PLDIDE 90(7) 837-976(2006)
ISSN 0191-2917
VOLUME 90, NUMBER 7
JULY 2006

plant disease

AN INTERNATIONAL JOURNAL OF APPLIED PLANT PATHOLOGY

First Report of *Meloidogyne arenaria* Parasitizing Lettuce in Southern Spain. P. Castillo, B. B. Landa, and J. A. Navas-Cortés, Institute of Sustainable Agriculture (IAS), CSIC, P.O. Box 4084, 14080 Córdoba, Spain; N. Vovlas, Istituto per la Protezione delle Piante, Sezione di Bari, Nematologia Agraria, Consiglio Nazionale delle Ricerche, (C.N.R.), Via G. Amendola 165/A, 70126 Bari, Italy; and R. M. Jiménez-Díaz, IAS-CSIC and College of Agriculture, University of Córdoba, P.O. Box 3048, 14080 Córdoba, Spain. Plant Dis. 90:975, 2006; published on-line as DOI: 10.1094/PD-90-0975A. Accepted for publication 13 April 2006.

During the 2005–2006 autumn to winter lettuce-growing (*Lactuca sativa* cv. Iceberg) season, severely stunted and yellowing lettuce plants with disease incidence ranging from 80 to100% were observed in four commercial, fall-sown fields at Almodóvar del Río (Córdoba Province) in southern Spain. Early symptoms consisted of severely reduced growth of the plants that continued with extensive leaf yellowing and the absence of tight-head formation. Attacks by the disease were estimated to cause near complete loss of the crop yields since the lettuce head produced in affected fields were unmarketable. Observations of affected lettuce plants revealed high parasitism of the root system by a root-knot nematode (*Meloidogyne* sp.) in the main and feeder roots as well as heavy soil infestations by the nematode. The nematode was identified by the female perineal pattern, esterases phenotype, and a sequence-characterized amplified region polymerase chain reaction (SCAR-PCR) technique (1,2,4). Measurements and morphological observations of 20 second-stage juveniles (J2s) (body length = 463 ± 28 µm, dorsal gland orifice from stylet base = 2.8 ± 0.6 µm, stylet length = 10.4 ± 0.5 µm, tail length = 54.4 ± 0.6 µm; hyaline tail terminus = 9.4 ± 0.6 µm) and 10 adult females (stylet length = 14.5 ± 0.7 µm, dorsal gland orifice from stylet base = 4.7 ± 0.5 µm, and perineal pattern with low and rounded dorsal arch with coarse striae) conformed to the description of *Meloidogyne arenaria* (3). On the basis of the characteristics of the perineal pattern, the 2-band esterase phenotype, and the 420-bp SCAR fragment, the causal agent was identified as the peanut root-knot nematode *M. arenaria*. Nematodes were extracted from soil and root samples by standard procedures and their populations quantified. *M. arenaria* was detected in nearly all soil and root samples assessed, with nematode population densities ranging from 206 to 1,072 eggs and J2s per 5 g of fresh roots. Different *Meloidogyne* spp. have been reported parasitizing lettuce roots, especially *M. hapla* in northern areas (2); however, to our knowledge this is the first time that *M. arenaria* is reported parasitizing lettuce roots in Spain and elsewhere.

References: (1) P. R. Esbenshade and A. C. Triantaphyllou. J. Nematol. 22:10, 1990. (2) N. A. Mitkowski et al. Plant Dis. 86:840, 2002. (3) K. J. Orton Williams. *Meloidogyne arenaria*. CIH Descriptions of Plant-Parasitic Nematodes. Set 5, No. 62. Commonwealth Institute of Helminthology, St. Albans, 1975. (4) C. Zijlstra et al. Nematology 2:847, 2000.

e-Xtra*

Occurrence of *Prunus necrotic ringspot virus* and *Arabis mosaic virus* on Rose in Iran. F. Rakhshandehroo, H. R. Zamani Zadeh, A. Modarresi, and S. Hajmansoor, Plant Pathology Department, College of Agriculture and Natural Resources, Science and Research Branch, Islamic Azad University, P.O. Box-14515-775, Tehran, Iran. Plant Dis. 90:975, 2006; published on-line as DOI: 10.1094/PD-90-0975B. Accepted for publication 10 April 2006.

Rose is an economically important crop for Iran and the world. A survey was carried out from March 2005 to January 2006 to identify viruses infecting rose plants (*Rosa* × *damascena*, *R. chinensis*, *R. canina*, *R. indica*, and *R. multiflora*) in five plantations (Damavand, Tehran, Karaj, Shahre-Rey, and Varamin) in and near the Tehran Province of Iran. Samples (526) from eight rose-growing plantations were collected. All samples were tested for *Prunus necrotic ringspot virus* (PNRSV), *Arabis mosaic virus* (ArMV), and *Cucumber mosaic virus* (CMV) using the dot-immunobinding assay (1) and double-antibody sandwich enzyme-linked immunosorbent assay (DAS-ELISA) according to the manufacturer's instructions (Bioreba, Basel, Switzerland). Among the samples tested, PNRSV and ArMV were found in 23.1 and 18.8% of the collection, respectively. No CMV was detected in any of the samples. The presence of ArMV and PNRSV was verified in samples by transmission to indicator test plants, cucumber (*Cucumis sativus*), French bean (*Phaseolus vulgaris*), and Cowpea (*Vigna unguiculata*). Inoculation with extracts from PNRSV-positive plants produced systemic mosaic, stunting, and vein banding on cucumber, and necrotic local lesions on cowpea. No symptoms were observed in French bean. Inoculation with extracts from ArMV-positive plants produced systemic vein banding on cucumber, chlorotic local lesions on French bean, and systemic mosaic on cowpea. These symptoms were similar to those that were described previously for these viruses (2,4). The symptoms observed on indicator plants for each virus corresponded to the results of DAS-ELISA. Examination of crude sap prepared from ArMV- and PNRSV-infected cucumber leaves using immunosorbent electron microscopy (IEM) revealed the presence of isometric virus particles with a diameter of approximately 30 and 25 nm, respectively. Frequencies of occurrence of these two viruses as determined by serological detection showed ArMV to be the most prevalent virus in high altitudes (1,700 to 1,900 m above sea level) compared with the lowland regions. Serological tests also indicate that PNRSV is mostly distributed through the red rose varieties (*Rosa* × *damascena*, *R. chinensis*, *R. canina*, and *R. multiflora*) and ArMV is within the white varieties (*R. canina*, *R. indica*, and *R. multiflora*). However, mixed infections of PNRSV and ArMV were detected in all rose samples tested. An infection by PNRSV and ArMV either singly or in combination is usually responsible for rose mosaic disease. PNRSV has been isolated in many rose-growing regions worldwide. ArMV alone or in complexes with ilarviruses infect garden and greenhouse rose in Europe and India (3). Mosaic is probably the most commonly found virus on roses. To our knowledge, this is the first report of a natural occurrence of ArMV and PNRSV on rose in Iran.

References: (1) E. E. Banttari and P. H. Goodwin. Plant Dis. 69:202, 1985. (2) M. Boulila and M. Marrakchi. Phytopathol. Mediterr. 40:125, 2001. (3) S. Kulshrestha et al. Curr. Sci. 89:1759, 2005. (4) N. Salem et al. Plant Pathol. 86:85, 2004.

* The *e*-Xtra logo stands for "electronic extra" and indicates this Disease Note online contains supplemental material not included in the print edition.

A Yellow Mosaic Disease of Soybean in Northern India is Caused by *Cotton leaf curl Kokhran virus*. S. K. Raj, M. S. Khan, and S. K. Snehi, Molecular Virology, National Botanical Research Institute (NBRI), Lucknow-226001 India; and S. Srivastava and H. B. Singh, Plant Pathology, National Botanical Research Institute (NBRI), Lucknow-226001, India. Plant Dis. 90:975, 2006; published on-line as DOI: 10.1094/PD-90-0975C. Accepted for publication 10 April 2006.

Soybean, *Glycine max* (L.) Merr., is a protein- and oil-rich crop cultivated in India and abroad. A yellow mosaic disease was observed on soybean with 80 to 90% disease incidence during August 2005 at fields of the National Botanical Research Institute, Lucknow, in northern India. Soybean plants were found to be infested with whiteflies (*Bemisia tabaci*) suggesting begomovirus etiology. The disease agent was transmitted experimentally by whiteflies, and symptoms developed after 23 days. Total DNA was isolated from 51 leaf samples collected from 42 symptomatic and 9 asymptomatic plants. Polymerase chain reaction was performed using begomovirus coat protein-specific primers 5′-ATGGCGAA GCGACCAG-3′ and 5′-TTAATTTGTGACCGAATCAT-3′ (AM180920/ AM180921). An amplicon of the expected size (~800 bp) was obtained in all 42 symptomatic leaves but not from any of the nine asymptomatic leaf samples. The amplicon was cloned, and the identical sequence of three clones was submitted to GenBank (Accession No. DQ343283). BLAST search of nucleotide sequences revealed 95% identity with *Cotton leaf curl Kokhran virus* (CLCKV) (GenBank Accession Nos. AJ002449, AJ002448, AJ496286, and AY456683) and 57% identity with *Mungbean yellow mosaic India virus* (MYMIV-Sb, GenBank Accession No. AY049772). Results indicated that the virus associated with yellow mosaic disease of soybean is an isolate of CLCKV rather than MYMIV-Sb (1) reported earlier on soybean from northern India. To our knowledge, this is the first report of soybean as a new host of *Cotton leaf curl Kokhran virus*.

Reference: (1) K. S. Usharani et al. Curr. Sci. 86:845, 2004.