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First report of tobacco rattle virus infecting ornamental paeony and trumpet creeper in France

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Trumpet creeper (*Campsis radicans*, Bignoniaceae) and paeony (*Paeonia lactiflora*, Paeoniaceae) are perennial ornamentals widely cultivated worldwide, including in France. Because they are clonally propagated, viruses can accumulate over successive propagation cycles. Only alfalfa mosaic virus (AMV, *Bromoviridae*) has been found to infect trumpet creeper, causing leaf mottling and mosaic symptoms (Pourrahim and Farzadfar 2016). In contrast, numerous viruses are reported from paeonies, causing leaf discolouration, stunting and reduced flowering (Lu et al. 2025). Virus-like symptoms, leaf deformation, ringspot and mosaic (Figures 1 and 2), were observed in a paeony in 2018 and in a trumpet creeper in 2025 at two different sites in western France (the departments of Maine-et-Loire and Vendée in the Pays de la Loire region, respectively). Double-stranded RNAs (paeony) and ribodepleted total RNAs (trumpet creeper) were extracted and subjected to high-throughput sequencing (2 × 150 nt paired-end; Illumina HiSeq3000 and NovaSeq, respectively).

A total of 2,179,922 reads (paeony) and 66,566,476 reads (trumpet creeper) were trimmed, de novo assembled using Geneious Prime 2026.0.2 software and subjected to BlastN analysis. In trumpet creeper, two viral contigs of respectively 6791 bp (average coverage: ×8580) and 3544 bp (×19,800) and showing 99.2% and 98.4% nt identities with tobacco rattle virus (TRV) California isolate RNA1 (GenBank accession no. MH614641) and RNA2 (MH614642) were identified. In paeony, a single viral contig of 6791 bp (×4497) was identified that showed 99.3% nt identity with TRV RNA1 California isolate (MH614641); no RNA2-related contig was detected. RNA1 sequences from both hosts shared 99.4% nt identity. The three TRV near-complete genome segments were deposited in GenBank (PZ016967-69).



FIGURE 1 | Paeony with distinct ringspot symptoms on the leaves.

No additional plant viruses were identified in trumpet creeper, whereas amalgavirus-like and partitivirus-like sequences were detected in paeony. TRV infection was confirmed by RT-PCR using primers targeting the RdRp gene (RNA1; Forward, 5′-TGAAGAACAAGCAAAGTGTAGATTC-3′; Reverse, 5′-ATCTCGGATGTCTCGACGCAT-3′; 392 bp) and the coat protein gene (RNA2; Forward, 5′-ATGACAGACGGTATGTACGATGA-3′; Reverse, 5′-TGGTAAACACCACCTCACGATT-3′; 665 bp). Sanger sequencing showed 100% nt identity with the HTS-derived sequences.

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FIGURE 2 | Trumpet creeper with distinct deformation and mosaic symptoms on the leaves.

To our knowledge, this is the first report of TRV infecting trumpet creeper worldwide, and TRV infecting paeony in France. The absence of RNA2 in paeony indicates a non-multiplying TRV isolate containing only RNA1 (Cadman and Harrison 1959). Such isolates are poorly mechanically transmissible, slow to become systemic, and do not form viral particles because the coat protein is encoded by RNA2, preventing serological detection (MacFarlane et al. 1999). Detection of this non-multiplying isolate in paeony highlights the value of HTS for virus diagnosis. Further studies are needed to assess the impact of TRV on ornamentals and their potential role as reservoirs of this nematode-transmitted virus, which also infects crops such as potato.

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