

Angelonia flower mottle, a new disease of *Angelonia angustifolia* caused by a hitherto unknown carmovirus

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Angelonia angustifolia (Scrophulariaceae), a Central American ornamental, is receiving increasing attention in the USA and Europe for its attractive flowers. In Germany, a number of accessions from commercial companies, subjected to evaluation for varietal release, exhibited conspicuous flower mottling symptoms, suggestive of virus infection. Carmovirus-like isometric particles (approx. 30 nm in diameter) were detected in plants with symptoms by electron microscopy. Sap inoculation studies revealed that the virus is mechanically transmissible to *Angelonia* plants, leading to mottling symptoms on the petals of flowers. When inoculated to *Nicotiana hesperis*, *N. occidentalis*, *N. glutinosa* and *N. clevelandii*, latent infections confined to the site of inoculation site resulted. An antiserum (DSMZ AS-858) raised against a purified virus preparation, reacted specifically with homologous antigen in western blot analyses. Virus was detected in flowers and in symptomless leaves.

Immunoelectron microscopic decoration tests showed no detectable cross-reaction to several other carmoviruses.

Clones of the complete coat protein gene were obtained by RT-PCR from viral RNA isolated from purified particles. Sequence analysis of the 1053 nucleotide coat protein gene (EMBL Acc. No. AM050058; encoding a predicted 351 amino acid product) confirmed this virus to be a typical, but distinct, carmovirus with 49 and 48% nucleotide sequence identity (37% and 35% amino acid sequence identity) to *Pelargonium flower break virus* and *Carnation mottle virus* respectively.

During cultivation of *Angelonia*, transient mild chlorotic spots appeared on the leaves of infected and non-infected plants, which are suspected to be stress-induced. Since the flower mottle symptoms consistently correlate with infection by the carmovirus, it is proposed naming this tentative new carmovirus species, *Angelonia flower mottle virus*.

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First report of *Ornithogalum mosaic virus* and *Ornithogalum virus 2* in New Zealand

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Ornithogalum thyrsoides, *Iris* sp. cv. Wedgewood and *Iris tingitana*, exhibiting mild mosaic leaf symptoms, were collected from a commercial grower's property near Palmerston North, New Zealand. All samples tested positive for potyvirus infection by ELISA using a universal potyvirus monoclonal antibody (Agdia Inc.). Universal potyvirus primers PV2/IT7 and PV1/SP6 (Mackenzie *et al.*, 1998) were used to amplify a ~1.7 kb product spanning part of the *Nib* gene, the entire *CP* gene and the 3' UTR. The amplicon was cloned into the vector pGEM®-T Easy (Promega Corporation) and the resultant sequences analysed using CLUSTALX (version 1.83), PAUP (version 4.0 Beta 10) and DNA-STAR (version 4.0).

Three distinct sequences related to *Ornithogalum mosaic virus* (OrMV) were deposited in GenBank: nzOrMV-1 from *O. thyrsoides* (AY994102), nzOrMV-2 from *Iris* cv. Wedgewood (AY994106), and nzOrMV-3 from *I. tingitana* (AY994107). Isolates nzOrMV-1 and nzOrMV-2 shared 95% nucleotide identity with each other and 90 and 91% identity, respectively, with a South African isolate of OrMV from *Ornithogalum* (D00615). Isolate nzOrMV-3 showed only ~88% identity with nzOrMV-1 and nzOrMV-2, but 99% nucleotide identity with an Australian isolate of OrMV, also obtained from *Iris* sp. (AF203528). A second potyvirus isolated from *O. thyrsoides* as a single infection (AY994103), showed between 79 and 99% nucleotide identity to partial *Nib* gene, complete *CP* gene and 3'UTR, when compared with previously published sequences of *Ornithogalum virus 2* (Fuji *et al.*, 2003). In common with the sequences of *Ornithogalum virus 2* from Japan, the New Zealand *Ornithogalum virus 2* isolate has an unusual cleavage site (V-Y-H-Q/T) between the *Nib* and *CP* genes.

OrMV is a distinct *Potyvirus* species, originally identified from *O. thyrsoides* in the USA by Smith & Brierley in 1944 (Van Regenmortel *et al.*, 2000), and can cause severe disease problems in some ornamentals (Fuji *et al.*, 2003). Reported susceptible hosts included *Chenopodium quinoa*, *Lachenalia* spp., *Nicotiana clevelandii*, *O. thyrsoides* and *Tetragonia tetragonioides*, whereas *I. germanica* was considered nonsusceptible (Burger, 1991). *Ornithogalum virus 2* was recently identified from Japan (Fuji *et al.*, 2003), where it was found coinfecting *O. thyrsoides* with OrMV and another previously unknown potyvirus, *Ornithogalum virus 3*. This is the first report of either OrMV and *Ornithogalum virus 2* in New Zealand.

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