First Report of Root and Collar Rot Caused by Fusarium tricinctum and Fusarium avenaceum on Carrot in France

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Résumé en anglais	In 2017, carrot (Daucus carota L.) seed production represented around 22% of the area devoted to the production of vegetable fine seeds. Since 2015, symptoms of root and collar rot have been observed in carrot seed parcels located in the Central Region, one of the most important production zone in France. Diseased plants became dried prematurely, compromising seed development. Depending on the year and the climatic conditions, the disease in a same field can be considered as epidemic (rate losses between 30 to 100% of plants in 2016) or can impact plants more sporadically (less than 10% in 2017 and 2018). Sixteen diseased carrot samples (Nantaise type) were collected from five fields of seed production in the Central Region: two fields in 2016 and 2017, one field in 2018. Seven fungal isolates, obtained from lesions, were grown on Potato Dextrose Agar (PDA) medium and incubated for one week at 20°C in darkness. From the colony top, fluffy mycelium pigmented in pink, red, purple or orange was observed, with a red color at the reverse. To induce sporulation, isolates were grown on Synthetischer Nährstoffarmer Agar (SNA) medium during three weeks at 24°C in near-UV radiations under a 12h-photoperiod. Four isolates (FT001, FT003, FT007, FT017) developed orange sporodochia with lunar or crescent-shaped macroconidia (40.3 ± 0.8 × 5.9 ± 0.1 µm; n=90) and lime or pear-shaped microconidia (10.7 ± 0.2 × 7.7 ± 0.2 µm; n=60), as described in Fusarium tricinctum (Leslie and Summerell 2006). Three isolates (FA001, FA002, FA006) developed orange sporodochia with sickle-shaped macroconidia (50.5 ± 1.1 × 5.0 ± 0.1 µm; n= 60), but no microconidia, as observed in Fusarium avenaceum (Leslie and Summerell 2006). To confirm the identification, DNA was extracted from the mycelium of the seven isolates and molecular markers (ATP citrate lyase, ACL1; RNA polymerase II, RPB2) were used for PCR amplification (Gräfenhan et al. 2011; O'Donnell et al. 2013). The ACL1 sequences from the seven field isolates (GenBank Accession numbers MK183788-MK183791; MK181528-MK181530) were 99-100% identical with the ACL1 sequence of a reference F. tricinctum isolate (query coverages 99-100%; E-values of 0.0) and a reference F. avenaceum isolate (query coverages 98-99%; E-values of 0.0) [respectively DAOM 235630 isolate, GenBank Acc. No. JX397813 and BBA64135 isolate, GenBank Acc. No. JX397768, Niessen et al. 2012]. Using RPB2, sequences from field isolates (GenBank Acc. No. MK183109-MK183115) were 98.5-99.9% identical with the RPB2 sequence of a reference F. tricinctum isolate (query coverages 96-100%; E-values of 0.0) and a reference F. avenaceum isolate (query coverages 95-100%; E-values of 0.0) [respectively MRC 1895 isolate, GenBank Acc. No. MH582113 and MRC 1413 isolate, GenBank Acc. No. MH582082, O'Donnell et al. 2018]. To confirm pathogenicity, FT001 and FA002 were inoculated on collars of 10-weeks old carrot plants in the greenhouse. Forty plants per isolate and 40 control plants were used. Ten microliters of a conidial suspension (105 conidia.mL-1) - or sterile water for the controls - were deposited at the collar, previously wounded using a scalpel blade. Necrotic lesions developed at 20 dpi (FT001) and at 30 dpi (FA002). Fusarium tricinctum and F. avenaceum were re-isolated from the lesions and identified by sequencing using ACL1 and RPB2 markers. No isolation of Fusarium was obtained from the controls. To our knowledge, this is the first report of F. tricinctum and F. avenaceum in carrot in France.
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