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Introduction of New Dengue Virus Lineages after COVID-19 Pandemic, Nicaragua, 2022

Appendix

Appendix Table. Sources of the samples sequenced from the 2022 dengue season in Nicaragua

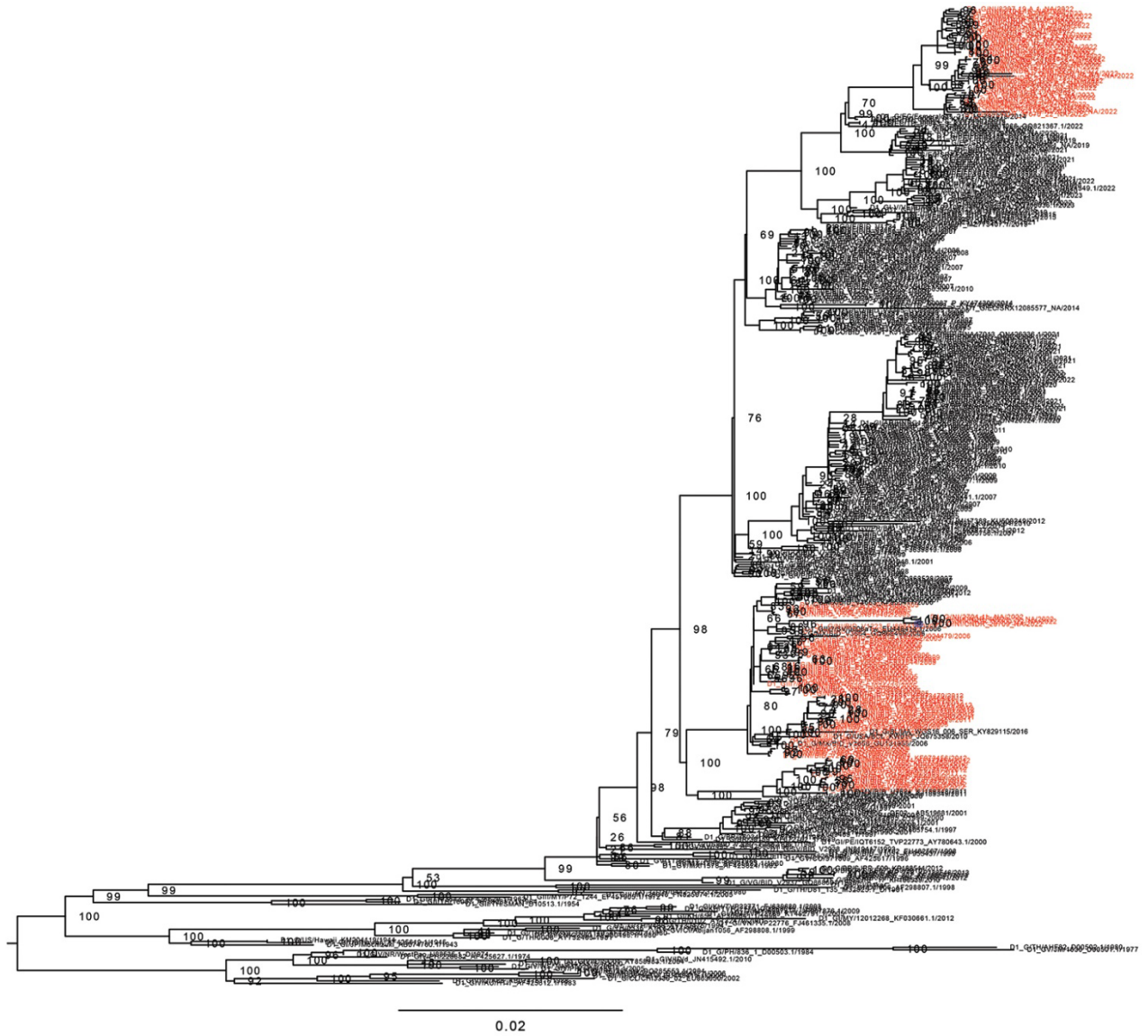
Sequences	Study sites			
	A2CARES (n=4) n (%) [*]	PDHS (n=13) n (%) [†]	PDCS (n=57) n (%) [‡]	MINSAs (n=61) n (%) [§]
DENV-1 genotype V (n=49)	2 (4.1)	8 (16.3)	10 (20.4)	29 (59.2)
DENV-2 Asian/American genotype IIIb (n=6)	Not applicable	Not applicable	6 (100.0)	Not applicable
DENV-3 Indian sub-continent genotype III (n=38)	Not applicable	1 (2.6)	35 (92.1)	2 (5.3)
DENV-4 genotype II (n=42)	2 (4.8)	4 (9.5)	6 (14.3)	30 (71.4)

^{*}A2CARES, American-Asian Arbovirus Research and Epidemiological Surveillance cohort study.

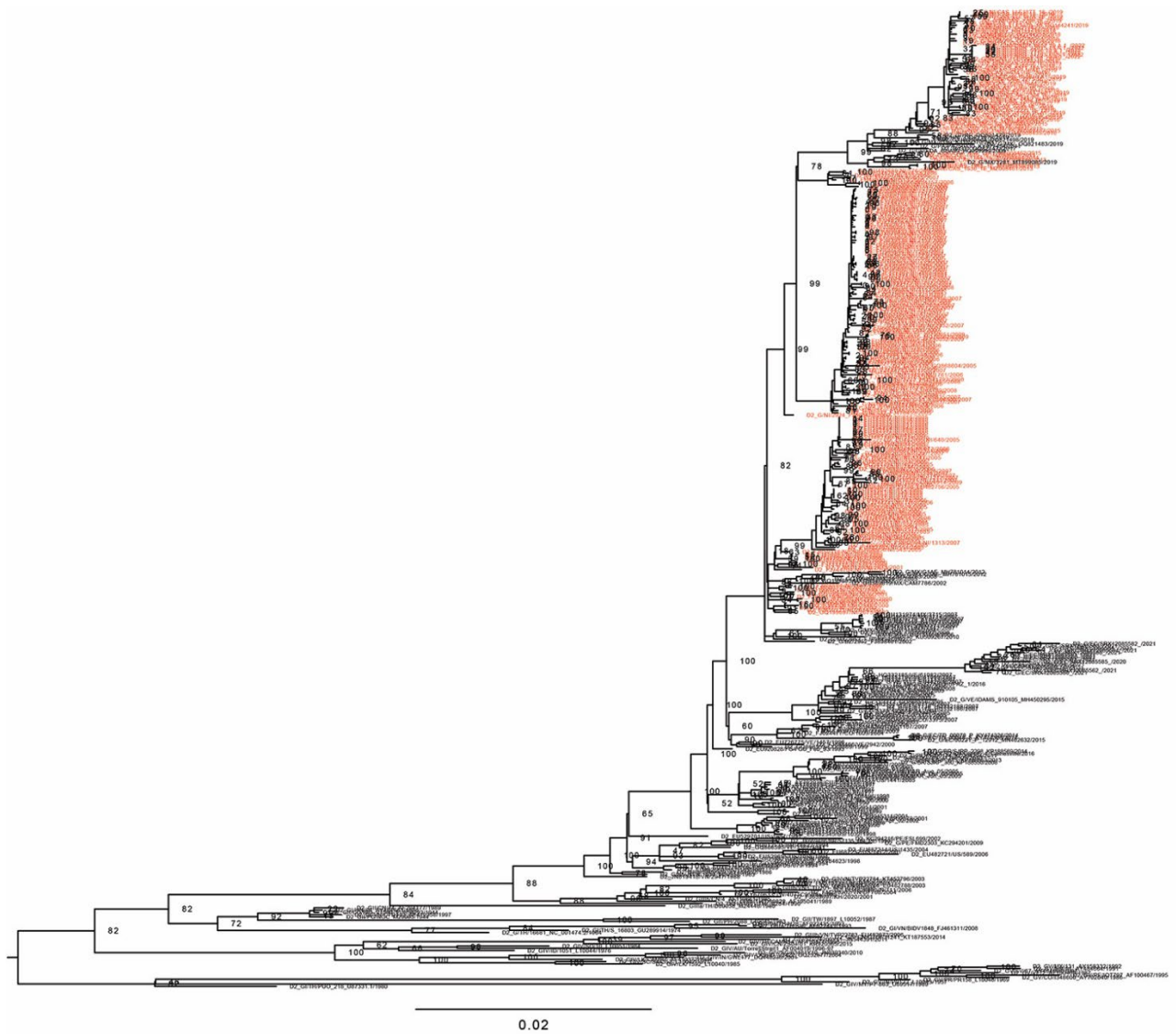
[†]PDCS, Pediatric Dengue Cohort Study.

[‡]PDHS, Pediatric Dengue Hospital-based Study.

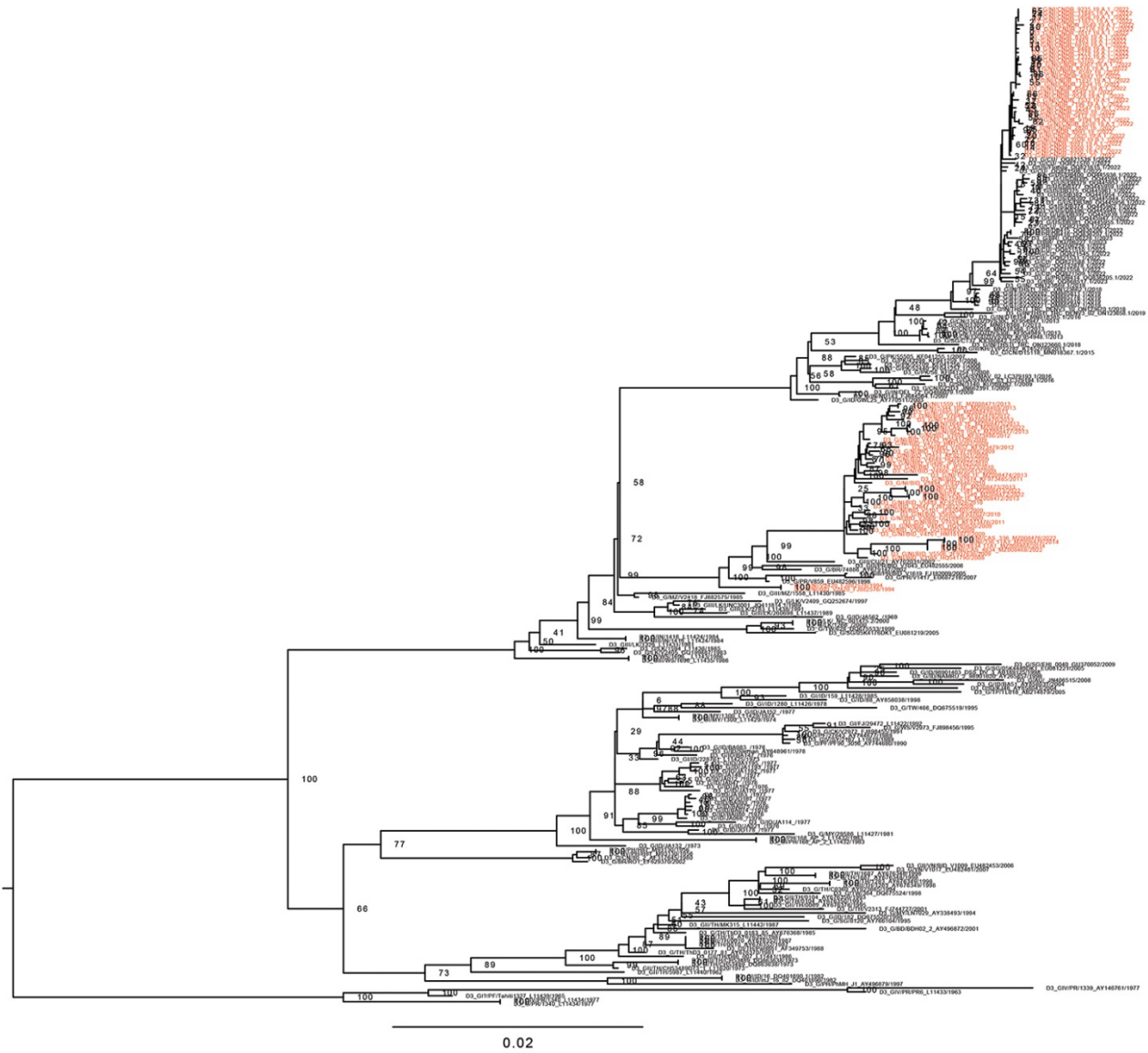
[§]MINSAs, Nicaragua Ministry of Health surveillance.



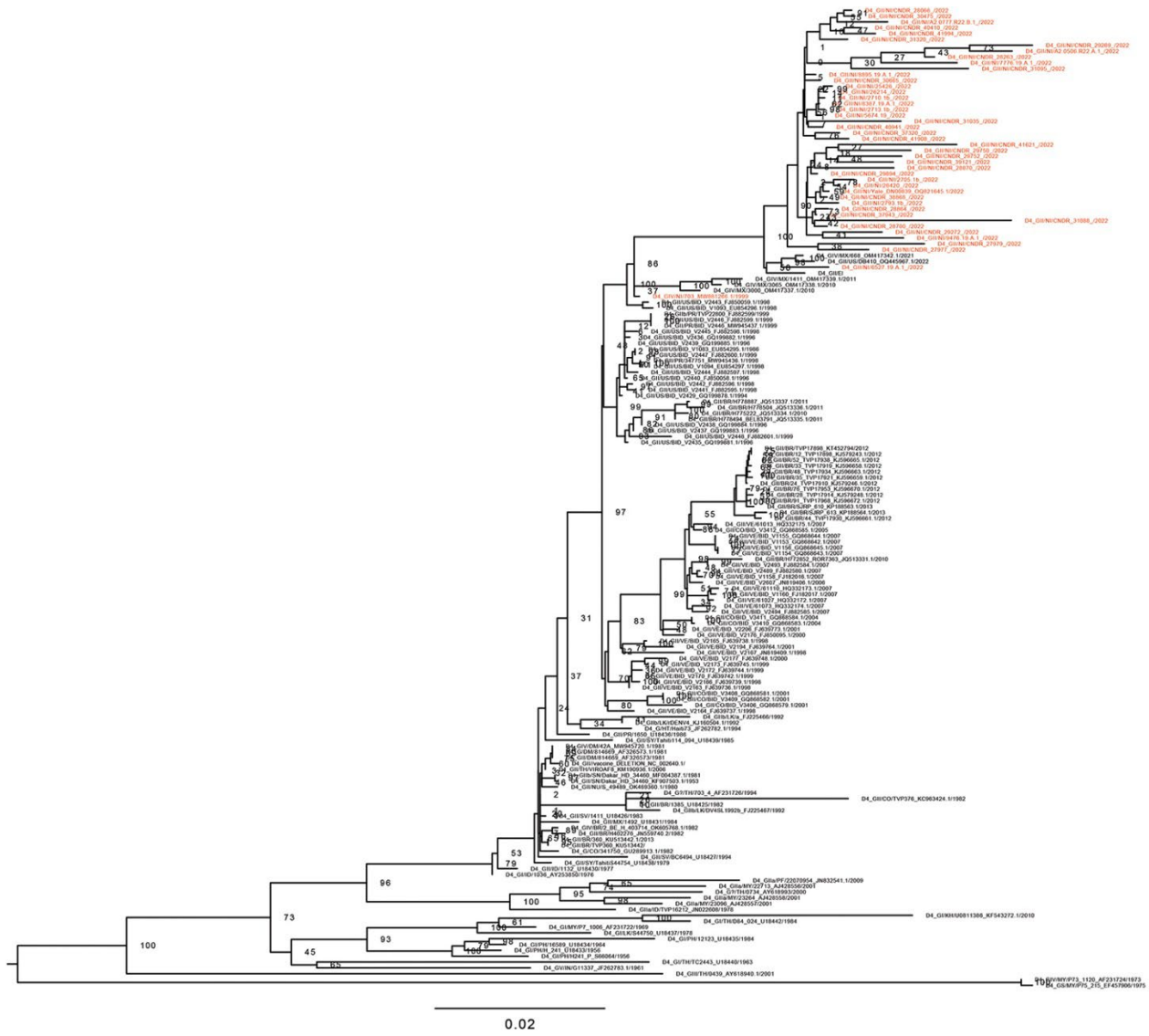
Appendix Figure 1. Maximum Likelihood tree of dengue virus serotype 1 generated in RAXML-HPC BlackBox v.8.2.12 based on an alignment of 408 sequences including those contributed by this study as well as publicly available sequences from [NCBI Virus](https://www.ncbi.nlm.nih.gov/virus/) via BLAST and a comprehensive search by region over time. Nicaraguan sequences colored red. Nodes are labeled with ML bootstrap support values (where default settings were used: RAXML halts bootstrapping automatically when convergence is achieved). Scale bar in substitutions/site.



Appendix Figure 2. Maximum Likelihood tree of dengue virus serotype 2 generated in RAXML-HPC BlackBox v.8.2.12 based on an alignment of 436 sequences including those contributed by this study as well as publicly available sequences from [NCBI Virus](https://www.ncbi.nlm.nih.gov/virus/) via BLAST and a comprehensive search by region over time. Nicaraguan sequences colored red. Nodes are labeled with ML bootstrap support values (where default settings were used: RAXML halts bootstrapping automatically when convergence is achieved). Scale bar in substitutions/site.



Appendix Figure 3. Maximum Likelihood tree of dengue virus serotype 3 generated in RAXML-HPC BlackBox v.8.2.12 based on an alignment of 253 sequences including those contributed by this study as well as publicly available sequences from [NCBI Virus](http://www.ncbi.nlm.nih.gov/nucl/) via BLAST and a comprehensive search by region over time. Nicaraguan sequences colored red. Nodes are labeled with ML bootstrap support values (where default settings were used: RAXML halts bootstrapping automatically when convergence is achieved). Scale bar in substitutions/site.



Appendix Figure 4. Maximum Likelihood tree of dengue virus serotype 4 generated in RAxML-HPC BlackBox v.8.2.12 based on an alignment of 168 sequences including those contributed by this study as well as publicly available sequences from [NCBI Virus](https://www.ncbi.nlm.nih.gov/virus/) via BLAST and a comprehensive search by region over time. Nicaraguan sequences colored red. Nodes are labeled with ML bootstrap support values (where default settings were used: RAxML halts bootstrapping automatically when convergence is achieved). Scale bar in substitutions/site.