



NEW DISEASE REPORT

First report of *Physostegia* chlorotic mottle virus in *Sarcococca* sp.

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In December 2021 a sample of *Sarcococca* sp. was submitted to Fera Science Ltd; the sample was taken following the inspection of a plant shipment originating from the Netherlands and destined for a nursery in England. The sample was sent due to the presence of vein clearing and leaf distortion symptoms consistent with viral infection (Fig 1.). The symptoms were observed on a single plant in a consignment of 75 plants.

The sample was initially tested by ELISA for cucumber mosaic virus (Agdia, USA), Arabis mosaic virus, potyviruses (DSMZ, Germany), strawberry latent ringspot virus and with broad spectrum antisera for tospoviruses (Bioreba, Switzerland). The sample tested negative. To determine the possible presence of virus(es) the sample was analysed by high throughput sequencing (HTS) as described by Fowkes et al. (2021). The total number of read pairs sequenced was 3,845,798 with 645,507 (16.8%) attributed to *Physostegia* chlorotic mottle virus (PhCMoV), with an average coverage of 11,210. The full coding sequence of PhCMoV was obtained, with 99% identity to a PhCMoV isolate from the Netherlands (GenBank Accession No. OK646031.1). The sequence was submitted to GenBank under accession PQ303396 and metagenomic sequence data was deposited under SRR30598214. To confirm the results of the HTS sequencing, the sample was tested using PhCMoV-specific primers (Gaafar et al., 2017), a 875 bp product was obtained and sent for Sanger sequencing (Eurofins, Germany),



FIGURE 1 Leaf of *Sarcococca* sp. with vein clearing symptom

and confirmed to be PhCMoV by nucleotide sequence comparison (PQ303397), with 99% identity to accession OK646031.1.

PhCMoV is assigned to the species *Alphanucleorhabdovirus physostegiae* in the family *Rhabdoviridae*. The virus was first found in 2014, but then reported in a German only institutional report in 2016, then formally reported from Austria in 2018, it has now been reported from several countries in mainland Europe (Temple et al., 2022; Temple et al., 2024). PhCMoV has been reported to be transmitted by a species within the genus *Anaceratagallia* (Temple et al., 2024).

PhCMoV has a broad host range and is known to infect members of the families *Asteraceae*, *Convolvulaceae*, *Cucurbitaceae*, *Lamiaceae*,

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Polygonaceae, *Ranunculaceae* and *Solanaceae*, (Temple et al., 2022). This report of PhCMoV from *Sarcococca* represents the first report of the virus infecting plants from the family *Buxaceae*. The virus has been associated with vein clearing in *Galinsoga parviflora*, *Solanum melongena*, and *Helleborus* (Temple et al., 2022). As no other viruses were detected by HTS in the sample, it is possible that the symptoms observed in *Sarcococca* are due to infection with PhCMoV, however, further epidemiological evidence would be required to confirm the association of infection with these symptoms in this host (Fox, 2020). With this first finding in the family *Buxaceae*, the host range of this emerging virus is broader than currently reported and further work needs to be conducted on the epidemiological significance of this virus.

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