Disease Note

ALTERNARIA ALTERNATA CAUSING LEAF SPOT ON *ULMUS MINOR* IN GREECE

G.T. Tziros

Hellenic Agricultural Organization, Forest Research Institute, 57006 Vassilika, Thessaloniki, Greece

A foliar disease of field elm (*Ulmus minor*) was observed in 2010 in two natural ecosystems in northern Greece (Serres and Thessaloniki) during a nationwide survey aiming at determining the current status of Dutch Elm Disease in the country. Symptoms consisted of small circular necrotic spots with yellow border on *ca*. 30% of the leaves. Single spore cultures from the fungus isolated on potato dextrose agar (PDA) gave rise to white colonies which turned to grayish-black and produced obpyriform, ovoid or ellipsoidal conidia in long chains. Conidia had 1 to 5 transverse and 0 to 3 longitudinal septa and measured 11.8-31.8.0 × 7.8-16.4 µm (average 18.4 × 8.3 µm). These morphological characteristics conform to those of *Alternaria alternata* (Fr.) Keissl. (Simmons, 2007). The ITS1-5.8S-ITS2 region was amplified with primers ITS1 and ITS4 and sequenced (GenBank accession Nos. KT893476, KT893477). A BLAST search of GenBank database showed 100% homology with the sequences of various *A. alternata* isolates (e.g. JX308308). Twenty healthy detached elm leaves were sprayed with a spore suspension (10^6 spores/ml), placed into 20 cm diameter Petri dishes containing a wet sterilized piece of cotton and incubated in a growth chamber at 25ºC. Pathogenicity tests were repeated three times and 10 days post inoculation spots similar to the original ones developed on all inoculated leaves, while control leaves sprayed with sterile distilled water remained symptomless. *A. alternata* was reisolated from artificially inoculated leaves fulfilling Koch's postulates. This is the first report of *A. alternata* as the cause of a leaf spot disease on *U. minor* in Greece.

Simmons E.G., 2007. Alternaria. An Identification Manual. 1st Ed. CBS Biodiversity Series, Utrecht, The Netherlands.

Corresponding author: G.T. Tziros
E-mail: gtziros@yahoo.gr

Received December 13, 2015
Accepted December 13, 2015

Disease Note

FIRST REPORT OF *RHYNCHOSIA GOLDEN MOSAIC YUCATAN VIRUS* INFECTING SOYBEAN IN CUBA

L. Chang-Sidorchuk[1,2], H. González[1], Y. Martínez-Zubiaur[1], J. Navas-Castillo[2] and E. Fiallo-Olivé[2]

[1]Centro Nacional de Sanidad Agropecuaria (CENSA), Carretera de Tapaste y Autopista Nacional, San José de las Lajas, Mayabeque, Cuba
[2]Instituto de Hortofruticultura Subtropical y Mediterránea "La Mayora", Universidad de Málaga - Consejo Superior de Investigaciones Científicas (IHSM-UMA-CSIC), 29750 Algarrobo-Costa, Málaga, Spain

In November 2014, commercial soybean (*Glycine max*) plants grown in Mayabeque (Cuba), showed mosaic symptoms. These plants also sustained populations of the whitefly *Bemisia tabaci*, the vector of begomoviruses (genus *Begomovirus*, family *Geminiviridae*). Symptomatic leaves were collected from 13 plants, total DNA was extracted and PCR was carried out with primers AV494 and AC1048 (Wyatt and Brown, 1996). A sample with a bright yellow mosaic in contrast with the milder symptoms shown by the others, yielded the expected *ca.* 550 bp DNA fragment. DNA from all samples was used as a template in rolling-circle amplification (RCA) using Phi29 DNA polymerase and digested with a set of restriction enzymes. Only the PCR-positive sample was amplified. *Eco*RV and *Hind*III fragments of *ca.* 2.6 kbp were cloned in pBluescript II SK(+) and sequenced. BLAST analysis showed that the clones corresponded to begomoviral DNA-A (2581 nt) and DNA-B (2554 nt), respectively. Pairwise identity scores with isolates selected after BLAST analysis were calculated with Sequence Demarcation Tool. DNA-A (KT381193) showed 93% nucleotide identity with *Rhynchosia golden mosaic Yucatan virus* (RhGMYuV) (EU021216), a begomovirus infecting *Rhynchosia minima* and *Desmonium* sp. in Mexico. DNA-B (KT381194) showed 91% nucleotide identity with RhGMYuV (FJ792608) and *Rhynchosia rugose golden mosaic virus* (HM236371), a begomovirus infecting *R. minima* in Cuba. DNA-A and DNA-B had a common region of 159 nt with an identity of 89.6% and identical iterons, indicating that they constitute a cognate pair. According to begomovirus species demarcation criteria (Brown *et al*., 2015), the begomovirus identified is an isolate of RhGMYuV. This is the first record of RhGMYuV infecting soybean and of the occurrence of this viral species in Cuba.

L. Chang-Sidorchuk was supported by a MAEC-AECID (Spain) fellowship.

Brown J.K., Zerbini F.M., Navas-Castillo J., Moriones E., Ramos-Sobrinho R., Silva J.C.F., Fiallo-Olivé E., Briddon R.W., Hernández-Zepeda C., Idris A., Malathi V.G., Martin D.P., Rivera-Bustamante R., Ueda S., Varsani A., 2015. Revision of *Begomovirus* taxonomy based on pairwise sequence comparisons. *Archives of Virology* **160**: 1593-1619.

Wyatt S.D., Brown J.K., 1996. Detection of subgroup III geminivirus isolates in leaf extracts by degenerate primers and polymerase chain reaction. *Phytopathology* **86**: 1288-1293.

Corresponding author: E. Fiallo-Olivé
E-mail: efiallo@eelm.csic.es

Received October 20, 2015
Accepted December 15, 2015