AMERICAN SOCIETY FOR MICROBIOLOGY | genomeAnnouncements

# Complete Genome Sequences of the *Potyvirus Sweet potato virus 2* from East Timor and Australia

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**We present here the first complete genome sequences of *Sweet potato virus 2* (SPV2) from sweet potato in Australia and East Timor, and compare these with five complete SPV2 genome sequences from South Korea and one each from Spain and the United States. Both were closely related to SPV2 genomes from South Korea, Spain, and the United States.**

**Received** 20 April 2016 **Accepted** 22 April 2016 **Published** 2 June 2016

**Citation** Maina S, Edwards OR, de Almeida L, Ximenes A, Jones RAC. 2016. Complete genome sequences of the *Potyvirus Sweet potato virus 2* from East Timor and Australia. Genome Announc 4(3):e00504-16. doi:10.1128/genomeA.00504-16.



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To examine possible connectivity between viruses infecting crops in Australia and Southeast Asia, we studied sweet potato viruses from East Timor and Australia. *Sweet potato virus 2* (SPV2; synonym, *Sweet potato virus Y*) is a single-stranded RNA virus within the genus *Potyvirus*, family *Potyviridae* (1). It was found previously in Australia, and six Australian coat protein sequences exist (AM050884 to AM050888 [1] and EF990648 [2]), but it is not reported from East Timor. Seven complete SPV2 genomes are available on GenBank, five from South Korea, and one each from Spain and the United States (3–5). Australian sample AusCan and sample Tm37 collected in May 2015 from the Dili district of East Timor were sequenced and their complete genomes obtained. AusCan and Tm37 were coinfected with *Sweet potato chlorotic fleck virus* (2, 6).

Fifteen East Timorese samples blotted onto Fast Technology for Analysis of nucleic acids (FTA) cards (7) were sent to Australia. A plant infected with AusCan (CP accession no. EF990648) was planted, and a scion from it was graft-inoculated to the indicator host *Ipomoea setosa*. Total RNA was extracted from the FTA cards, and from an *I. setosa* leaf sample with virus symptoms, using the ZR plant RNA MiniPrep kit (Zymo Research). The total RNA extracts were treated with RNase-free DNase (Invitrogen) and measured using Qubit (Invitrogen). RNA integrity was confirmed using RNA screen tape (TapeStation 2200; Agilent Technologies). Libraries were prepared from total RNA using a TruSeq stranded Total RNA sample preparation Ribo-Zero plant kit (catalog no. RS-122-2401; Illumina). The final size and concentration of each library were verified using Qubit and D1000 ScreenTape (TapeStation 2200; Agilent Technologies). Sequencing was performed by HiSeq 2500 using a TruSeq SBS kit version 4 (Illumina) with 151 cycles of paired-end reads. The reads were assembled and genomes annotated using CLC Genomics Workbench 6.5 (CLC bio) and Geneious 8.1.7 (Biomatters) (8).

FTA card sample Tm37 yielded 14,721,488 reads and, after trimming, 14,546,337 reads remained. *De novo* assembly generated 1,307 contigs and 13,415 reads mapped to the contig of interest, with a coverage of 298×. Sample AusCan yielded 6,260,728 reads, and, after trimming, 5,405,928 reads remained. *De novo* assembly generated 832 contigs, with 964,917 reads mapping to the contig of interest, giving a coverage of 1,460×. Both Tm37 and AusCan SPV2 sequences coded for 10 proteins, as occurs with other potyviruses (5, 9). The pairwise nucleotide sequence identity between Tm37 and AusCan was 97.7%, which is well within the species demarcation limit of 76% for complete *Potyvirus* genomes (10, 11). The closest pairwise identity for Tm37 was 98.7% to accession no. KP115617 from South Korea, and for AusCan, identity was 98.6% to accession no. KU511270 from Spain, followed by 98.3% to accession no. JN613807 from the United States. Thus, the Australian and East Timorese isolates were marginally less closely related to each other than to isolates from other parts of the world.

**Nucleotide sequence accession numbers.** The sequences were deposited in GenBank under accession numbers KX017447 (Tm37) and KX017448 (AusCan).

## ACKNOWLEDGMENTS

Martin Barbetti and Mingpei You of the School of Plant Biology, The University of Western Australia (UWA), provided administrative support. The UWA ARC Centre of Excellence in Plant Energy Biology and School of Chemistry and Biochemistry and Laura Boykin also provided initial administrative support at the beginning of this project.

## FUNDING INFORMATION

This work, including the efforts of Solomon Maina, was funded in part by Cooperative Research Centres, Australian Government Department of Industry (CRCs) (Project PBCRC61056).

The Cooperative Research Centre for Plant Biosecurity and The University of Western Australia provided a scholarship and operating funds to Solomon Maina. Both organizations and The Commonwealth Scientific and Industrial Research Organisation provided additional operating funds. The University of Western Australia and the Department of Agriculture and Food Western Australia provided laboratory and glasshouse facilities to this project.

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