

Supplementary

Molecular Characterization of Dengue Type 2 Outbreak in Pacific Islands Countries and Territories, 2017–2020

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Abstract: Dengue virus (DENV) serotype-2 was detected in the South Pacific region in 2014 for the first time in 15 years. In 2016–2020, DENV-2 re-emerged in French Polynesia, Vanuatu, Wallis and Futuna, and New Caledonia, co-circulating with and later replacing DENV-1. In this context, epidemiological and molecular evolution data are paramount to decipher the diffusion route of this DENV-2 in the South Pacific region. In the current work, the E gene from 23 DENV-2 serum samples collected in Vanuatu, Fiji, Wallis and Futuna, and New Caledonia was sequenced. Both maximum likelihood and Bayesian phylogenetic analyses were performed. While all DENV-2 strains sequenced belong to the Cosmopolitan genotype, phylogenetic analysis suggests at least three different DENV-2 introductions in the South Pacific between 2017 and 2020. Strains retrieved in these Pacific Islands Countries and Territories (PICTs) in 2017–2020 are phylogenetically related, with strong phylogenetic links between strains retrieved from French PICTs. These phylogenetic data substantiate epidemiological data of the DENV-2 diffusion pattern between these countries.

Keywords: dengue; phylogeny; molecular evolution; Pacific

Table S1. Path Sampling and Stepping Stone Sampling Marginal Likelihood Estimates of tested Bayesian models.

Population Size	Strict clock	Relaxed clock - lognormal relaxed distribution	Relaxed clock - exponential relaxed distribution
Constant	PS ¹ -2869.47	PS -2879.79	PS -2869.06
	SS ² -2869.47	SS -2880.47	SS -2869.32
Bayesian Skygrid	PS -2865.73	PS -2871.37	PS -2864.95
	SS -2865.90	SS -2871.65	SS -2865.18

¹ PS = Path Sampling, ² SS = Stepping Stone Sampling

>Ancestral state DENV-2 Pacific

ATGCGTTGTATAGGAATATCAAATAGAGACTTGTGGAAGGGGTTCAGGAGGAAGCTGG
 GTTGACATAGTCTTAGAACATGGAAGCTGTGACGACGATGGCGAAAAATAAACCAACA
 TTGGACTTGAAGTATAAAAACCGAAGCCAAACATCCGCCACTTAAGGAAGTATTGT
 ATAGAGGCAAAGCTGACCAACACAACACTACAGCATCTCGTGCACACAAGGAGAACCC
 AGCCTAAATGAAGAACAGGACAAAGGTTGTCTGCAAACACTCCATGGTAGACAGAGGA
 TGGGGAAATGGATGCGGATTGTTGGAAAGGGAGGCATCGTACCTGTGCAATGTTCACA
 TGCAAAAAGAACATGGAAGGAAAAGTCGTGCAACCAGAAAACCTGGACTATAACCATTGT
 ATAACACCTCACTCAGGGAAAGAGAACAGTCAGTCGAAATGACACAGGAAACACGGCACG
 GAAATTAAAGTAACGCCACAGAGTTCCATCACAGAACGCGAACTGACAGGCTATGGCACT
 GTCACGATGGAATGCTCTCCGAGAACCGGCCTCGACTTAATGAGATGGTGTGCTGCAA
 ATGGAAGACAAGGCTTGGCTGGCACAGGCAATGGTCTTAGACCTGCCGTACCATGG
 CTGCCCGAGCAGACAAACAAGGATCAAATTGGATACAGAAGGAGACATTGGTCACITTC
 AAAAATCCCCATGCGAAGAACAGGATGTTGTTAGGATCCAAGAAGGGGCCATG
 CATAACAGCACTCACAGGGCCACGGAAATCCAGATGTCATCAGGAAACTACTGTTCACA
 GGACATCTCAAGTGCAGGCTGAGAACAGGAAACTACAGCTCAAAGGAATGTCATATTCT
 ATGTGTACAGGAAAGTTAAAGTTGAAGGAAATAGCAGAAACACAACATGGAACAATA
 GTTATCAGAGTACAATATGAAGGGACGGTTCTCCGTGCAAGATCCCTTTGAAATAATG
 GATTGGAAGAACAGACATGCTTAGGCCGTTGATCACAGTCACCCAAATTGTTACAGAA
 AAAGACAGCCCAGTCAACATAGAAGCAGAACCTCCATTGGAGACAGTTACATCGTTATA

GGAGTAGAACCGGGACAACCTGAAGCTCAGCTGGTCAAGAAAGGGAGTTCTATTGGCAA
ATGTTGAGACAACAATGAGAGGAGCGAAGAGAATGCCATTAGGTGACACAGCTTGG
GATTTGGATCCCTGGGAGGAGTGTTCACATCTATAGAAAGGCCCTCCACCAAGTTTT
GGAGCAATCTATGGGCTGCCTTAGCGGGTTCATGGACTATGAAAATCCTTATAGGA
GTCGTCATCACATGGATAGGAATGAATTACGCAGCACCTCACTGTCTGTGTCAGTA
TTAGTGGG

Figure S1. Ancestral state reconstruction of the sequence of The Most Recent Common Ancestor to all strains retrieved in the South Pacific between 2014 and 2020.