New Disease Reports

First report of *Iris yellow spot virus* infecting onion in the Pichincha and Tungurahua provinces of Ecuador

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Onion (Allium cepa) is one of the most important vegetable crops and is widely cultivated throughout the world. In Ecuador onion is grown on an area of 16,000 ha with a production of 103,316 tonnes (Ministerio de Agricultura, Ganadería, Acuacultura y Pesca, 2012). Iris yellow spot virus (IYSV) was first reported in Idaho, United States of America in 1993 and has since spread to many other onion-producing areas in the world (Gent et al., 2006). IYSV is an emerging virus and belongs to the family Bunyaviridae, genus Tospovirus. IYSV infects monocotyledonous and dicotyledonous plants (Kritzman et al., 2000) and can be transmitted by mechanical inoculation and by Thrips tabaci in a persistent manner (Cortêz et al., 1998). During April 2015, straw-coloured, irregularly shaped, chlorotic or necrotic lesions on leaves were observed (Fig. 1) in two onion fields, one in the province of Pichincha and the other in Tungurahua in Ecuador. The disease incidence observed in both fields was 10-15% and plants were heavily infested with thrips. Based on symptomatology, a tospovirus infection was suspected.

The presence of the IYSV in diseased leaves of twenty plants was initially confirmed by DAS-ELISA using IYSV polyclonal antibodies (Agdia, USA). Total RNA was isolated from leaf tissues of ten onion plants (five from each province). RT-PCR was done using IYSV-specific primers designed to detect sequences flanking the nucleocapsid-coding region on the S-segment (Robène-Soustrade et al., 2006) and resulted in a c. 890 bp amplicon. One product amplified from a sample from each province was sequenced (Macrogen, Seoul, Korea) and deposited in GenBank with Accession Nos. KP772267 (Onion-IYSV: Pichincha-Ecuador) and KT207939 (Onion-IYSV: Tungurahua-Ecuador). Sequence analysis using BioEdit v. 7.05 (Hall, 1999), of isolates from the present study compared with previously reported IYSV isolates showed a maximum of 99.1% nucleotide and 99% amino acid identities in the coat protein coding region. A phylogenetic tree constructed with nucleotide sequences of the coat protein region using MEGA v. 4.1 showed that the Onion-IYSV: Pichincha-Ecuador isolate was closely related to IYSV isolates from Mexico (JX946658), Canada (EU287943), New Zealand (EU477515), USA (DQ233468 and JQ973067), Guatemala (DQ838590), Japan

(AB871447), Bosnia & Herzegovina (KF733020), Chile (DQ150107) and Spain (EF427447), and formed one cluster. Whereas, the Onion-IYSV: Tungurahua–Ecuador isolate was closely related to IYSV isolates from India (DQ270004), Greece (FJ785835), Australia (AY556424 and AY345227) and Japan (AB871438), forming a separate cluster (Fig. 2). To the best of our knowledge this is the first report of the natural occurrence of IYSV in onion in Ecuador.

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Figure 1