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New Disease Reports

Occurrences of a new fruit rot of peach caused by *Hyphodermella rosae* in northern Iran

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Peach (*Prunus persica*) is among the major fruit crop species grown in Mazandaran province, Iran. Peach trees are often cultivated in alternate rows or in rows among citrus species. In the summer of 2011, symptoms of a previously unknown disease were observed on fruits approaching maturity. The symptoms initially consisted of greyish, circular necrotic spots 1-2 cm in diameter that gradually turned brown, developing into a dry rot. The lesions expanded in size and assumed a somewhat depressed appearance (Fig. 1). The fruits that were severely affected had a tendency to drop. Incidence of trees yielding infected fruit was noticeable (>20%) throughout most of the province where the average relative humidity exceeded 80%.

In attempts to isolate the potential causal agent, a section of the fruit bearing a younger lesion was removed using a scalpel and surface sterilised in 0.5% sodium hypochlorite for two minutes followed by one minute in 70% ethanol. The segment was rinsed twice with sterile distilled water, partially blotted on sterile filter papers and plated on potato dextrose agar (PDA) amended with 100 µg/ml streptomycin. Plates were incubated at 25°C for 7-10 days. The resulting fungus growing from the tissue was subcultured on PDA and pure cultures were established through isolation of hyphal tips. A fungus resembling a species of *Hyphodermella* was consistently isolated from the fruit lesions. The basidiomata were effuse, resupinate, crustaceous, 15 x 10 µm in size. Tubercules were small, light orange to greyish orange and bore apical bristles. Subhymenium was about 30 µm thick and composed of vertically-arranged, short-celled, non-agglutinated hyphae. Subhymenial hyphae were 3-4 µm in diameter. Basidiospores were ellipsoid, 7.5-8.5 x 4.5-5.5 (average 8.0 x 5.0 µm; n=100) with a thin, hyaline, smooth cell wall. On the basis of these morphological characteristics, the isolates were identified as *Hyphodermella rosae* (Nakasone *et al.*, 2008). Genomic DNA was extracted from a representative isolate (isolate 10) using a CTAB method (Winnepenninckx *et al.*, 1993) and used for the PCR amplification with the ITS4 (5-TCCTCCGCTTATTGATATGC-3) and ITS5 (5-GGAAGTAAAAGTCGTAACAA-3) universal primer pairs (White *et al.* 1990). A 604 bp fragment was amplified in PCR and sequenced by the dideoxy chain termination method followed by multiple sequence alignments with the CLUSTAL W software. The sequences, submitted to GenBank (Accession No. JQ920375) were compared with those in GenBank using BLAST and showed 99% similarity with *H. rosae* (FN600385.1).

Pathogenicity of two isolates (10 and 25) was confirmed by placing blocks of three-day-old colonies grown on PDA on surface-sterilised peach fruits, 10 fruits per isolate. The inoculated fruits and controls (fruits inoculated with PDA alone) were placed in polyethylene bags and then placed in desiccators used as humid chambers at 25-28°C. Fruit symptoms, similar to those observed in the field, started to appear four to six days after inoculation. The fungus was re-isolated from the inoculated fruits, while the control fruits remained symptomless. The genus *Hyphodermella* has been reported causing wood rot on apricot and sweet and sour cherry (Ogawa *et al.*, 2003; Uyemoto *et al.*, 2012). To our knowledge, this is the first report on the occurrence of dry fruit rot of peach fruits, as a new disease, caused by *H. rosae*.

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Figure 1

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