DISEASE NOTES

First Report of Turnip Yellows Virus on Cabbage in Serbia

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Cabbage (*Brassica oleracea* var. *capitata* L.) is a cruciferous vegetable consumed worldwide and is used in traditional medicine (Tjitraresmi et al. 2017). In October 2018, during a survey to determine the presence of viral diseases in cabbage, virus-like symptoms were observed on cabbage plants (cv. 'Srpski melez') growing in the Futog locality, South Bačka District, the main cabbage-producing area in Serbia. Disease incidence was estimated at 40%. Plants exhibiting symptoms of stunting and purpling of the leaves were collected and tested by commercial double-antibody sandwich (DAS)-ELISA diagnostic kits (Loewe Biochemica, Germany) against turnip yellows virus (TuYV), turnip mosaic virus, and cauliflower mosaic virus. Out of 20 samples tested, 15 were positive for TuYV and negative for the other tested viruses. The aphid transmissibility of the selected serologically positive sample (364Cb) was tested using *Myzus persicae*

(Sulzer) as the vector. Nymphs of aphids were allowed to feed for an acquisition access period of 24 h and thereafter transferred onto three plants of each *Physalis floridana* and *Sinapis alba* for a 4-day inoculation access period, with a 16-h photoperiod at 22°C. All inoculated *P. floridana* plants manifested a very mild interveinal chlorosis, whereas all inoculated *S. alba* plants reacted with a mild reddening of leaf margins and yellowi weeks postinoculation (wpi). In the same manner, the virus was successfully transf to cabbage plants (cv. 'Futoški'), which reacted with a mild yellowing symptom 6 w ELISA was used to confirm the presence of TuYV in all inoculated plants. Total RNAs were extracted from all 15 ELISA-positive cabbage samples using an RNeasy Plant Mini Kit (Qiagen, Hilden, Germany) and tested by conventional reverse transcription PCR using the OneStep RT-PCR Kit (Qiagen) with specific primers TuYVorf0F/TuYVorf0R (Wilson et al. 2012). Total RNAs obtained from the Serbian TuYV oilseed rape isolate (GenBank accession no. KR351306) and healthy cabbage leaves were used as positive and negative controls, respectively. A 780-bp fragment, covering the fragment of the TuYV P0 gene, was obtained from all naturally infected plants as well as the positive control. No amplicon was recorded in the negative control. The amplified product derived from two selected isolates, 345Cb and 364Cb, was sequenced directly in both directions and deposited in GenBank (MN602973 and MN165558, respectively). BLAST analysis revealed that the Serbian isolates 345Cb and 364Cb shared the highest nucleotide identity of 97.83% with TuYV-SA isolate (MH427303) of TuYV from Australia and 98.5% with *Raphanus sativus* isolate (Raph M) of TuYV from Germany (Y16876). In additional, a neighbor-joining tree constructed using the partial sequences of the P0 gene showed that the Serbian TuYV isolates 345Cb and 364Cb grouped in the cluster with the known TuYV isolates. The virus has been recorded on *Brassica napus* in Serbia (Milošević et al. 2015), but to our knowledge, this is the first report of TuYV on *B. oleracea* in the country. Vectors of TuYV are widespread in Serbia. With both *B. oleracea* and *B. napus* serving as a reservoir of TuYV in Serbia, production of these and other important brassica hosts of the virus is threatened.

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