

First report of a potyvirus infecting *Albucca rautanenii* in the Namib Desert

O. D. J. Zablocki;

Centre for Microbial Ecology and Genomics (CMEG), University of Pretoria, Pretoria, 0002;

E. P. Rybicki,

Institute of Infectious Diseases and Molecular Medicine, University of Cape Town, Observatory, 7925 Cape Town, South Africa;

and D. A. Cowan,

Centre for Microbial Ecology and Genomics (CMEG), University of Pretoria, Pretoria, 0002, South Africa

Chlorotic, streak-like symptoms were observed in April 2013 on a single specimen of *Albucca rautanenii* (Schinz) J.C.Manning & Goldblatt (Family: *Hyacinthaceae*) found among other plants near Homeb in the Namib Desert, Namibia. No potential insect vectors (e.g. aphids) were observed around and on the infected plant. An extract from symptomatic leaves was assessed by transmission electron microscopy (leaf dip method) to ascertain if the symptoms were viral in origin. Long, flexuous threadlike particles 687-825 nm in length and 12.5 nm in diameter were observed. The morphology and size of the particles were indicative of a putative member of the taxonomic family *Potyviridae*. To confirm this, RT-PCR using universal potyvirus primers which amplify part of the nuclear inclusion b gene (Nib) was conducted (1) on total RNA extracted from leaf tissue (Qiagen RNeasy Plant Mini Kit). The triplicated reaction yielded amplicons of the expected size (~350 bp), which were cloned into the pJET 1.2 vector (Thermo Scientific, Waltham, MA) according to manufacturer's instructions. The sequences of 10 clones were trimmed to remove vector and primer ends and were deposited in the EBI database under the accession numbers LK995422-LK995431. Curated sequences were used to search the GenBank database using BLASTn and tBLASTx, as well as for phylogenetic analysis. Intra-clonal nucleotide sequence similarity ranged from 97.99-99.72%. BLASTn searches showed all clones were 72% identical to *Papaya ringspot virus* isolate 1 accession JQ314105.1 (87% coverage), followed by *Bean yellow mosaic virus* clone Brn167 accession JF707769.1 (72% identity with 86% sequence coverage). The translated peptide fragment was most similar to *Sugarcane mosaic virus* isolate Beijing (accession AY042184.1), with a query cover of 98% and a similarity of 81%. Phylogenetic analysis was performed with a set of 57 reference potyvirus genomes, with their Nib regions aligned with the cloned nucleotide sequences according to the parameters used previously (1). The clones formed a distinct cluster, at a node with Cocksfoot streak virus (CSV, accession NC_003742.1). An identity matrix of the aligned Nib clones and CSV showed a nucleotide identity range of 68.79-70.23%. These results suggest that the virus isolate belongs to the family *Potyviridae*, genus *Potyvirus*, supported by the characteristic morphological features of the virion and its relatedness to CSV. Moreover, the clustering of all sequences at a single node suggests a homogeneous viral population, without significant strain variation. Genetic distance inferred by phylogenetic analysis further suggests that the

isolate is a novel species within the genus, which we tentatively name *Albuca mosaic virus*, AlbMV. To our knowledge, this is the first report of any plant virus infection in the native Namib Desert ecosystem. This is particularly relevant due to the scarcity and uniqueness of plant life in this hyperarid desert environment, and additional monitoring of this virus infection and other desert plant species is encouraged.

References

1. L. Zheng et al. *Plant Pathol.* 59:211, 2010.