

First report of *Citrus concave gum associated virus* (CCGaV) on apple (*Malus* spp.) in South Africa.

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Citrus concave gum-associated virus (CCGaV), species *Coguvirus citri*, in the family *Phenuiviridae* is a flexuous, nonenveloped virus with a bipartite genome of negative-stranded RNA coding for the viral RNA-dependent RNA polymerase (RdRp), and an ambisense RNA (RNA2) with two open reading frames (ORF) encoding a putative movement protein and nucleocapsid protein. This graft transmissible virus has been reported from Italy, Hungary, the Czech Republic, the USA, and Brazil on either citrus or apple. Here, leaf samples of 12 apple trees displaying reduced vigor relative to other trees in the orchard were collected from the Elgin and Ceres production areas of the Western Cape, South Africa. One sample was sequenced through preparation of a TruSeq Stranded Total RNA with Ribo-Zero Plant library and sequenced at Lifesequencing on an Illumina NextSeq500 platform while the other libraries were prepared according to Shishkin et al (2015) and sequenced using an Illumina NextSeq 2K sequencer (University of Leeds, UK). Reads were trimmed using CLC Genomics Workbench 21 (Qiagen Bioinformatics, Aarhus, Denmark) and were deposited in NCBI sequence read archive PRJNA1026321. Reads were assembled using metaSPAdes. Complete/near complete CCGaV genomes were assembled for all 12 samples, with an average length of 6,651 and 2,728 nucleotides for RNA1 and 2 respectively (OR728660-OR728683). The identification was confirmed with reverse-transcriptase (RT) PCR using CCGaV-specific primers (Navarro et al. 2018) and Sanger sequencing. All extant CCGaV genomes share >97% nucleotide identity for both RNA1 and RNA2 but variants from apple and citrus while closely related are distinct (Minutolo et al. 2021). This was confirmed through the generation of a percent identity matrix with genomes from this study and those available from GenBank. Concave gum symptoms have been closely associated with CCGaV on citrus, however, less is known about the symptomatology on apple. CCGaV has not been found present on citrus in South Africa (Maree, *per comm.*).

References

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Ethical Statement: The submitted work is the original work of the authors and has not been published or submitted for publication elsewhere in any form or language (partially or in fully).

Data availability: Confirmed sequences deposited with Genbank numbers OR728660 to OR728683. The high throughput sequencing data are under accession number PRJNA1026321. The reviewer link to the data is: <https://dataview.ncbi.nlm.nih.gov/object/PRJNA1026321?reviewer=2ee828113e7jbp0hp9mqjljke31>