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DISEASE NOTES



First Report of *Peyronellaea lethalis* Associated With *Ascochyta* Blight Complex of Field Pea in Serbia

K. Petrović, L. Riccioni, M. T. Valente, V. Đorđević, D. Živanov, R. Jevtić, and G. Malidža

Affiliations

Authors and Affiliations

K. Petrović, Institute of Field and Vegetable Crops, 21000 Novi Sad, Serbia

L. Riccioni

M. T. Valente, Consiglio per la Ricerca in Agricoltura e L'analisi Dell'economica Agraria - Centro di Ricerca per la Patologia Vegetale, I-00156 Rome, Italy

V. Đorđević

D. Živanov

R. Jevtić

G. Malidža, Institute of Field and Vegetable Crops, 21000 Novi Sad, Serbia.

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Ascochyta blight complex is a significant and widespread disease of field pea (*Pisum sativum* L.) caused by *Peyronellaea pinodes*, *P. pinodella*, and *Ascochyta pisi* (Ahmed et al. 2015). During the 2015 growing season, screening of isolates revealed a previously unknown member of this complex. Thirteen single-conidial isolates were obtained using standard phytopathological protocols. Three pathogens from this complex were recognized on potato dextrose agar according to their morphological features: *A. pisi*, *P. pinodes*, and *P. pinodella* (Aveskamp et al. 2010; Chilvers et al. 2009). Due to the plasticity of morphological characters, species identification can be challenging. Therefore, we used comparative BLAST sequence analysis of a portion of the β -tubulin (TUB) region to confirm the identity of the isolates (Aveskamp et al. 2009). It was determined that: two isolates were *A. pisi* (KX838492–93); seven were *P. pinodes* (KX838481–87); two were *P. pinodella* (KX838488–89); and the final two were *Peyronellaea lethalis* isolates (KX838490–91). All showed 100% identity to authenticated reference isolates CBS126.54 (GU237531), CBS159.78 (GU237569), CBS567.97 (GU237567), and CBS103.25 (GU237564), respectively. To verify the pathogenicity, 15 2-week-old field pea plants were sprayed with a spore suspension (10^6 conidia/ml) of the *P.*

lethalis isolate and incubated in a humid chamber for 72 h at 22°C. Control plants were sprayed with sterile water. After 7 days, inoculated plants showed *Ascochyta* blight symptoms on leaves. The control plants were symptomless. Koch's postulates were fulfilled by reisolation from infected leaves and species identity was again confirmed by β -tubulin sequencing. To our knowledge, this is the first report of *P. lethalis* associated with *Ascochyta* blight complex of field pea in Serbia. Moreover, *P. lethalis* has never been detected before in field pea and this legume is not listed as a potential host plant. Therefore, future research should focus on epidemiological studies, pathogenicity tests, and screening for field pea resistance to the newly discovered pathogen.



The American Phytopathological Society

(APS)

📍 3352 Sherman Court, Suite 202, St. Paul, MN

55121 USA

☎ +1.651.454.7250

FAX +1.651.454.0766

🐦 APS

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