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NEW DISEASE REPORT

First report of Tradescantia mild mosaic virus infecting Tradescantia × andersoniana in Germany

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Cultivars of the perennial *Tradescantia* × *andersoniana* (spiderwort, family *Commelinaceae*) are popular bedding and border plants, that spread easily by seed. In spring 2009 spiderwort plants with yellow streak symptoms on the leaves, conspicuously indicating virus infection, were observed in a garden in Lower Saxony, Germany. To test for the presence of the potyvirus *Tradescantia mild mosaic virus* (TraMMV), which was earlier reported in another *Tradescantia* species (*Tradescantia fluminensis*) from Italy (Ciuffo et al. 2006), a fragment of c. 1.4 kb in the 3′-proximal region of the genome was amplified by RT-PCR using a specific primer designed on the available sequence (GenBank Accession no. NC_043166) (Trad-s: 5′-CAGATCTTGGTATGAAGTACGA-3′) and an oligo(dT) primer. The sequence obtained (GQ847531) was 76% identical to the TraMMV isolate from Italy, identifying the associated virus as a deviant isolate of TraMMV.

In 2020, numerous spiderwort plants showing similar symptoms were observed in another public garden in Lower Saxony which prompted us to use a high-throughput sequencing (HTS) approach for an unbiased analysis of the virome associated with the disease. An Illumina Nextera XT library was prepared from total RNA (QIAGEN RNeasy Mini Kit, Germany) isolated from a symptomatic sample (Fig. 1) and sequenced on a MiSeq instrument as paired-end reads (2 × 301 bp). The raw reads were *de novo* assembled with Geneious Prime ver. 2022.01 (Biomatters, New Zealand) following a workflow established at DSMZ. A near complete virus genome was reconstructed from raw HTS reads and the terminal ends were completed by 5' and 3' standard RACE. The full-length genome was 9621 nt in length, excluding the 3'-terminal poly(A) tail, and showed a nucleotide sequence identity of 99.5% to the sequence of 2009, and 74.7% to the partial sequence of the ICTV exemplar isolate from Italy (NC_043166).



FIGURE 1 Symptoms observed on *Tradescantia* × *andersoniana* infected by *Tradescantia mild mosaic virus*

This is just below the species demarcation threshold value of 76% in nucleotide sequence for potyviruses (Wylie et al., 2017). In regard to

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the amino acis sequence identity, the obtained value of 80.2% is also below the threshold value of 82%, but for the coat protein alone, the aa sequence identity of 82% is slightly above the recommended demarcation value of 80%, supporting assignment to the same species. The German isolate is comparably distantly related (72.3% nt identity to KT633608) to the TraMMV isolate identified in another *Tradescantia* species in New Zealand (Tang et al., 2016), which was close to the Italian isolate (97.4% nt identity). No other viral sequences were found in the HTS analysis and thus TraMMV can be assumed to be the causative agent of the disease. In accordance with the results reported by Ciuffo et al. (2006), the German as well as the Italian TraMMV isolate did not react with a broad spectrum potyvirus antiserum (ACP-ELISA, DSMZ AS-0573/1).

The full genome sequence has been deposited in GenBank under Accession. no. OL584375 and reference material is available at the DSMZ Plant Virus Collection (PV-1308). In addition to verifying the presence and establishment of TraMMV in *Tradescantia* × *andersoniana* in Germany, we provide the first complete genome sequence of an isolate of this virus species.

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