

DISEASE NOTE

FIRST REPORT OF TOMATO INFECTIOUS CHLOROSIS VIRUS IN GLOBE ARTICHOKE ECOTYPES IN APULIA, SOUTHERN ITALY

R. Spanò¹, A. Corrado² and A. Di Franco²

¹Istituto per la Protezione Sostenibile delle Piante, CNR,
Via Amendola 122/D, 70126 Bari, Italy

²Dipartimento di Scienze del Suolo, delle Piante e degli Alimenti,
Università degli Studi di Bari Aldo Moro,
Via Amendola 165/A, 70126 Bari, Italy

Apulia (southern Italy) hosts a rich variety of globe artichoke ecotypes of high interest for breeding programs and industrial production. Most of the ecotypes are at risk of genetic erosion because of the high incidence of plant pathogens, which include infections from taxonomically different viruses. In the early autumn of 2014 and 2016 five samples were collected from each of the early-flowering ecotypes, Brindisino, Carciofo di Lucera, Francesina di Brindisi, Francesina di Trinitapoli, Locale di Mola, Nero di Ostuni, Tricasino, Troianella, Verde di Putignano, Violetto di Putignano and the late-flowering ecotypes Bianco di Taranto and Locale di Mola tardivo, and tested for viral infections by dot blot hybridization with Dig-labeled DNA probes and RT-PCR (Minutillo *et al.*, 2012). In the five samples of the ecotypes Verde di Putignano, Violetto di Putignano, Nero di Ostuni and Troianella the hybridization signal revealed the presence of tomato infectious chlorosis virus (TICV) that in the ecotype Troianella was in mixed infection with artichoke Italian latent virus and turnip mosaic virus. TICV infection was confirmed by RT-PCR with TICV-specific primer pair for 5'-TCAGTGCCTACGTTAATGGG-3' and rev 5'-CACAGTATACAGCAGCGGCAG-3' (Minutillo *et al.*, 2012). Amplicons from the ecotypes Verde di Putignano and Troianella were sequenced. Nucleotide sequence analyses revealed 99% identity with a TICV isolate from USA (accession No. FJ542306). Previous surveys detected TICV in globe artichoke in Liguria, Sardinia, Latium, Campania and Sicily but this is the first report of TICV in artichoke in Apulia and in the ecotypes Verde di Putignano, Violetto di Putignano, Nero di Ostuni and Troianella. Artichoke plants infected by TICV did not show symptoms and thus may act as perennial TICV reservoirs.

Minutillo S.A., Mascia T., Gallitelli D., 2012. A DNA probe mix for the multiplex detection of ten artichoke viruses. *European Journal of Plant Pathology* **134**: 459-465.

Corresponding author: R. Spanò
E-mail: roberta.spano@ipsp.cnr.it

Received July 29, 2017
Accepted July 31, 2017

DISEASE NOTE

FIRST REPORT OF BROAD BEAN WILT VIRUS 2 AND YOUCAI MOSAIC VIRUS INFECTING WOOLLY FOXGLOVE (*DIGITALIS LANATA*)

J.L. Dong, Y. Li, W.L. Ding and R. Wang

Institute of Medicinal Plant Development, Chinese Academy of
Medical Sciences and Peking Union Medical College, No. 151
Malianwa North Road, Beijing, 100193, China

Broad bean wilt virus 2 (BBWV2), a member of genus *Fabavirus*, in the family *Secoviridae*, is an economically important virus in China (Zhou *et al.*, 1994). Similarly, *Youcai mosaic virus* (YoMV), a member of genus *Tobamovirus* in the family *Virgaviridae*, causes serious disease in many plants (Aguilar *et al.*, 1996). In April of 2017, woolly foxglove (*Digitalis lanata*) plants displaying foliar virus-like mottling symptoms were found at the Beijing Medicinal Plant Garden. To detect possible pathogenic virus(es), total RNA was extracted from symptomatic leaves and used in reverse transcription (RT)-PCR with six pairs of primers for the detection of BBWV2 (BBWV-F: 5'-TTGGGHTC-WAGYYTGGGACGYTTRT-3' and BBWV-R: 5'-TTRTAR-AACTTCTTGCTCCCACGM-3'), cucumber mosaic virus (CMVCPf: 5'-ATGGACAAATCTGAATCAACCA-3' and CMVCPr: 5'-TCAGACTGGGAGCACCCCAGACGT-3'), tobamo- (Tob-Uni1: 5'-ATTTAAGTGGASGGAAAACVACT-3' and Tob-Uni2: 5'-GTYGTTGATGAGTTCRTGGA-3'), poty- (PotyF: 5'-ATGGTHTGGTGYATHGARAAYGG-3' and PotyR: 5'-TGCTGCKGCVTTCATYTG-3'), potex- (Potex5: 5'-CAYCARCARGCMAARGAYGA-3' and Potex2RC: 5'-AGCATRGCNSCRTCYTG-3'), and polerovirus (PoconF: 5'-TGYTCYGGTTTTGACTGG-3' and PocoCPR: 5'-CGTC-TACCTATTSGGRTTN-3'). A 1,347 bp fragment (GenBank accession No. MF671980) partially covering the coat protein (CP) gene was amplified from symptomatic plants using BBWV2 primers. This fragment shared the highest identity (92.2% and 98.2% at the nucleotide and amino acid levels, respectively) with a BBWV2 isolate from *Rebmannia glutinosa* in China (GQ202215). In addition, a 680 bp fragment (MF671981) covering the complete CP gene was also amplified from symptomatic plants with tobamovirus primers. This fragment showed the highest identity (100%) with YoMV isolate Shanghai (AF254924). No RT-PCR product was amplified from asymptomatic plants. To our knowledge, this is the first report of BBWV2 and YoMV in *Digitalis lanata*.

This work was supported by CAMS Innovation Fund for Medical Sciences (2016-I2M-3-017).

Aguilar I., Sánchez F., Martín A.M., Martínez-Herrera D., Ponz F., 1996. Nucleotide sequence of Chinese rape mosaic virus (oilseed rape mosaic virus), a crucifer tobamovirus infectious on *Arabidopsis thaliana*. *Plant Molecular Biology* **30**: 191-197.
Zhou X.P., Qian X.H., Zhang L.C., 1994. Isolation and identification of broad bean wilt virus in faba bean. *Journal of Zhejiang University* **28**: 271-277.

Corresponding author: R. Wang
E-mail: rwang@implad.ac.cn

Received August 28, 2017
Accepted August 31, 2017