



## NEW DISEASE REPORT

# First report of *Turnip yellows virus* in Brazil

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BBSRC, Grant/Award Numbers: BB/M017206/1, BB/J500070/1, BB/M017923/1; Fundação de Amparo à Pesquisa do Estado de São Paulo, Grant/Award Numbers: 2014/22594-2, 2015/50076-9, 2017/50334-3, 2018/17287-4; Coordenação de Aperfeiçoamento de Pessoal de Nível Superior; Conselho Nacional de Desenvolvimento Científico e Tecnológico

**KEYWORDS***Brassicaceae*, vegetables, virus aetiology

*Turnip yellows virus* (TuYV, family *Solemoviridae*, genus *Polerovirus*; syn. *Beet western yellows virus*, BWYV) has a single-stranded, positive-sense RNA genome. It is phloem-limited and aphid-transmitted in a persistent (circulative, non-propagative) manner. The virus represents a serious threat to Brazilian brassica production as it has been shown to cause yield losses of up to 65% in vegetable brassicas (Walsh *et al.*, 2011). In the 1970's and 1980's, infections of wild radish plants with yellowing symptoms in lower leaves were reported in Brazil, probably caused by BWYV (Kitajima, 2020) though the aetiology was not confirmed.

In May 2017, a cabbage (*Brassica oleracea* var. *capitata*) plant with reddening of leaves was discovered in a commercial field in the municipality of Araucária, Paraná State, Brazil (Fig. 1). Enzyme-linked immunosorbent assay of the symptomatic leaf tissue for TuYV (Hackenberg *et al.*, 2019) gave a clear positive result. No infection by *Turnip mosaic virus* (TuMV) or *Cole latent virus* (CoLV) was detected following RNA extraction and RT-PCR with specific primers. *Cauliflower mosaic virus* (CaMV) was not detected following DNA extraction and PCR. Mechanical inoculation of symptomatic leaf tissue to a range of indicator plants failed to detect the presence of any virus.

In July 2021, leaves from six cabbage plants showing reddening symptoms in older leaves were collected from two commercial fields in the municipality of Ibiúna (Fig. 2), in the main vegetable brassica-producing region in São Paulo State, Brazil. The incidence of symptomatic plants was c. 1%. All symptomatic plants tested by RT-PCR with



**FIGURE 1** Cabbage (*Brassica oleracea* var. *capitata*) plant in the field in Araucária, Paraná, Brazil with reddening symptoms infected by *Turnip yellows virus* (right).

TuYV-specific primers (Congdon *et al.*, 2019) were infected. CaMV, CoLV, or TuMV were not detected in the symptomatic plants by PCR or RT-PCR.

The TuYV genome of the Araucária isolate was reverse transcribed, PCR amplified and sequenced following Newbert (2016). Sequencing

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**FIGURE 2** Cabbage (*Brassica oleracea* var. *capitata*) plant in the field in Ibiúna, São Paulo State, Brazil with reddening symptoms infected by *Turnip yellows virus*.

files were trimmed and assembled in SeqMan Pro (DNASTAR Laser-gene v15) using the program's default parameters. Sequences were assembled with at least a 40 nucleotide overlap at each end, to reveal the complete genome (5,615 nucleotides; Genbank Accession No. MZ313372). The Brazilian isolate shared the highest nucleotide identity (93.6%) with an Australian TuYV isolate MK107 from oilseed rape (MT586590.1; Filardo *et al.*, 2021). The Brazilian isolate's P3 protein (ORF3, the most conserved TuYV protein) had 92.6% amino acid identity with that of MK107 and the P5 coat protein read-through domain (ORF5 region of ORF3+5, the most variable region) had 95.7% amino acid identity with that of MK107.

This is the first report of TuYV in Brazil. The finding has been reported to the Ministry of Agriculture of Brazil (MAPA), which approved the notification (SEI process 21052.012367/2021-73, 66/2021/DSV/SDA). Further work is required to determine the distribution and prevalence of TuYV and its impact on brassica cultivation in Brazil.

#### ACKNOWLEDGEMENTS

This study was supported BBSRC grants BB/M017206/1, BB/J500070/1 and BB/M017923/1, Limagrain, the FAPESP-University

of Warwick Joint Fund, FAPESP grants 2014/22594-2, 2015/50076-9, 2017/50334-3, 2018/17287-4, CAPES, Brazil, Finance Code 001, a CAPES Ph.D. fellowship, a FAPESP Ph.D. fellowship and a CNPq research fellowship.

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**How to cite this article:** Greer, S.F., Newbert, M.J., Rodrigues, L.K., Oliveira, A.M., Chaves, A.L.R., Calegario, R.F., *et al.* (2021) First report of *Turnip yellows virus* in Brazil. *New Dis Rep*, 44, e12045. <https://doi.org/10.1002/ndr2.12045>