

Phylogenomics of Dengue Virus Isolates Causing Dengue Outbreak, São Tomé and Príncipe, 2022

Lazismino Lázaro, Doris Winter, Katia Toancha, Adjaia Borges, Anabela Gonçalves, Asmiralda Santos, Marcos do Nascimento, Nilton Teixeira, Yardlene Sacramento Sequeira, Anery Katia Lima, Bakissy da Costa Pina, Andreza Batista de Sousa, Jürgen May, Rosa Maria Afonso Neto, Kathrin Schuldt

Author affiliations: National Reference Laboratory for Tuberculosis and Emerging Diseases, Ministry of Health, São Tomé, São Tomé and Príncipe (L. Lázaro, K. Toancha, A. Borges, A. Gonçalves, A. Santos, M. do Nascimento, N. Teixeira, Y. Sacramento Sequeira, A.K. Lima, R.M. Afonso Neto); Bernhard Nocht Institute for Tropical Medicine, Hamburg, Germany (D. Winter, J. May, K. Schuldt); National Emergency Operating Center, Ministry of Health, São Tomé (B. da Costa Pina); National Surveillance Department, Ministry of Health, São Tomé (A. Batista de Sousa); German Center for Infection Research, Hamburg–Lübeck–Borstel–Riems, Germany (J. May); University Medical Center Hamburg–Eppendorf, Hamburg (J. May)

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We determined that the dengue outbreak in São Tomé and Príncipe during 2022 was caused by dengue virus serotype 3 genotype III. Phylogenomic analyses showed that the outbreak strain was closely related to the newly identified GIII-American-II lineage and that the virus probably was introduced from the Americas.

Globally, dengue case numbers have increased dramatically over recent decades; an estimated 96 million clinical dengue cases per year have been reported in >100 countries (1). Dengue is an acute febrile disease that can evolve into a severe life-threatening disease. Dengue is caused by an infection with the dengue virus (DENV), a member of the family *Flaviviridae*, and has 4 different serotypes (DENV-1–4) and distinct infection dynamics (2).

In 2022, São Tomé and Príncipe, an island state with ≈210,000 inhabitants in the Gulf of Guinea in sub-Saharan Africa, reported the occurrence of dengue cases in the country. During epidemiologic weeks 15–50 in 2022, a total of 1,152 dengue fever cases confirmed by positive rapid diagnostic tests (RDTs) were reported. The first cases were reported April 15, and case numbers peaked at 178 notifications in week 24 (Appendix Figure, <https://wwwnc.cdc.gov/EID/>

article/30/02/23-1316-App1.pdf). Among the 1,152 RDT-confirmed cases, the most frequent observed symptoms were fever (92%), headache (78%), and myalgia (38%). A total of 144 (12.5%) persons were admitted to the hospital (Appendix Table 1), and 8 persons died from infection with the virus. The presumptive index patient was described as a 27-year-old man from São Tomé and Príncipe who had traveled to the island of Guadeloupe before arriving in São Tomé on March 26, 2022, and whose onset of symptoms occurred on April 4, 2022 (3). A previous study analyzed the seroprevalence of DENV antibodies in the São Tomé and Príncipe population. In that study, 31 of 78 tested pregnant women were found to be seropositive for DENV, indicating that the country's population might have experienced exposure to the virus before 2003–2004, during which the collection of the analyzed serum samples took place (4).

This study was approved by the Health Ethics Committee for Scientific Research at the Ministry of Health of STP (approval no. 015B/2022). During May 6–16, 2022, we collected 7 plasma samples from dengue RDT-positive patients in São Tomé and Príncipe (Appendix Table 2). All 7 infections were confirmed by real-time PCR, and subtyping revealed the presence of DENV-3 (Appendix Table 2). Long-read whole-genome sequencing and subsequent assembly (reference strain GenBank accession no. NC_001475) resulted in 48–64,440 assembled reads (Appendix Table 3) with an average depth of coverage of 4–4,148× (Appendix Figure 2). We classified all 7 isolates as DENV-3 genotype III (GIII) by using a flavivirus genotyping tool (5) with bootstrap support of 100.

To study the evolutionary relationship of the virus isolates from São Tomé and Príncipe, we included 4 reconstructed genomes with best assembly results (>10 kb, genome coverage >98%, depth of coverage >250×) in a phylogenomic analysis together with 1,168 DENV-3 GIII genomes (Appendix Table 4) sampled worldwide. All 1,172 sequences passed the IQ-TREE2 composition test. The best-fitting evolutionary model according to Bayesian information criterion (BIC) was the general time-reversible plus empirical frequencies plus invariable sites plus FreRate model. The reconstructed consensus tree revealed that the newly sequenced DENV-3 isolates from São Tomé and Príncipe clustered with and are closely related to the new monophyletic clade consisting of 218 DENV-3 sequences detected in the Americas during 2022–2023 (Figure). A recent study by Naveca et al. (6) demonstrates that this new lineage (GIII-American-II lineage) was most likely introduced to Cuba from the Indian subcontinent in

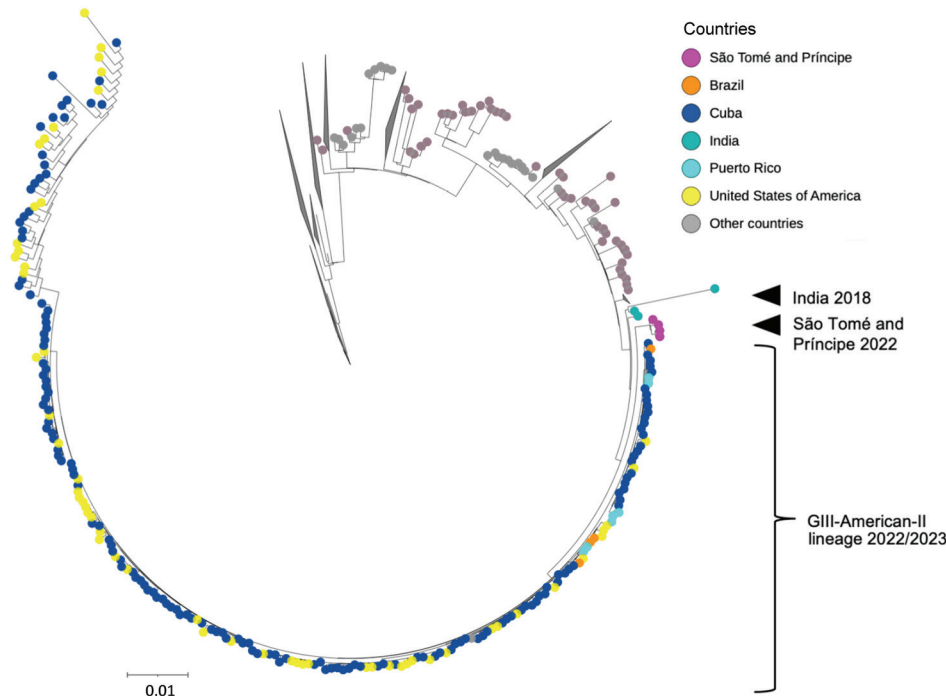


Figure. Reconstructed consensus tree of newly sequenced dengue virus serotype 3 isolates from São Tomé and Príncipe. The isolates clustered with and are closely related to a new monophyletic clade consisting of 218 dengue virus serotype 3 sequences detected in the Americas during 2022–2023. To improve visualization, several clades have been collapsed. Scale bar indicates nucleotide substitutions per site.

2019 (6). Consistent with their findings, our consensus tree (Figure) shows 3 DENV-3 sequences collected in India in 2018 as part of the next bigger clade comprising the GIII-American-II lineage and the 4 isolates from São Tomé and Príncipe.

Because the index patient reportedly had traveled to Guadeloupe before arriving in São Tomé and Príncipe, the likely scenario of virus importation is that after the introduction of the DENV-3-GIII lineage from Asia to America during 2018–2020, the virus might have circulated in the region, and from there it was introduced to São Tomé and Príncipe in 2022. Although we did not conduct formal phylogeographic analysis as part of this study, 2 points support our conclusions: the epidemiologic information that the index patient visited Guadeloupe; and the results of the previous study from Brazil, describing the new DENV-3, GIII-American-II lineage and how it arose in America (6). Thus, our results suggest that the São Tomé and Príncipe outbreak originated from the new American lineage.

According to surveillance data of the Pan American Health Organization, Guadeloupe has experienced yearly dengue outbreaks since 2018, and in the year 2020, the serotypes 1–3 were detected (7). Unfortunately, no information is available on the DENV serotype or genomic sequences on the DENV circulating in 2022 in Guadeloupe, and only sparse information is available on dengue cases from countries in Africa.

The results of our study corroborate a possible global expansion of the new DENV-3 GIII-American-II clade previously described by Naveca et al. (6). Furthermore, finding this American lineage in Africa reinforces the importance of genomic surveillance of DENV in countries at risk for future outbreaks.

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We deposited the 4 dengue virus whole-genome sequences from this study in the European Nucleotide Archive at European Molecular Biology Laboratory–European Bioinformatics Institute (accession no. PRJEB65577).

Author contributions: L.L., D.W., K.T., A.B., A.G., A.S., M.N., N.T., Y.S.S., and A.K.L. performed the RNA extraction and the laboratory analyses; B.C.P and A.B.S. contributed the public health surveillance data; J.M. contributed to obtain funds; L.L., R.M.A.N., and K.S. designed the study and performed the bioinformatic analyses; and K.S. wrote the manuscript. All authors have read and approved the manuscript.

About the Author

Mr. Lázaro is a laboratory expert from the National Reference Laboratory for Tuberculosis and Emerging Diseases in São Tomé and Príncipe. His primary research interests include molecular surveillance of pathogens by whole-genome sequencing and bioinformatic analyses.

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Address for correspondence: Kathrin Schuldt, Infectious Diseases Epidemiology Department, Bernhard Nocht Institute for Tropical Medicine, Bernhard-Nocht-Str. 74, 20359 Hamburg, Germany; email: schuldt@bnitm.de

Integrating Veterinary Diagnostic Laboratories for Emergency Use Testing during Pandemics¹

Natasha F. Hodges, McKenzie Sparrer, Tyler Sherman, Treana Mayer, Danielle R. Adney, Izabela Ragan, Molly Carpenter, Christie Mayo,² Tracy L. Webb²

Author affiliations: Colorado State University, Fort Collins, Colorado, USA (N.F. Hodges, M. Sparrer, T. Sherman, T. Mayer, I. Ragan, M. Carpenter, C. Mayo, T.L. Webb); Lovelace Biomedical, Albuquerque, New Mexico, USA (D.R. Adney)

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The SARS-CoV-2 pandemic showed limitations in human outbreak testing. Veterinary diagnostic laboratories (VDLs) possess capabilities to bolster emergency test capacity. Surveys from 26 participating VDLs found human SARS-CoV-2 testing was mutually beneficial, including One Health benefits. VDLs indicated testing >3.8 million human samples during the pandemic, which included some challenges.

After emergence of SARS-CoV-2 in late January 2020, diagnostic testing was fraught with challenges. As cases increased, public health agencies struggled to provide timely support, prompting veterinary diagnostic laboratories (VDLs) to assist with processing human SARS-CoV-2 samples (1). VDLs regularly conduct diagnostic testing for infectious agents and maintain the necessary equipment, personnel, facilities, and protocols for animal disease testing. Currently, there are 60 university- or state-affiliated VDLs across the United States (2). On April 1, 2020, the World Organization for Animal Health published guidance stating that VDLs possess the resources and personnel expertise to help human diagnostic laboratories meet the demand for SARS-CoV-2 testing (3,4).

To assess VDL participation in human testing, we distributed a 14-question survey (Appendix, <https://wwwnc.cdc.gov/EID/article/30/2/23-0562-App1.pdf>) to 52 VDLs across the United States that had available email addresses. The study was reviewed by Colorado State University's Institutional Review Board (Protocol no. 3620), and respondent answers were deidentified before analysis. The first question queried whether human SARS-CoV-2 samples were tested and required an affirmative response to continue the survey. Subsequent questions were optional. Responses were gathered during July 7–December 22, 2022. Two follow-up reminders were sent during the open survey period. Responses were received from 26 (43.3%) of the 60 VDLs overall or 26 (50%) of the 52 VDLs that were contacted. Nine respondents indicated no human testing, and 17 (65.4%) of the 26 responding VDLs reported performing human testing. When >1 response was received from the same VDL (5 VDLs submitted >1 survey), numeric data were averaged, and all free text entries were included.

The duration of human testing across responding VDLs ranged from 5 to 31 months; average

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²These authors were co-principal investigators.

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Appendix

Material and Methods

Sample collection and RNA extraction

Seven plasma samples were collected randomly from patients that had an RDT positive test at the Hospital Dr. Ayres Menezes between 6th and 16th of May 2022 (Appendix Table 2). RNA was extracted from plasma using the QIAamp Viral RNA Mini Kit (Qiagen #52906) according to the manufacturer's instructions. Aliquots of the extracted nucleic acid were stored at -80°C until further analyses.

Real-time PCR and serotype identification

To detect DENV and identify the serotype real-time PCR was carried out using the RealStar Dengue RT-PCR Kit 3.0 (Altona Diagnostics #283003) and the RealStar Dengue Type RT-PCR Kit 1.0 (Altona Diagnostics #621003) according to manufacturer's instructions on a 7500 real-time PCR Instrument (Applied Biosystems).

Oxford Nanopore Technologies (ONT) library preparation

cDNA synthesis and multiplex PCR amplification were performed as previously described (1). Because the subtyping by real-time PCR did not reveal any evidence of infections with other serotypes than DENV-3, we used two pools of serotype-specific multiplex primer sets specifically designed for whole genome sequencing (WGS) of DENV-3 (1). Following PCR amplification, the two reactions were pooled and the final steps of the library preparation for the portable MinION sequencer (Oxford Nanopore Technologies) were performed as described (2).

Whole genome sequencing and consensus genomes

The sequencing run was performed on a MinION M1kc device (Oxford Nanopore Technology) and conversion from raw data to nucleotide sequences (“basecalling”) in high-accuracy mode was performed with ONT Guppy basecalling software version 6.5.7. Fastq files for each of the seven DENV-3 isolates were uploaded into the Genome Detective Platform for default viral analyses and assembly of the consensus sequence based on DENV-3 reference sequence NC_001475 using the Genome Detective Virus Tool v2.12.2 (<https://www.genomedetective.com>) (3).

Genotype identification

For genotype identification based on the consensus sequences of the seven DENV-3 virus isolates we used the web application Flavivirus Genotyping Tool v0.1 (<https://www.rivm.nl/mpf/typingtool/flavivirus/>) (4).

DENV-3 dataset and phylogenomic reconstruction

The alignment and subsequent reconstruction of phylogenomic relationships of all publicly available DENV-3 genotype III genomes together with the four DENV-3 from STP was carried out as described previously (5). Before the analysis, the four STP sequences were visually inspected. None of them contained any undetermined nucleotide in the consensus sequence. All DENV-3 genotype III genomes with a genome length >10,000bp that were available from GenBank via the NCBI Virus portal were downloaded for the phylogenomic analyses. The search on the assessment day (30–06–2023) resulted in a total of 1,168 DENV-3 genomes (Appendix Table 3). Hence, the complete dataset used for alignment with MAFFT v7.520 (6) included 1,172 DENV3 genomes. The reconstruction of the phylogenomic relationships was done by maximum likelihood (ML) using IQ-TREE 2 multicore v2.2.2.6 (7). The best-fitting evolutionary model was selected. A ML phylogenetic tree was constructed using the best-fitting model based on Bayesian information criterion (BIC) tests with ModelFinder (8) and Ultrafast bootstrap with 2,000 replicates (9). Visualization of the best fitting consensus tree was done in iTOLv6 (10).

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Appendix Table 1. Age and sex distribution of 144 RDT-positive Dengue cases admitted to hospital during the 2022 Dengue outbreak in the Democratic Republic of São Tomé and Príncipe

Age interval [years]	No. of cases	Percentage [%]	Gender [M/F]
0–9	17	11.8	9/8
10–19	26	18.1	19/7
20–29	26	18.1	15/11
30–39	18	12.5	9/9
40–49	26	18.1	9/17
50–59	13	9.0	6/7
>60	18	12.5	5/13
Total	144	100.0	72/72

Appendix Table 2. Real-time PCR results for seven analyzed DENV-3 GIII isolates from the 2022 Dengue outbreak in the Democratic Republic of São Tomé and Príncipe*

ID	Collection date	Age [years]/		District	Ct	Serotype	Genotype
		Gender					
DENVSTP01	16.05.22	24/M		Água-Grande	24.9	3	III
DENVSTP02	06.05.22	40/M		Água-Grande	18.9	3	III
DENVSTP03	06.05.22	17/F		Água-Grande	28.3	3	III
DENVSTP04	12.05.22	8/F		Mezóchi	20.6	3	III
DENVSTP05	16.05.22	34/F		Água-Grande	20.6	3	III
DENVSTP06	16.05.22	25/F		Água-Grande	18.4	3	III
DENVSTP07	16.05.22	43/F		Água-Grande	16.1	3	III

*Ct, value of cycle threshold from real-time PCR

Appendix Table 3. Assembly statistics for seven sequenced DENV-3 GIII isolates from the 2022 Dengue outbreak in the Democratic Republic of São Tomé and Príncipe*

Sample ID	Ct value	#Reads	Coverage depth	NT Identity [%]	AA Identity [%]	Genome Coverage [%]	#Contigs	Genome length	ENA Accession number
DENVSTP01	24.9	3,460	169	95.7	98.5	91.5	3	9,798	–
DENVSTP02	18.9	51,915	2,302	95.7	98.4	97.9	1	10,484	ERS16303457
DENVSTP03	28.3	48	4	94.6	quality too low	45.9	10	4,911	–
DENVSTP04	20.6	1,108	71	95.6	98.3	66.2	8	7,083	–
DENVSTP05	20.6	5,166	259	95.7	98.6	97.7	1	10,461	ERS16303458
DENVSTP06	18.4	24,339	1,288	95.7	98.6	97.7	1	10,460	ERS16303459
DENVSTP07	16.1	64,440	4,148	95.8	98.7	98.3	1	10,526	ERS16303460

*The four in bold highlighted isolates were included in the phylogenomic analysis. Ct, real-time PCR cycle threshold; NT, nucleotide; AA, amino acid; Reference sequence used for assembly: NC_001475; ENA, European Nucleotide Archive.

Appendix Table 4. Publicly available DENV-3 GIII genomes used in the phylogenomic analysis (assessed on 30-06-2023)

Accession	Country	Collection date
AY099336	Sri Lanka	2000
AY099337	Martinique	1999
AY662691	Singapore	2004
AY679147	Brazil	2002
AY770511	India	2003
DQ675533	Taiwan	1999
EF629366	Brazil	2004-11
EF629367	Brazil	2004-11
EF629368	Brazil	2004-11
EF629369	Brazil	2002-01
EF643017	Brazil	2003
EU081181	Singapore	2004
EU081182	Singapore	2005
EU081183	Singapore	2005
EU081184	Singapore	2005
EU081185	Singapore	2005
EU081186	Singapore	2005
EU081187	Singapore	2005
EU081188	Singapore	2005
EU081189	Singapore	2005
EU081190	Singapore	2005
EU081191	Singapore	2005
EU081192	Singapore	2005
EU081193	Singapore	2005
EU081194	Singapore	2005
EU081195	Singapore	2005
EU081196	Singapore	2005
EU081197	Singapore	2005
EU081198	Singapore	2005
EU081199	Singapore	2005
EU081200	Singapore	2005
EU081201	Singapore	2005
EU081202	Singapore	2005
EU081203	Singapore	2005
EU081204	Singapore	2005
EU081205	Singapore	2005
EU081206	Singapore	2005
EU081207	Singapore	2005
EU081208	Singapore	2005
EU081209	Singapore	2005
EU081210	Singapore	2005
EU081211	Singapore	2005
EU081212	Singapore	2005
EU081213	Singapore	2005
EU081214	Singapore	2005
EU081215	Singapore	2005
EU081216	Singapore	2005
EU081217	Singapore	2005
EU081218	Singapore	2005
EU081219	Singapore	2005
EU081220	Singapore	2005
EU081222	Singapore	2005
EU081224	Singapore	2005
EU081225	Singapore	2005
EU482555	USA	2006
EU482558	USA	1998
EU482559	USA	1998
EU482563	USA	1998
EU482564	USA	2003
EU482566	USA	1998
EU482595	USA	2003
EU482596	USA	1998
EU482612	Venezuela	2001
EU482613	Venezuela	2001
EU482614	Venezuela	2001
EU529683	Venezuela	2007

Accession	Country	Collection date
EU529684	Venezuela	2001
EU529685	Venezuela	2001
EU529686	Venezuela	2001
EU529687	Venezuela	2001
EU529688	Venezuela	2001
EU529689	Venezuela	2001
EU529690	Venezuela	2001
EU529691	Venezuela	2001
EU529692	USA	2006
EU529696	USA	1999
EU529697	USA	2000
EU529698	USA	2006
EU529699	USA	2006
EU529702	USA	2003
EU529703	USA	1998
EU529704	USA	2004
EU529705	USA	2004
EU569688	Venezuela	2001
EU569689	Venezuela	2001
EU569690	Venezuela	2001
EU569691	Venezuela	2001
EU596492	USA	2007
EU596493	USA	2007
EU596494	USA	2007
EU660420	Venezuela	2001
EU687196	USA	2002
EU687197	USA	2003
EU687198	USA	2003
EU687218	USA	1998
EU687219	USA	1999
EU687221	USA	2000
EU687226	USA	1999
EU687233	USA	2002
EU687234	USA	2002
EU687239	USA	2003
EU726768	USA	2000
EU726769	USA	2003
EU726771	USA	1998
EU726772	USA	1998
EU726773	USA	1999
EU726774	USA	1999
EU781136	USA	1999
EU781137	USA	1999
EU854291	Venezuela	2004
EU854292	Venezuela	2005
EU854298	USA	2002
EU932687	Venezuela	2007
EU932688	Venezuela	2007
FJ024465	USA	2004
FJ024466	USA	2004
FJ024467	USA	2004
FJ024468	USA	2004
FJ024469	USA	2004
FJ024470	USA	2004
FJ024471	USA	2004
FJ177308	Brazil	2001
FJ182004	USA	2004
FJ182005	USA	2004
FJ182006	USA	2004
FJ182007	USA	2005
FJ182008	USA	2005
FJ182009	USA	2005
FJ182010	USA	2005
FJ182011	USA	2005
FJ182013	USA	1998
FJ182015	Venezuela	2001
FJ182037	USA	2005
FJ182038	USA	2005
FJ182039	USA	2005

Accession	Country	Collection date
FJ182040	USA	2005
FJ182041	USA	2005
FJ205870	USA	2003
FJ205871	USA	1999
FJ373302	USA	2004
FJ373303	Venezuela	2001
FJ373304	Venezuela	2004
FJ373306	USA	2002
FJ390371	USA	2003
FJ390372	USA	2003
FJ390373	USA	2002
FJ390375	USA	1999
FJ390376	USA	1999
FJ390377	USA	1999
FJ410176	USA	2000
FJ410177	USA	2000
FJ410178	USA	2002
FJ478456	USA	2002
FJ547069	USA	1999
FJ547070	USA	1998
FJ547071	USA	2000
FJ547072	USA	2000
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FJ547078	USA	2000
FJ547079	USA	2001
FJ547080	USA	2001
FJ547081	USA	2001
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FJ547084	USA	2002
FJ547085	USA	2006
FJ562107	USA	2000
FJ639746	Venezuela	2000
FJ639747	Venezuela	2000
FJ639749	Venezuela	2000
FJ639750	Venezuela	2000
FJ639751	Venezuela	2001
FJ639752	Venezuela	2001
FJ639753	Venezuela	2001
FJ639754	Venezuela	2001
FJ639755	Venezuela	2001
FJ639756	Venezuela	2001
FJ639757	Venezuela	2001
FJ639758	Venezuela	2001
FJ639759	Venezuela	2001
FJ639760	Venezuela	2001
FJ639761	Venezuela	2001
FJ639762	Venezuela	2001
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Accession	Country	Collection date
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FJ744700	Venezuela	2001
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FJ882575	Mozambique	1985
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FJ882577	Venezuela	2001
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FJ898458	Peru	2002
FJ898459	Trinidad and Tobago	2002
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Accession	Country	Collection date
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Accession	Country	Collection date
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JN662391	China	2009-08-06
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KF955474	Sri Lanka	1989
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Accession	Country	Collection date
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KJ830751	Saudi Arabia	2014-01-26
KT726340	Cuba	2001
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KU509281	India	2009
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KY921907	Singapore	2015-04
LC379193	Gabon	2016-05-15
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MF142763	Thailand	2015-09
MF370226	China	2013-08-20
MG721059	India	2016
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MH544647	Colombia	2015-08-23
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MK858151	India	2016-11-08
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MN018371	China	2015-08-08
MN018372	China	2016-03-18
MN018375	China	2015-10-23
MN018376	China	2015-07-06
MN018378	China	2015-09-30
MN018381	China	2016-05-06
MN018385	China	2016-09-20
MN018386	China	2013-07-28
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MN227698	China	2019-07-02
MN227699	China	2019-06-30
MN227700	China	2019-07-08
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MN253124	India	2017-08-10
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MN448966	Thailand	2012-09-25
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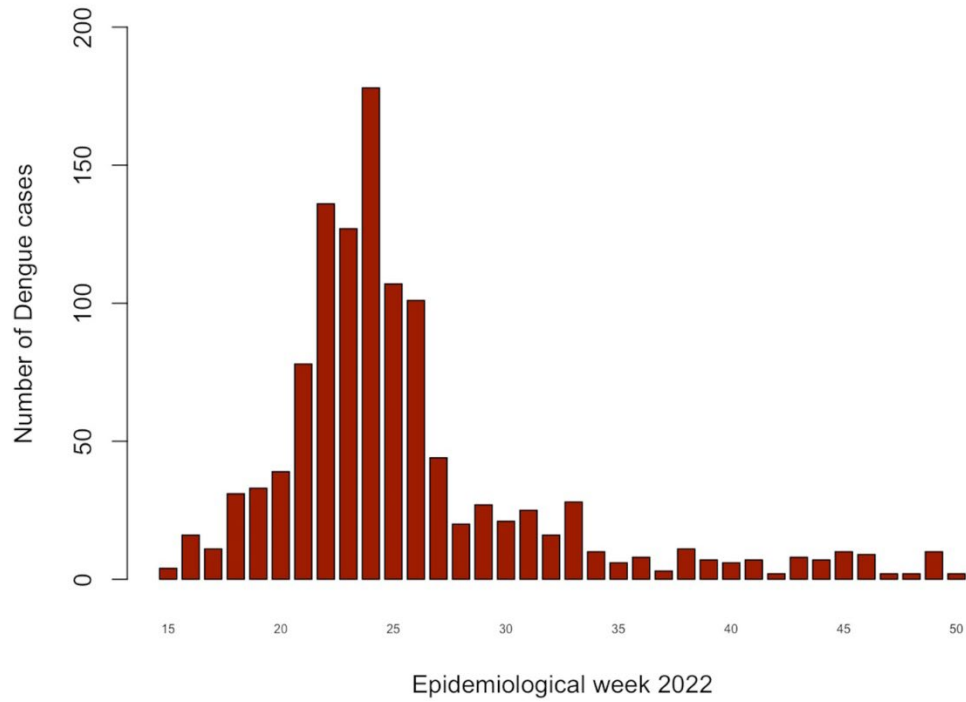
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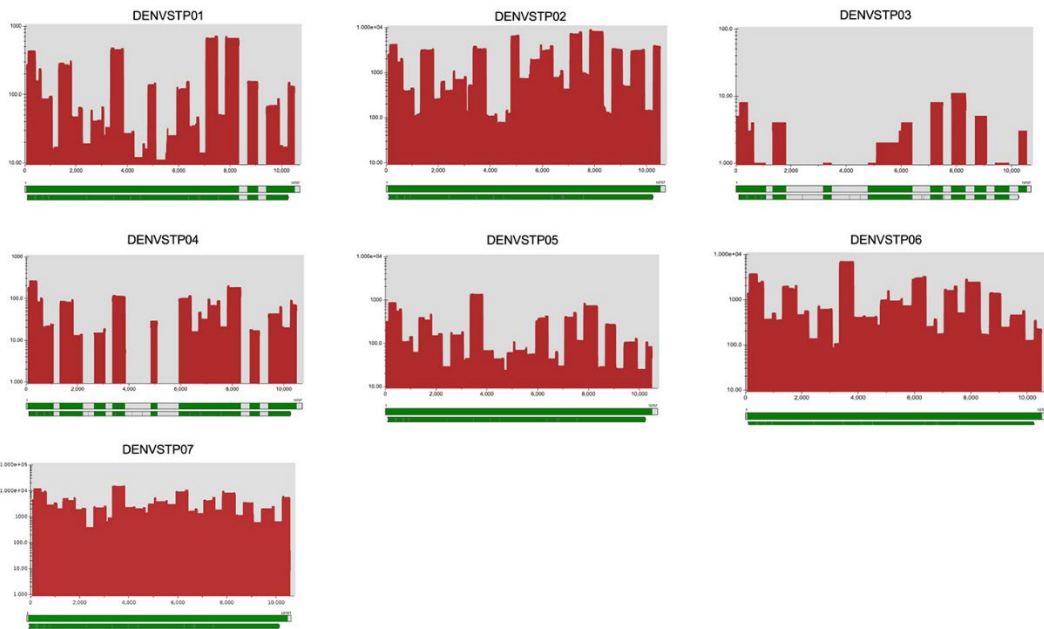
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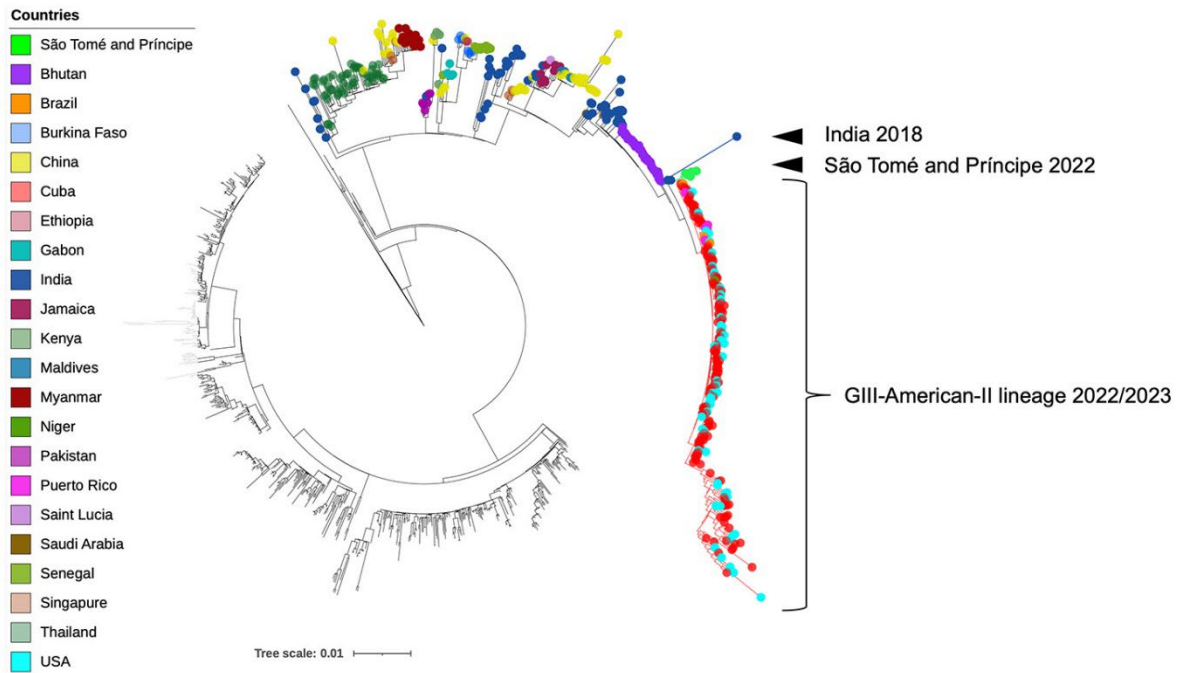
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Appendix Figure 1. Epidemiological curve of the Dengue virus outbreak in the Democratic Republic of São Tomé and Príncipe, 2022. Notified Dengue disease cases were confirmed by a positive rapid test.



Appendix Figure 2. Genome coverage plots for seven sequenced DENV-3 GIII isolates from the Dengue virus outbreak in São Tomé and Príncipe, 2022. Assembled to reference NC_001475.



Appendix Figure 3. Unrooted phylogenomic tree including the four DENV-3 genomes from the Dengue outbreak in São Tomé and Príncipe in 2022 and 1,168 DENV-3 G III genomes sampled worldwide. The four STP sequences are clustered and branched between virus genomes isolated in India 2018 (dark blue) and the branch of the recent GIII-American-II lineage comprising isolates from Cuba (red), Brazil (orange), USA (light blue), and Puerto Rico (pink). Scale bar indicates nucleotide substitutions per site.