

## DISEASE NOTES



# First Report of *Fusarium flocciferum* Causing Root Rot of Pea (*Pisum sativum*) and Faba Bean (*Vicia faba*) in Germany

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Pea (*Pisum sativum*) and faba bean (*Vicia faba*) are important cash crops that could in cooler areas partially replace soybean imports as a source of protein for human and animal nutrition. They require long rotations mainly owing to problems with root diseases caused by a complex of soil-borne fungal pathogens (Finckh et al. 2015). In the period between 2016 and 2018, plants with brown to black necrotic lesions on tap and lateral roots, as well as some plants with softened root tips, were received from 12 conventional and organic pea and faba bean fields (six fields of each crop, 20 samples per field) at full flowering from seven German states: Hessen, Mecklenburg Vorpommern, Niedersachsen, Rheinlandpfalz, Sachsen, and Thüringen. The roots were washed under running tap water, surface

disinfected in 3% NaOCl for 10 s, rinsed in distilled water, and air dried. Three 1-cm root pieces were placed on Coon's medium and incubated for 7 to 12 days (Šišić et al. 2018a). The morphological studies of the resulting colonies were conducted from the pure cultures grown on potato dextrose and synthetic nutrient-poor agar following the methods described by Leslie and Summerell (2006). Out of 587 *Fusarium* isolates obtained, a group of 27 isolates, 18 recovered from pea and nine from faba bean, were initially identified as *Fusarium torulosum*-like based on morphology. Species identity was confirmed for two randomly selected isolates, one from each host, by sequencing portions of the internal transcribed spacer region (GenBank accession nos. MN055984 and MN055985), the translation elongation factor 1-alpha (MN061495 and MN061496), and the RNA polymerase II second largest subunit (MN061497 and MN061498) (Šišić et al. 2018b). Depending on the locus and the isolate, analyses of the sequences in the NCBI and the *FUSARIUM*-ID databases showed 99 to 100% identity match with the *Fusarium flocciferum* NRRL accession numbers 54147, 52933, 25473, 45999, and 52714. The pathogenicity of the two isolates was examined in a greenhouse assay. Inoculum was prepared on sterile sand-millet mix infested with five agar plugs of each of the isolates. Two seeds of pea cultivar Respect and faba bean cultivar Taifun were planted in 300-ml pots in autoclaved sand amended with inoculum at a ratio (by volume) of one part fungal inoculum to seven parts of sand. Noninoculated controls were amended with sterilized inoculum. Four replicates were arranged in a completely randomized design, and the experiment was conducted twice. Root rot was assessed 21 days after planting. The *F. flocciferum* isolate recovered from faba bean roots was highly aggressive on both hosts, causing decay of the entire taproot and/or dark black lesions on the root system and reduced seedling emergence. In contrast, plants inoculated with the isolate recovered from pea did not show any visible disease symptoms. However, both isolates were successfully reisolated from the roots of both hosts but not from the noninoculated controls. To the best of our knowledge, this is the first report of *F. flocciferum* causing root rot on pea and faba bean in Germany. The wide distribution of the species and the presence of highly aggressive strains in the population of *F. flocciferum* suggest that the fungus is an additional important component of the grain legume root rot complex in Germany. Our results also show that the presence of certain fungi in the root system is not proof of ongoing disease infection, and often additional tests are needed to confirm the aggressiveness of the isolates.

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