FIRST REPORT OF LEAF RUST CAUSED BY MELAMPSORA MAGNUSIANA ON POPULUS ALBA IN ITALY

L. Giordano1,2, A. Giorelli3, P. Gonthier1 and M.L. Gullino1,2
1Department of Agricultural, Forest and Food Sciences (DISAFA), University of Torino, Largo Paolo Braccini 2, I-10095 Grugliasco (TO), Italy
2Centre of Competence for the Innovation in the Agro-Environmental Field (AGROINNOVA), University of Torino, Largo Paolo Braccini 2, I-10095 Grugliasco (TO), Italy
3CREA – PLF Consiglio per la Ricerca in Agricoltura e l’Analisi dell’Economia Agraria – Unità di Ricerca per le Produzioni Legnose Fuori Foresta, Strada Frasneto 35, I-15033 Casale Monferrato (AL), Italy

In October 2016, Melampsora spp. hypophyllous uredinia (0.3-0.5 mm in diameter) were observed on leaves of Populus alba L. clones cultivated in Casale Monferrato at CREA-PLF (Piedmont, northern Italy). Morphological observations and DNA sequencing of the Internal Transcribed Spacer (ITS) region were performed to identify the fungus at the species level. Urediospores were yellowish, obovate, verrucose and on average 23.3 ± 18.8 μm (wall 1.22-2.44 μm thick). DNA was extracted from urediospores with the Quiagen Plant DNeasy Mini-kit following manufacturer’s instructions. The ITS region was amplified and sequenced with taxon-selective primers ITS1-F and ITS4-B (Gardes and Bruns, 1993). Sequences were deposited in GenBank (accession Nos. KY364897, KY364898) and compared with those of known Melampsora species using the NCBI GenBank nucleotide BLAST search. Based on morphological features of uredinia and urediospores and DNA sequences the fungus was identified, according to Vialle et al. (2011), as Melampsora magnusiana G.H. Wagner, belonging to M. populeae complex and associated with P. alba, P. tremula L. and P. × canescens (Aiton) Sm. telial hosts. The identification of this Melampsora species was also supported by the presence of its known aecial hosts Chelidonium majus L. and Corydalis spp. in the neighborhood of the sampling site (Picco, 2010). Telia were not observed. Disease symptoms consisting of chlorotic spots were reproduced on the abaxial surface of ten leaves cut from five Melampsora telial hosts. The fungal isolate was confirmed as P. ultimum.

During summer 2016, fruit rot symptoms were observed on tomato (Solanum lycopersicum L.) plants in the field. Symptoms appeared as small circular water-soaked lesions and enlarged with time. Lesions destroyed sub-epidermal tissue and white mycelium emerged from the lesions, leading to collapse of the fruits. Symptomatic fruit portions were surface sterilized with 1% NaOCl solution and placed on corn meal agar (CMA) plates at 18 ± 2°C. White depressed colonies appeared on plates; oogonia were globose, 19.5 μm in diameter. Fungal isolate produced globose intercalary and terminal sporangia 21.5 μm in diameter. Crook necked antheridia were found on oogonium, mostly emerging very close to the oogonial stalk. Main hyphae were up to 7.5 μm wide and oospore was single, globose aplerotic, 18-22 μm in diameter. Fungal DNA was extracted and used as a template for PCR with ITS1 and ITS4 primers (White et al., 1990). BLASTn analysis of the ITS sequences (GenBank accession No. LT670911) showed 100% homology with Pythium ultimum. The fungal isolate was confirmed as P. ultimum on its morphological and molecular basis. A pathogenicity test was performed by using cork borer prick method on twenty fruits and the experiment was repeated three times. After inoculation, fruits were kept in a plastic bag and incubated at 18 ± 2°C in a growth chamber. All inoculated fruits exhibited symptoms similar to those recorded in the field and control inoculated fruits did not show infection. The pathogen was re-isolated and confirmed as P. ultimum, thus fulfilling Koch’s postulates. According to our knowledge, P. ultimum causing symptoms of fruit rot in tomato is the first record in Pakistan.

Corresponding author: L. Giordano
E-mail: luana.giordano@unito.it

Received March 5, 2017
Accepted April 24, 2017

DISEASE NOTE

FIRST REPORT OF FRUIT ROT OF TOMATO CAUSED BY PYTHIUM ULTIMUM IN PAKISTAN

W. Anwar, K. Nawaz, S. Iftikhar and M.N. Subhani
Institute of Agricultural Sciences, University of the Punjab, Lahore, Pakistan

During summer 2016, fruit rot symptoms were observed on tomato (Solanum lycopersicum L.) plants in the field. Symptoms appeared as small circular water-soaked lesions and enlarged with time. Lesions destroyed sub-epidermal tissue and white mycelium emerged from the lesions, leading to collapse of the fruits. Symptomatic fruit portions were surface sterilized with 1% NaOCl solution and placed on corn meal agar (CMA) plates at 18 ± 2°C. White depressed colonies appeared on plates; oogonia were globose, 19.5 μm in diameter. Fungal isolate produced globose intercalary and terminal sporangia 21.5 μm in diameter. Crook necked antheridia were found on oogonium, mostly emerging very close to the oogonial stalk. Main hyphae were up to 7.5 μm wide and oospore was single, globose aplerotic, 18-22 μm in diameter. Fungal DNA was extracted and used as a template for PCR with ITS1 and ITS4 primers (White et al., 1990). BLASTn analysis of the ITS sequences (GenBank accession No. LT670911) showed 100% homology with Pythium ultimum. The fungal isolate was confirmed as P. ultimum on its morphological and molecular basis. A pathogenicity test was performed by using cork borer prick method on twenty fruits and the experiment was repeated three times. After inoculation, fruits were kept in a plastic bag and incubated at 18 ± 2°C in a growth chamber. All inoculated fruits exhibited symptoms similar to those recorded in the field and control inoculated fruits did not show infection. The pathogen was re-isolated and confirmed as P. ultimum, thus fulfilling Koch’s postulates. According to our knowledge, P. ultimum causing symptoms of fruit rot in tomato is the first record in Pakistan.


Corresponding author: K. Nawaz
E-mail: Kirannawaz34@gmail.com

Received March 1, 2017
Accepted March 3, 2017