, indicating that viral spread occurred primarily through densely populated corridors and coastal regions.

Supplementary Files

This is a list of supplementary files associated with this preprint. Click to download.

- [SupplementaryCLIMADEConsortiumContributingAuthorsJuly2026.docx](#)
- [SupplementaryCLIMADEConsortiumContributingAuthorsJuly2026.docx](#)
- [SupplementaryCLIMADEConsortiumContributingAuthorsJuly2026.docx](#)
- [SupplementaryCLIMADEConsortiumContributingAuthorsJuly2026.docx](#)
- [Supplementaryinformation.docx](#)
- [Supplementaryinformation.docx](#)
- [Supplementaryinformation.docx](#)
- [Supplementaryinformation.docx](#)