Diseases Caused by Viruses

First Report of Turnip Yellow Virus Infecting Cabbage (*Brassica oleracea* var. *capitata*) in the United States

Saritha Raman Kavalappara,¹ Hayley Milner,¹ David G. Riley,² and Sudeep Bag^{1,†}

¹ Department of Plant Pathology, University of Georgia, Tifton, GA

² Department of Entomology, University of Georgia, Tifton, GA

Funding: Funding was provided by USDA-UGA Cooperative Agreement (58-6080-9-006) and USDA-HATCH (1020319). Plant Dis. 106:2273, 2022; published online as <https://doi.org/10.1094/PDIS-10-21-2174-PDN>. Accepted for publication 24 January 2022.

During the spring of 2021, cabbage (*Brassica oleracea* var. *capitata*) planted in the research farm at the University of Georgia, Tifton, exhibited leaf distortion, yellow and purple discoloration at the leaf margin of older leaves, and severe stunting. Symptoms were present on nearly 30% of plants in the field. To identify the potential associated agents, leaf tissues from two symptomatic plants were sent for high throughput sequencing (HTS) of small RNA (sRNA; DNB sequencing, SE read 1 × 75 bp) to Beijing Genomics Institute, China. From each sample, ~18 million raw reads were generated. The reads with poor quality and adapter sequences were removed using CLC Genomics Workbench 21.2 (Qiagen, Germantown, MD). Of the total reads, 2,093 and 3,889 reads aligned to the genome of turnip yellow virus (TuYV) in samples one and two, respectively. Reads of turnip mosaic virus (TuMV) were also detected. Partial sequences of TuYV assembled from samples one and two showed an 89.5 and 89.9% match and 86 and 93% coverage, respectively, with the genome of the type isolate of TuYV (NC_003743) from the United Kingdom. To confirm the presence of TuYV in the samples collected from the same location, specific primers were designed targeting the P0 region (FP-5'ACAAAAGAAACCAG-GAGGGAATCC3'; RP-5'GCCTTTT CATACAAACATTTTCGGTG3') and coat protein (CP) region (FP-5'GTT AATGAATACGGTCGTGGGTAG3'; RP-5'ATTCTGAAAGAACCAGCT ATCGATG3') of the virus. Eight of 20 (40%) symptomatic samples were determined to be infected with TuYV based on the amplification of expected size products of the P0 (786 nt) and the CP gene (581 nt) in reverse transcription (RT)-PCR. All samples were also tested for the presence of TuMV by RT-PCR as in Sánchez et al. (2003), but none tested positive despite being identified in HTS. Symptoms on samples from which neither virus could be

detected indicate the involvement of other factors and would require further studies. The partial P0 and CP gene amplicons of TuYV from two samples each were Sanger sequenced bidirectionally at Genewiz (South Plainfield, NJ) and confirmed as TuYV using BLASTn. The partial CP gene sequences from two samples shared 98.7% nucleotide sequence identity with each other and 88.0 (OK349421) and 87.1% (OK349422) identity with the type isolate. The partial P0 gene sequences (OK349423 and OK349424) shared 99.6% nucleotide sequence identity with each other and 92.2% identity with the type isolate. TuYV, formerly known as beet western yellows virus (BWYV) (Mayo 2002), genus *Polerovirus*, family *Solemoviridae* (Walker et al. 2021), is transmitted persistently by aphids (Stevens et al. 2008) and distributed throughout temperate regions of the world (Kawakubo et al. 2021). TuYV has a wide host range, including *Brassica* spp., vegetables, and weeds (Stevens et al. 2008). However, losses have been reported primarily on canola (*Brassica napus*) in Australia (Jones et al. 2007) and Europe (Stevens et al. 2008). On cabbage, TuYV infections have been reported from China (Zhang et al. 2016), Serbia (Milošević et al. 2020), and the Philippines (Buxton-Kirk et al. 2021). TuYV (BWYV) has been found infecting shepherd's purse (*Capsella bursa-pastoris*) in California (Falk and Duffus 1984), but there are no reports of the virus from any cultivated crops in the United States. To our knowledge, this is the first report of TuYV in cabbage in the United States. More studies are needed to understand its occurrence and impact on cabbage crops in Georgia and other regions in the United States.

References:

- Buxton-Kirk, A., et al. 2021. New Dis. Rep. 44:e12020.
- Falk, B. W., and Duffus, J. E. 1984. Phytopathology 74:1224.
- Jones, R. C. A., et al. 2007. Aust. J. Agric. Res. 58:788.
- Kawakubo, S., et al. 2021. PNAS 118:e2021221118.
- Mayo, M. A. 2002. Arch. Virol. 147:2254.
- Milošević, D., et al. 2020. Plant Dis. 104:997.
- Sánchez, F., et al. 2003. Virus Res. 94:33.
- Stevens, M., et al. 2008. Research Review 69. Home-Grown Cereals Authority, Kenilworth, UK. <https://citeserx.ist.psu.edu/viewdoc/download?doi=10.1.1.518.7795&rep=rep1&type=pdf> (accessed January 19, 2022).
- Walker, P. J., et al. 2021. Arch. Virol. 166:2633.
- Zhang, X., et al. 2016. Virol. J. 13:189.

The author(s) declare no conflict of interest.

Keywords: cabbage, Georgia U.S.A., *Polerovirus*, *Solemoviridae*, turnip yellows virus

[†]Indicates the corresponding author.
S. Bag; sudeepbag@uga.edu