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NEW DISEASE REPORT

First report of *Wisteria badnavirus 1* infecting *Wisteria sinensis* in Iran

M. Mehrvar[1] | **Z. Moradi**[2] | **M. S. Al-Jaberi**[1]

[1]Department of Plant Pathology, Faculty of Agriculture, Ferdowsi University of Mashhad, P.O. BOX 91779-1163, Mashhad, Iran

[2]Department of Plant Pathology, Faculty of Crop Sciences, Sari Agricultural Sciences and Natural Resources University, P.O. Box 578, Sari, Iran

Correspondence
M. Mehrvar, Department of Plant Pathology, Faculty of Agriculture, Ferdowsi University of Mashhad, P.O. BOX 91779-1163, Mashhad, Iran.
E-mail: mehrvar@um.ac.ir

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Iran, Wisteria sinensis, Wisteria badnavirus 1

Badnaviruses are members of the family *Caulimoviridae* with a 7.2 to 9.2 Kb circular double-stranded DNA genome and non-enveloped bacilliform virions (Bhat et al., 2016; Geering & Hull, 2012). They are responsible for yield and quality losses in several economically important crops (Borah et al., 2013) and are spread efficiently by mealybugs in a semi-persistent mode (Bhat et al., 2016). The first badnavirus infecting *Wisteria sinensis* was discovered in 2017 in China and named *Wisteria badnavirus 1* (WBV1) (Li et al., 2017).

Three leaf samples of *W. sinensis* showing virus-like symptoms including mosaic (Figure 1) were collected in 2020 from the urban area of Mashhad, Razavi Khorasan province, Iran. Genomic DNA was extracted from fresh leaves of the samples using a DNeasy Plant Mini Kit (Qiagen, Germany) following the manufacturer's protocol. PCR was done using the primer pair WBV1-F (5′-CTTGGAGGATGCAGTTTGAA-3′) / WBV1-R (5′-GACATTGGTTCATCAGGGTC-3′) which amplify a 727 bp fragment of the capsid protein coding region within ORF3. The PCR cycling conditions were as follows: initial denaturation as 94°C for 3 minutes, followed by 35 cycles of 94°C for 30 s, 56°C for 30 s, and 72°C for 70s; and a final extension step at 72°C for 7 min. PCR products were separated by agarose gel electrophoresis and visualised using DNA Green Viewer staining under ultraviolet light. DNA fragments of approximately 730 bp were amplified for all three isolates (IR, IR2, and IR3) using specific primers, confirming infection with WBV1.

The amplified product derived from isolate IR was purified (DENAzist PCR Clean-up kit, Iran), directly sequenced in both directions and deposited in GenBank (Accession No. OP484939). BLAST analysis of the sequence (727 nt) against the GenBank database, revealed a nucleotide identity of 78.34% (92.53% amino acid identity) with the previously reported sequence of WBV1 (ZT-1, KX168422). To our knowledge, this is the first report of WBV1 in Iran. This finding complements previous reports of viruses associated with wisteria diseases in Iran (Al-Jaberi *et al*., 2021; Moradi & Mehrvar, 2021).



FIGURE 1 Mosaic symptoms on wisteria leaves infected with *Wisteria badnavirus 1*, collected from Mashhad in the province of Razavi Khorasan, northeastern Iran.

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ORCID

M. Mehrvar https://orcid.org/0000-0003-1042-8660

Z. Moradi https://orcid.org/0000-0002-8989-6450

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