

NEW DISEASE REPORT

First report of turnip vein clearing virus (*Tobamovirus rapae*) infecting *Silene flos-cuculi* in Portugal

W. Menzel¹  | D. Knierim¹ | P. Margaria¹ | A. Silva²¹Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures, Plant Virus Department, Braunschweig, Germany²Novo Sol Plantas Lda, Taipadas Canha, Portugal

Correspondence: W. Menzel, Leibniz Institute DSMZ - German Collection of Microorganisms and Cell Cultures, Plant Virus Department, Inhoffenstraße 7 B, 38124 Braunschweig, Germany. Email: wulf.menzel@dsMZ.de

KEYWORDS

Caryophyllaceae, ornamentals, Tobamovirus, TVCV



FIGURE 1 Diseased *Silene flos-cuculi* leaf samples infected with turnip vein-clearing virus

Few viruses have been identified in species of the genus *Silene* (syn. *Lychnis*) and none are reported in *Silene flos-cuculi* (ragged robin). Viruses infecting the genus include, for example, Melandrium yellow fleck virus (GenBank Accession No. MT153870) and cucumber mosaic virus (OQ388340) in *Silene latifolia*, *Lychnis* mottle virus (KR011033) in *Silene cognata* and *Lychnis* ringspot virus (MG913811) in *Lychnis* sp.

In May 2024, about 50 *Silene flos-cuculi* plants with symptoms suspected of being viral (mottled and slightly deformed leaves) were observed in a production facility in Portugal (Figure 1). To identify the viruses putatively involved, a diseased leaf sample was mechanically inoculated on *Nicotiana tabacum* cv. Samsun nn, which developed leaf mottling and deformation, indicating the successful transmission of a putative viral pathogen (Figure 2). To identify it, total RNA was



FIGURE 2 Symptoms caused by turnip vein-clearing virus on *N. tabacum* cv. Samsun nn 18 days post inoculation

extracted using a Qiagen RNeasy Plant Mini kit and sequenced on an Illumina NextSeq2000 high-throughput sequencing (HTS) platform. Analysis of the assembled sequences (Geneious Prime v. 2024.0.5, Dotmatics) revealed the almost complete genomic sequence of a

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tobamovirus (PQ072296), which showed the highest nucleotide identity (98.9%) to turnip vein-clearing virus (TVCV; OQ446799). Pairwise alignment with the sequence of the exemplar isolate of this species (NC_001873) showed 98.7% identity, thus clearly identifying it as an isolate of the species *Tobamovirus rapae*. No further viruses were detected. Based on this information, eight individual diseased samples were tested using a generic tobamovirus RT-PCR (Li et al., 2018), all of which were positive. A representative amplicon was sequenced (with forward and reverse PCR primers) and showed 100% identity to the sequence originally obtained by Illumina HTS (PQ072296).

This is the first evidence of TVCV infecting species of the genera *Silene*/*Lychnis*. Following the successful transmission to *N. tabacum* cv. Samsun nn, the isolate was deposited in the DSMZ Plant Virus Collection under accession PV-1452. TVCV has been found increasingly in various vegetatively propagated ornamental plants of different families, which indicates a broad host range. The ease of mechanical transmissibility during cultivation facilitates the spread of this tobamovirus and represents a fundamental problem for the propagation of orna-

mental plants, thus imposing higher demands on operational hygiene procedures.

ORCID

W. Menzel  <https://orcid.org/0000-0002-3614-161X>

REFERENCE

Li, Y., Tan, G., Lan, P., Zhang, A., Liu, Y., Li, R. et al. (2018) Detection of tobamoviruses by RT-PCR using a novel pair of degenerate primers. *Journal of Virological Methods*, 259, 122–128. <https://doi.org/10.1016/j.jviromet.2018.06.012>

How to cite this article: Menzel, W., Knierim, D., Margaria, P. & Silva, A. (2025) First report of turnip vein clearing virus (*Tobamovirus rapae*) infecting *Silene flos-cuculi* in Portugal. *New Disease Reports*, vol.51, e70019. <https://doi.org/10.1002/ndr2.70019>