Welcome Sign in | Register | Mobile

APS Journals The premier source for peer-reviewed plant pathology research since 1911.

Journals Home Books Home APS Home IS-MPMI Home My Profile Subscribe Search Advanced Search Help

Share | Subscribe Free alerts RSS

About the cover for October 2011

ISSN: 0191-2917
e-ISSN: 1943-7692

SEARCH

Enter Keywords

MPMI
Phytobiomes
Phytopathology
Plant Disease

search
Advanced Search

Resources

Subscribe
About Plant Disease
First Look
Most Downloaded Articles
Journals Impact
Submit a Manuscript
Customer Care
About My Password
Rights and Permissions
Plagiarism and Ethics
Advertise
e-Xtra
Open Access
ORCID Registry

ORCID Connecting Research and Researchers
REGISTRATION IS FREE AND FAST.
ORCID is an open, non-profit, community driven organization.
Your ORCID iD ensures you get credit for your work throughout your career.
Register today at orcid.org

plant disease

Editor-in-Chief: Alison E. Robertson
Published by The American Phytopathological Society

October 2011, Volume 95, Number 10
Page 1321
https://doi.org/10.1094/PDIS-10-10-0708

Disease Notes

First Report of *Chickpea chlorotic stunt virus* Infecting Legume Crops in Tunisia

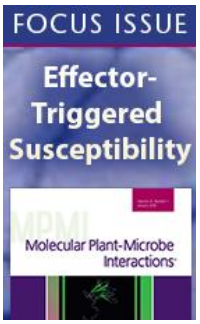
A. Najar, Laboratoire de Protection des Végétaux, Institut National de Recherche Agronomique de Tunisie, Rue Hedi Karray 2049 Ariana, Tunisia; and **S. Kumari**, **N. Attar**, and **S. Lababidi**, International Center for Agricultural Research in the Dry Areas (ICARDA), P.O. Box 5466, Aleppo, Syria

Quick Links

Add to favorites
E-mail to a colleague
Alert me when new articles cite this article
Download to citation manager
Related articles found in APS Journals

Open Access.

During a survey of legume crops in the northeast and northwest regions of Tunisia in April 2010, plants showing yellowing, reddening, and stunting symptoms were observed. A total of 281 symptomatic samples were collected: 142 plants from 10 chickpea (*Cicer arietinum* L.) fields, 84 plants from six faba bean (*Vicia faba* L.) fields, and 55 plants from six pea (*Pisum sativum* L.) fields. All samples were tested by the tissue-blot immunoassay procedure with the following monoclonal antibodies (MAbs): a broad-spectrum legume-luteovirus MAb (5G4), *Faba bean necrotic yellows virus* (FBNYV; genus *Nanovirus*, family Nanoviridae) (3-2E9; provided by J. Vetten, BBA, Braunschweig, Germany), *Beet western yellows virus* (BWYV; genus *Polerovirus*, family Luteoviridae) (A5977; Agdia, Elkhart, IN), *Bean leafroll virus* (BLRV; genus *Luteovirus*, family Luteoviridae) (4B10), *Soybean dwarf virus* (SbDV; genus *Luteovirus*, family Luteoviridae) (ATCC PVAS-650; American Type Culture Collection ATCC, Rockville, MD,), and a mixture of three MAbs (5-2B8, -3D5, and -5B8) to a Syrian isolate of *Chickpea chlorotic stunt virus* (CpCSV) (1). Serological tests showed that CpCSV was detected in 121 samples (43.06%) (62 chickpea, 57 faba bean, and 2 pea), followed by FBNYV (detected in three faba bean and three pea), BWYV (detected in three chickpea and one faba bean), and BLRV (detected in one pea sample). FBNYV, BLRV, and BWYV have been previously detected in faba bean and chickpea in Tunisia (4), but to our knowledge, this is the first report of CpCSV affecting legumes in Tunisia, which was found in seven chickpea, seven faba bean, and two pea fields. CpCSV has been reported to naturally infect legume crops such as chickpea, lentil, field pea, and faba bean as well as some leguminous weeds and a few wild non-legume plants species in many countries in West Asia and North Africa and causes economic losses on chickpea in Eritrea, Ethiopia, and Syria (1–3). Serological results of CpCSV was confirmed in four (two pea, one faba bean, and one chickpea) samples by reverse transcription (RT)-PCR using CpCSV specific primers (F:5′-TAGGCGTACTGTTCAGCGGG-3′ and



R:5′-TCCTTTGTCCATTCGAGGTGA-3′) (3), which produced an amplicon of expected size (413 bp). No amplification was observed from healthy plant extracts. Sequence analysis revealed that the four Tunisian isolates (TuV 258-201 collected from faba bean [GenBank Accession No. HQ199310], TuC 215-201 collected from chickpea [HQ199307], and TuP 163-201 [HQ199308] and TuP 166-201 collected from pea [HQ199309]) were most similar to each other with a high sequence identity (99%) and clustered with isolates of CpCSV from Syria (GenBank Accession No. EU541270), Egypt (EU541269), and Morocco (EU541267), to which they were most closely related (98%). The Tunisian isolates also showed high sequence identity (96%) in the coat protein region with Ethiopian (GenBank Accession No. EU541257) and Sudanese (EU541263) isolates. However, all isolates are distinct from BWYV, BLRV, and SbDV (less than 70% sequence identity). Since CpCSV is transmitted by aphids only, additional studies are needed to identify the host range of the virus and the efficient aphid vectors to better understand the epidemiology of this virus under Tunisian conditions

References: (1) A. D. Abraham et al. Arch.Virol. 154:791; 2009. (2) N. Y. Asaad et al. J. Phytopathol. 157:756, 2009. (3) S. G. Kumari et al. Phytopathol. Mediterr. 47:42, 2008. (4) A. Najar et al. Phytopathol. Mediterr. 39:423, 2000.

WHITE PAPER
Foundational and Translational Research Opportunities to Improve Plant Health
Molecular Plant-Microbe Interactions
Read Article Comments

View publication stats