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DISEASE NOTES



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



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