Disease Note

**Fusarium solani** Causing Lemon Verbena Root Rot in Iran

D. Moshrefi Zarandi¹ and A. Sharzei²

¹ Young Researchers and Elite Club, Science and Research Branch, Islamic Azad University, Tehran, Iran, 14778-93855
² Department of Entomology and Plant Pathology, Aburraiban Campus, University of Tehran, Tehran, Iran

Lemon verbena (Lippia citriodora) is a medicinal plant whose use and growing surface is increasing in Iran (Malekirad et al., 2011). Leaf chlorosis and necrosis associated with root rot symptoms were observed in the course of surveys in lemon verbena farms of Kerman province (southeast Iran) in November 2012. More than 45% of 140 randomly examined plants were symptomatic. Infected root tissues were surface-sterilized, cultured onto PDA and incubated at 25°C for a week. Cream-colored colonies developed, with thin-walled, hyaline, ovoid, 1-2 celled microconidia (7.1-15.6×2.1-4.7 μm). Macroconidia (30-62×4.1-5.8 μm) were 3-5 septate, thick walled, hyaline and slightly curved. Chlamydospores were rounded, thick-walled, single, double or several in chains. Based on the morphological features, the isolated fungi were identified as *Fusarium solani* (Leslie and Summerell, 2006). Based on the ITS sequences, the isolate cluster with other *F. solani* isolates in phylogenetic analysis. A preliminary report on the isolation and morphological identification of *F. solani* from lemon verbena in Fars province (south of Iran) was previously published (Bagheri et al., 2014). This study confirms the presence and pathogenicity of *F. solani* in a wider range in lemon verbena farms in southern Iran and to our knowledge is the first molecularly-supported report of this fungal pathogen on lemon verbena in the world.


Corresponding author: D. Moshrefi Zarandi
E-mail: delbar.moshrefi@yahoo.com

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Disease Note

**First Report of Southern Tomato Virus in Tomato in the Canary Islands, Spain**

M. Verbeek¹, A.M. Dullemans¹, A. Espino², M. Botella³, A. Alfaro-Fernández³ and M.I. Font³

¹ Wageningen University and Research Centre, Droevedaalsesteeg 1, 6708 PB Wageningen, The Netherlands
² Laboratorio de Sanidad Vegetal Tenerife, Ctra. Boquerón s/n, La Laguna, Tenerife, Spain
³ Instituto Agroforestal Mediterráneo, Universidad Politécnica de Valencia, Cno de Vera s/n, 46022 Valencia, Spain

In October 2006, tomato plants with torrado disease were sampled in Spain. In a sample of cv. Mariana, originating from Gran Canaria, Tomato torrado virus (ToTV, genus *Tospovirus*) was detected (isolate GCN06; Alfaro-Fernández et al., 2010). In 2013, the sample was further analysed using next-generation sequencing (NGS). Total RNA, extracted from ca. 150 mg of leaf tissues, was used for an RNA library suitable for Illumina HiSeq paired end sequencing. A de novo assembly (using CLC Genomic Workbench v.6.5) resulted in 1380 sequence contigs. BLAST searches revealed the presence of ToTV and *Tomato chlorosis virus* (ToCV, genus *Crinivirus*). One contig (3427 nts, 8901 reads), showed 99.85% identity with *Southern tomato virus* (STV, genus *Amalgavirus*), isolate Mexico-1 (GenBank accession No. EF442780), a dsRNA seed-transmitted virus (Sabanadzovic et al., 2009). Reference assembly with the Mexico-1 sequence resulted in a partial sequence of 3420 nts (GenBank KJ174690). The presence of STV in sample GCN06 was verified in RT-PCR using the specific primers STV-fw and STV-rev (Candresse et al., 2013) and sequencing of the obtained amplicon. A new sampling in May 2014 in Gran Canaria revealed the presence of STV in six out of seven tomato samples of cv Mariana. All these samples were co-infected with *Pepino mosaic virus* (PepMV, genus *Potexvirus*), *Tomato spotted wilt virus* (TSWV, genus *Tospovirus*), and *Tomato yellow leaf curl virus* (TYL CV, genus *Begomovirus*). Because STV was generally found in samples co-infected with other viruses, its symptomatology in tomato remains unclear. To our knowledge, this is the first report of STV in the Canary Islands and Spain.

Alfaro-Fernández A., Medina V., Córdoba-Sellés M.C., Font M.I., Jornet J., Cebrián M.C., Jordá C., 2010. Ultrastructural aspects of tomato leaves infected by *Tomato torrado virus* (ToTV) and co-infected by other viruses. *Plant Pathology* 59: 231-239.


Corresponding author: M. Verbeek
E-mail: martin.verbeek@wur.nl

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