



Occurrence of *Xanthomonas campestris* pv. *campestris* in wild radish (*Raphanus raphanistrum* L.) in Brazil

João César da Silva¹ · Tadeu Antônio Fernandes da Silva Júnior² · José Marcelo Soman¹ · Ricardo Marcelo Gonçalves³ · Antonio Carlos Maringoni¹

Received: 27 July 2018 / Accepted: 13 September 2018 / Published online: 4 October 2018
© Società Italiana di Patologia Vegetale (S.I.Pa.V.) 2018

Wild radish (*Raphanus raphanistrum* L.) is considered an important weed in agricultural fields, because it competes with crops for water, nutrients and light, apart from acting as a host for pathogens and pests. Herbicide resistant populations have hampered the management of this weed (Heap, 2017), contributing to survival of pathogens in fields of cultivation during the off season. Wild radish plants naturally infected with *Xanthomonas campestris* pv. *campestris* (Xcc), causal agent of brassicas black rot, were reported in the USA (Schaad and Dianese 1981). In Brazil, this weed is common in fields cultivated with *Brassica* spp. with black rot occurrence. It has not been described, however, as Xcc host so far. During 2016, wild radish plants with symptoms of yellowing and leaf marginal necrosis were collected in a broccoli (*Brassica oleracea* var. *italica*) producing property with a black rot history, located in Pardinho, São Paulo state, Brazil. Bacterial isolation was performed on nutrient sucrose agar (NSA)

followed by incubation at 28 °C for 48 h. The presence of yellow colonies, mucoid and shiny, characteristic of *Xanthomonas* genus were observed. The strain obtained (Nab3175) hydrolyzed starch, was pathogenic to cauliflower plants (cultivar ‘Teresopolis’) and showed positive PCR result using the specific primers HrcCF2 and HrcCR2, that amplified a 519 bp fragment (Zaccardelli et al. 2007). The 16S rDNA gene region of the Nab3175 strain was amplified by PCR using primers FD1 and RD1 (Weisburg et al. 1991) and sequenced, being identified by the degree similarity with GenBank (NCBI). Nab3175 strain (Accession N° MG993191) showed a 100% nucleotide similarity with Xcc strain ATCC 33913 (NR_074936.1), originally isolated from brussels sprout (*Brassica oleracea* var. *gemmifera*) in 1957, United Kingdom. To our knowledge this the first report of the natural occurrence of Xcc in wild radish in Brazil.

Acknowledgements The first author thanks the São Paulo Research Foundation (FAPESP) for granting the doctoral scholarship and for the financial support (FAPESP process number: 2017/13822-0).

✉ João César da Silva
joaoacesar.silva@outlook.com

- ¹ Departamento de Proteção Vegetal, Faculdade de Ciências Agronômicas (FCA), Universidade Estadual Paulista “Júlio de Mesquita Filho” (UNESP), Avenida Universitária, 3780, Botucatu, São Paulo 18610-034, Brazil
- ² Pró-Reitoria de Pesquisa e Pós-Graduação (PRPPG), Universidade do Sagrado Coração, Rua Imã Armanda, 10-50, Bauru, São Paulo 17011-160, Brazil
- ³ Instituto Federal de Educação, Ciência e Tecnologia de Minas Gerais, Campus Santa Luzia, Rua Érico Veríssimo, 317, Santa Luzia, Minas Gerais 33115-390, Brazil

References

- Heap I (2017) The International Survey of Herbicide Resistant Weeds. Available at: <http://www.weedscience.org/>. Accessed 29 October 2017
- Schaad NW, Dianese JC (1981) Cruciferous weeds as sources of inoculum of *Xanthomonas campestris* in black rot of crucifers. *Phytopathology* 71:1215–1220
- Weisburg WG, Barns SM, Pelletier DA, Lane DJ (1991) 16S ribosomal DNA amplification for phylogenetic study. *J Bacteriol* 173:697–703
- Zaccardelli M, Campanile F, Spasiano A, Merighi M (2007) Detection and identification of the crucifer pathogen, *Xanthomonas campestris* pv. *campestris*, by PCR amplification of the conserved Hrp/type III secretion system gene hrcC. *Eur J Plant Pathol* 118:299–306