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**First Report of Narcissus mosaic virus From Iris and From  
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Review

## First Report of *Narcissus mosaic virus* From Iris and From Australia

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*Narcissus mosaic virus* (NMV) is a little studied member of the genus *Potexvirus* (family Alphaflexiviridae). It was first described in Britain from *Narcissus* sp (family Amaryllidaceae) in 1966 (1). Later, aspects of its encapsidation biology were reported (2). In 1989, the type isolate of NMV from The Netherlands was one of the first plant virus genomes to be fully sequenced (GenBank accession D13747) (4). In 2001 a partial genome sequence (AJ270988) from the Netherlands was released, and in 2003 another complete genome from New Zealand became available (AY225449). To our knowledge, no other reports of NMV detection exist, and all reports are from narcissus. Here we report the detection and sequencing of the complete genome of an isolate of NMV infecting *Iris xiphium* Desf. (cv Telstar Blue) (Spanish Iris, Dutch Iris, family Iridaceae) in Australia. Iris bulbs were purchased from a retail hardware supply store in Perth, Australia, and grown within a greenhouse. Leaves displayed mild streaking patterns. Previously we used a high-throughput sequencing approach to identify multiple viruses infecting other *I. xiphium* plants (3), and in this case, a similar procedure was followed. Briefly, total RNA was extracted from a symptomatic leaf, and cDNA was synthesized using random primers before library preparation. Sequencing was done on a Roche GS Junior machine. Sequence reads were edited where necessary and contigs and consensus sequences were constructed *de novo* using CLC Genomics workbench software v6.0.1. Blast analysis revealed a sequence of 6,957 nucleotides (nt) that shared 97% nt identity across the genomes of both the Dutch and New Zealand isolates of NMV, confirming its identity as an isolate of *Narcissus mosaic virus*. The new isolate was designated NMV-SW13-Iris. Like other NMV isolates, the NMV-SW13-Iris genome is predicted to encode a replicase calculated at 184.8 kDa, a triple gene block involved in viral movement consisting of three proteins of 25.9 kDa, 12.8 kDa, and 11.1 kDa encoded from overlapping reading frames, a coat protein (CP) of 24.4 kDa, and a protein of unknown function of 10.1 kDa encoded within the CP gene in the +1 reading frame. The nucleotide sequence of the NMV-SW13-Iris genome was granted Genbank accession KF752593. Only one RNA virus, NMV, was present in the symptomatic plant tested. To our knowledge, this isolate represents the first report of *Narcissus mosaic virus* from a host other than narcissus, and the first report of its presence in Australia. Although this virus has not been widely reported, the significance of this discovery is that NMV has a broader host range than previously thought. It is possible, therefore, that NMV is under diagnosed. This has implications for production in the floriculture industry, and for the diagnosis of viruses infecting internationally traded flower bulbs. The high-throughput sequencing approach used is a powerful generic tool for the detection of unexpected and unknown viruses.

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