



First Complete Genome Sequences of Dengue Virus Serotype 2 Strains from the Solomon Islands and Vanuatu

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ABSTRACT Isolates of dengue virus serotype 2 (DENV-2) were recovered from a female resident of the Solomon Islands in 2016 and another female patient who had traveled from Vanuatu to Australia in 2017. Here, we describe the first complete genome sequences of DENV-2 strains from Vanuatu and the Solomon Islands.

Dengue virus serotype 2 (DENV-2; genus *Flavivirus*, family *Flaviviridae*) (1) has recently caused several outbreaks of dengue disease in the Pacific region, including the Solomon Islands and Vanuatu (2–4). Between August 2016 and April 2017, 12,250 dengue virus cases with 10 hospitalizations were recorded in the Solomon Islands, and in Vanuatu, 2,838 cases with 147 hospitalizations were reported between November 2016 and May 2017 (2).

In October 2016, a female in her 70s residing in the Solomon Islands presented with headache, fever, and body aches. In January 2017, a second female patient in her 20s developed symptoms of diarrhea and joint pain after traveling from Vanuatu to Brisbane, Australia. DENV-2 RNA was detected in acute-phase serum from both patients by reverse transcription real-time PCR (RT-rtPCR) (5, 6), and DENV-2 isolates, namely, SI 2016 and Van 2017, were subsequently recovered from each serum sample.

Here, we describe the whole-genome sequencing (WGS) of SI 2016 and Van 2017 and the first report of complete DENV-2 genome sequences from isolates obtained from the Solomon Islands and Vanuatu. Briefly, DENV-2 RNA was extracted from the SI 2016 and Van 2017 isolates (C6/36 cell culture supernatant, passage 1) using the QIAamp viral RNA extraction kit (Qiagen, Chadstone, Australia). The extracted viral RNAs were circularized to enable complete sequencing of the terminal 5' and 3' untranslated regions using a tobacco decapping enzyme (Enzymax LLC, USA) and T4 RNA ligase (New England Biolabs, Genesearch, Arundel, Australia) as reported previously (7). To remove host and potentially contaminating microbial DNA, the circularized RNA was then DNase treated (Heat & Run kit, ArcticZymes, Scientifix, South Yarra, Australia). Whole-genome sequencing was performed on a NextSeq 500 instrument (Illumina, San Diego, CA) as described previously (7, 8) using the Nextera XT kit for cDNA library construction, followed by paired-end (2 × 151-nucleotide [nt]) sequencing using the V2 mid output kit. Ethical approval for this study was granted by the Forensic and Scientific Services Human Ethics Committee.

Illumina sequencing yielded 15,050,786 and 10,303,566 for SI 2016 and Van 2017, respectively, and raw sequence reads were processed using Geneious R10 (version 10.2.3) software (9). Low-quality reads were removed using BBDuk (version 37.25; minimum quality score, 20). Trimmed reads were assembled by mapping to a reference genome (GenBank accession number [AB189124](https://www.ncbi.nlm.nih.gov/nuccore/AB189124)) with complete 5' and 3' untranslated terminal sequences using default parameters and the low-sensitivity setting. To compare the SI 2016 and Van 2017 genome sequences with all other available DENV-2 sequences on GenBank, BLASTN analyses were performed using an expect threshold of 10. For SI 2016, a total of 3,861,001 (from 5,400,568) reads mapped to the reference

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genome (AB189124), with an average coverage depth of 48,014×. The SI 2016 complete genome (10,723 nt; G+C content, 45.7%) and envelope (E) gene (1,485 nt) sequences demonstrated 97% nt sequence identity with the reference genome and 99% nt sequence identities with DENV-2 strains from Papua New Guinea in 2013 (KU517845) and the Solomon Islands in 2016 (KY495808). For Van 2017, a total of 1,916,389 (from 3,144,522) reads mapped to the reference genome, with an average coverage depth of 23,840×. The Van 2017 complete genome (10,722 nt; G+C content, 46.2%) and E gene (1,485 nt) sequences demonstrated 98% nt sequence identity with the reference genome and 98% and 100% nt sequence identities with DENV-2 strains from China in 2001 (KR920365) and French Polynesia in 2017 (from a patient who had traveled to Vanuatu; KY782126), respectively. The complete genomes of SI 2016 and Van 2017 (both belonging to the DENV-2 Cosmopolitan genotype) share only 96% nt sequence identity, highlighting the potential diversity of DENV-2 strains responsible for concurrent outbreaks in the Pacific. These data are important for the ongoing surveillance and monitoring of DENV strains which continue to be a major public health threat throughout the Pacific and wider global regions in which *Aedes* mosquito vectors are prevalent.

Data availability. Raw sequencing reads were deposited in NCBI under the BioProject accession number PRJNA493303 (SRA numbers SRX4776970 and SRX4776971). The consensus genome sequences have been deposited in GenBank under accession numbers MH985858 (SI 2016) and MH985859 (Van 2017).

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