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First Report of *Fusarium avenaceum* , *Fusarium oxysporum* , *Fusarium redolens* , and *Fusarium solani* Causing Root Rot in Pea in France

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1 **First Report of *Fusarium avenaceum*, *Fusarium oxysporum*, *Fusarium redolens* and *Fusarium***
2 ***solani* Causing Root Rot in Pea in France**

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19 Pea (*Pisum sativum* L.) is a commonly cultivated legume in France. It can be affected by root rot diseases
20 caused by a pathogenic complex of soilborne fungi (Harveson et al. 2021). Symptomatic peas with black
21 rot lesions on their root system, sometimes associated with stunting, yellowing or wilting of the aerial parts,
22 were collected in 2017 and 2018 in the Hauts-de-France, a pea-producing region in France. Fungal colonies
23 were obtained from diseased roots, purified by single-spore culturing, and cultivated on potato dextrose
24 agar and carnation leaf agar to characterize them morphologically. Sixteen isolates, with morphological
25 characteristics similar to those of *Fusarium* (Nelson et al. 1983), were identified using the translation
26 elongation factor 1- α gene (*TEF1*) (O'Donnell et al. 2015). *TEF1* was amplified with primers EF1/EF2

(O'Donnell et al. 1998) or primers Fa/Ra (Edel-Hermann et al. 2015) and sequenced. Their GenBank acc. nos. are MW694287 through MW694302. A BLAST search showed that the sequences of strains MIAE07688, MIAE07689, MIAE07690, and MIAE07691 had 100% similarity with sequences of *F. avenaceum*, and 98.6 to 100% similarity with the sequence KU587615 of *F. avenaceum* collected from symptomatic pea in Canada. The sequences of strains MIAE07692, MIAE07693, MIAE07694, and MIAE07695 had 100% similarity with sequences of *F. oxysporum* collected from symptomatic peas in UK (acc. nos. MT630325, MT630331, MT630325, and MT630322, respectively). The sequences of strains MIAE07696, MIAE07697, MIAE07698, and MIAE07699 showed 100% similarity with sequences of *F. redolens*, and 99.3 to 99.5% similarity with the sequence KU587620 of *F. redolens* collected from symptomatic pea in Canada. The sequences of strains MIAE07700, MIAE07701, MIAE07702, and MIAE07703 showed 99 to 100% similarity with sequences of *F. solani*, and 99.7 to 100% similarity with the sequence KY556458 of *F. pisi* comb. nov. lineage (formerly *F. solani* f. sp. *pisi*) (Šišić et al. 2018). To assess pathogenicity, surface-sterilized pea seeds (cv. Firenze) were placed on malt agar and after 48 h, germinated seeds were transferred into sterile glass tubes containing 20 ml of Hoagland's No. 2 basal salt mixture at 1.6 g/liter added with 8 g/liter of agar. They were inoculated 5 days post germination with 1 ml of a conidial suspension at 10^5 conidia/ml or sterile deionized water for the control plantlets. Eight tubes per strain and eight control tubes were prepared. The tubes were incubated in a growth chamber at 25°C day / 23°C night and 16 h light / 8 h dark for 30 days. The control plantlets were asymptomatic. The four *F. avenaceum* strains caused brown rot symptoms on the roots and wilting of aerial parts, leading to 62 to 100% of dead plantlets. The four *F. oxysporum* strains caused discolored to brown symptoms on the roots and wilting of the aerial parts, causing 100% death. The four *F. redolens* strains caused honey-colored to brown symptoms on the roots and wilting of the aerial parts, leading to 75 to 100% of dead plantlets. Finally, the four *F. solani* strains caused brown to black rot symptoms on the entire root systems up to the base of the stem, causing 100% death. Strains reisolated from infected plants had the same morphological characteristics as the inoculated strains. To our knowledge, this is the first report of *F. avenaceum*, *F.*

52 *oxysporum*, *F. redolens* and *F. solani* pathogenic in pea in France. A large sampling and isolation campaign
53 is currently being performed to determine the contribution of each pathogen.

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