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DISEASE NOTES

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First Report of Tobacco Streak Virus Infecting Sunflower in Argentina

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Sunflower (*Helianthus annuus*) is one of the main oleaginous crops in the world, and Argentina is positioned among the top sunflower seed producers worldwide (FAO 2019). During the 2018 to 2019 crop season, sunflower plants showing symptoms similar to those reported for the tobacco streak virus (TSV) were observed in one field of Rivera, Buenos Aires province. The symptoms included leaf mosaic and severe necrosis of stem, petioles, leaves, and pith, often progressing to complete collapse and death of affected plants. Samples from symptomatic leaf tissue were collected from five plants, and leaves of sunflower seedlings maintained under greenhouse conditions were used as the healthy control. Leaf extracts obtained from symptomatic leaves were positive by double antibody sandwich ELISA test, using a polyclonal antibody against TSV (Bioreba, Reinach, Switzerland). The average optical density of infected samples was 0.384, eight times higher than the mean plus three standard deviations of four healthy controls. Total RNA was extracted from collected samples using an RNeasy Plant Mini Kit (Qiagen, Hilden, Germany) and tested by reverse transcription polymerase chain reaction (RT-PCR) with specific TSV primers (Almeida et al. 2005). Only infected samples produced expected amplicons (~1 kb). The RT-PCR products obtained in duplicate from two symptomatic plants were purified and sequenced in both directions. The sequences were generated by individually sequencing and assembling each product to avoid assemble possible variants. The obtained sequences were assembled using DNASTAR Lasergene SeqMan software (DNASTAR, Madison, WI) and generated a consensus 969-bp sequence, which included the gene of the 714-nt coat

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No. 12
December
2019

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ISSN: 01
91-2917
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Caption

Chlorotic
symptom
of *Paris
polyphyll
a var.
yunnanen
sis*
infected
by
PMMoV-
QJ (Wen
et al.).
Photo
credit: M.
F. Zhao.
Symptom
s of
*Puccinia
tritici*
on wheat
(Brar et
al.).
Photo
credit: G.
S. Brar.Metrics 

protein and a 255-nt 3' untranslated region. The obtained sequences were identical, and a single nucleotide sequence was deposited in the GenBank database under the accession number MK732934 and used in the analysis. A BLASTn analysis of the obtained sequence with those available in the GenBank database showed the highest nucleotide sequence identity (91%, 78 to 100% query coverage) with TSV isolates from Australia (JX463336, EU871659, and EU375481). Phylogenetic trees obtained by using Bayesian inference in Mr. Bayes 3.2.6 (Ronquist et al. 2012) indicated that the TSV isolate from Argentina clustered together with those from Australia (JX463336, EU871659, and EU375481) and Brazil (AY354406). TSV has been associated with disease epidemics in sunflower and a range of legume and vegetable crops worldwide (Bag et al. 2019; Gracia and Feldman 1974; Sharman et al. 2009). To our knowledge, this is the first report of the occurrence of TSV infecting sunflower crops in Argentina. According to Sharman et al. (2016), the use of tolerant germplasm is critical to minimize the risk of TSV epidemics in sunflower. This finding should be addressed in future studies of resistant-cultivar selection in Argentina.

The author(s) declare no conflict of interest.



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Vol. 103,
No. 12
December
2019

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ISSN: 01
91-2917
e-ISSN: 1
943-7692

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Caption

Chlorotic symptom of *Paris polyphylla* var. *yunnanensis* infected by PMMoV-QJ (Wen et al.). Photo credit: M. F. Zhao. Symptoms of *Puccinia triticina* on wheat (Brar et al.). Photo credit: G. S. Brar.

Metrics

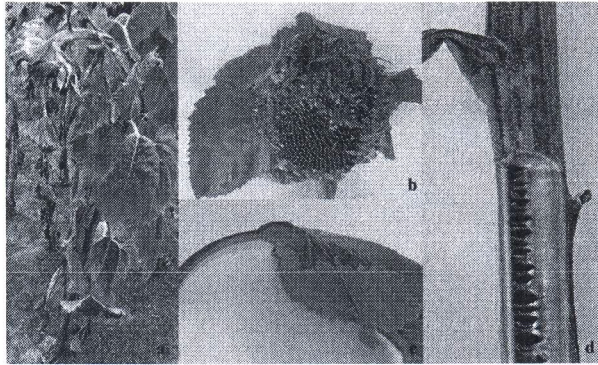


Figure S1. Symptoms of an Argentine tobacco streak virus on naturally infected sunflower field: a) severe stem and terminal necrosis, b) distortion of mature flower head, c) necrotic lesions on petioles and leaves, d) blackened pith.

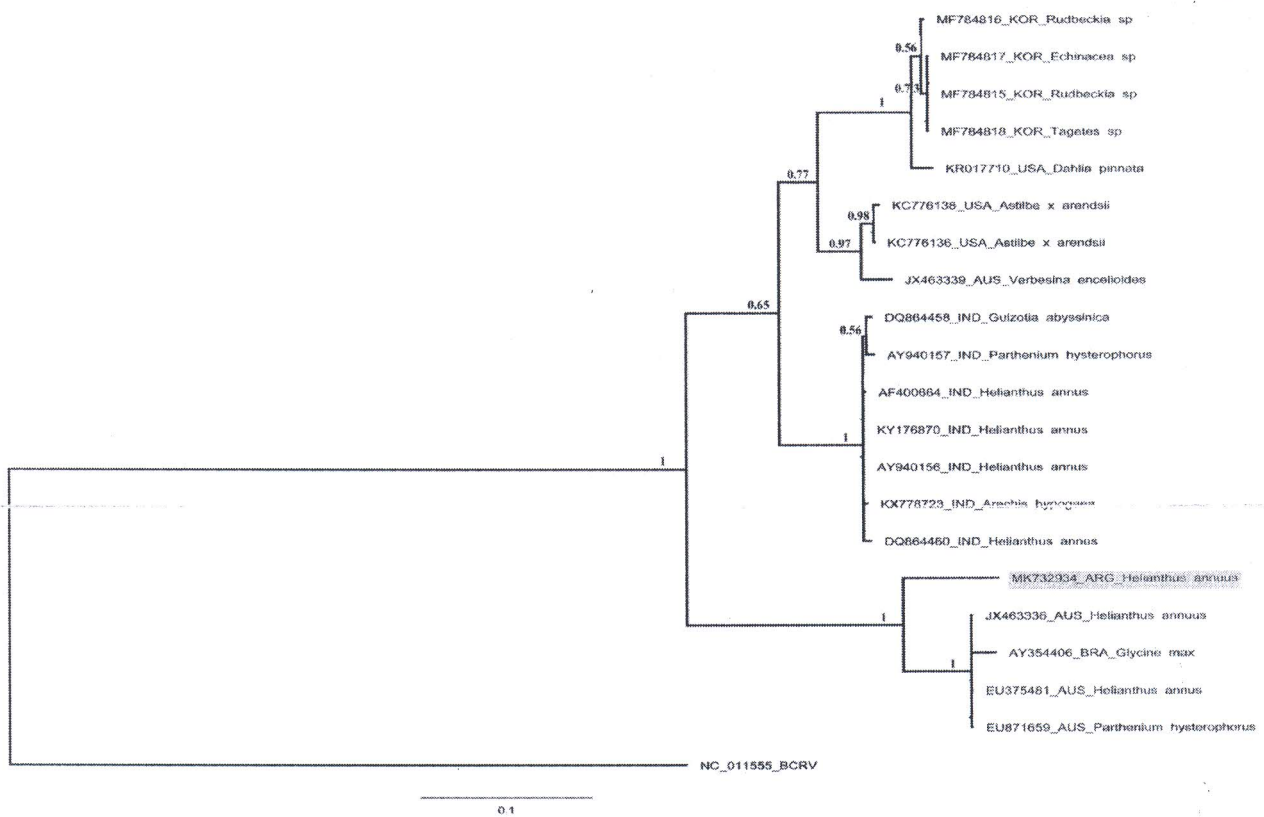


Figure S2. Bayesian phylogenetic tree obtained from the analysis of coat protein nucleotide sequences of an Argentine tobacco streak virus isolate (MK732934) and other isolates available at GenBank database. Branch lengths are proportional to genetic distances and branch significance is indicated at nodes for posterior probability values higher than 0.5. For each isolate, the GenBank accession number, geographic origin and host were indicated. Blackberry chlorotic ringspot virus (BCRV) (NC_011555) was used as out group.