
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 to 100% 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, esters 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.


e-Xtra*

Occurrence of Prunus necrotic ringspot virus and Arabis mosaic virus on Rose in Iran. F. Rakhshandehroo, H. R. Zamani Zadeh, A. Modarresi, M. Hassanpour, R. Rajabi, and S. Hajmansoor, Plant Pathology Department, College of Agriculture, 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. The survey was carried out from March 2005 to January 2006 to identify viruses infecting rose plants (Rosa × damascena, R. chinesis, R. canina, R. indica, and R. multiflora) in five plantations (Damavand, Tehran, Karaj, Shahre-Ray, and Qazvin) and in 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. chinesis, 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 lilyviruses 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.


*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. Shehri, 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 near Lucknow, in 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′-ATGCCTGGA GCGACCACG-3′ and 5′-TTAAATTTTGACCGAATCAT-3′ (AM180920 and AM180921). An amplon 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, AJ149628, and ATY456683) and 57% identity with Mungbean yellow mosaic India virus (MYMV-Sb, GenBank Accession No. AY049772). Results indicated that the virus associated with yellow mosaic disease of soybean is an isolate of CLCKV rather than MYMV-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.