



# First report of *Fusarium lateritium* causing fruit rot of yellow peach (*Amygdalus persica*) in China

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Yellow peach (*Amygdalus persica*) is an economically important fruit crop in China, and is a specialty of Fengxian district in Shanghai. During July to September 2017, losses of at least 10% associated with fruit rot of yellow peaches (cv. Jinxiu) were observed in several commercial orchards in Fengxian districts of Shanghai, China.

Affected fruit showed brown, water-soaked lesions and white mycelium was observed on c. 80% of the fruit. As infection continued, the lesions became wrinkled and slightly sunken on the outer surface of the fruit. The mesocarp tissues were soft, brown to dark brown, water-soaked in appearance and white mycelium developed on the tissues. Sometimes orange conidial masses were produced in the centre of the lesions under high humidity (Fig. 1).

Diseased lesions from different fruit were cut into pieces (5 × 5 mm), surface-sterilised in 5% sodium hypochlorite solution for one minute, 70% ethanol solution for 30 seconds, rinsed three times with sterile distilled water, air dried, plated on potato dextrose agar (PDA) and incubated at 25°C for three days. The pure cultures were obtained by single spore isolation. Twelve uniform isolates produced pale pink, sparse aerial hyphae on PDA, and a brick red pigment was produced in the agar. Colonies grew slowly with a mean mycelia growth rate of 3.24 ± 0.26 mm per day at 25°C in the dark on PDA. Macroconidia were thin, falcate to almost straight, with parallel walls, apical cell with a distinct beak, basal cell foot-shaped, 3- to 5-septate, measuring 27.2 to 45.4 µm long (average 37.5 µm) and 4.1 to 7.8 µm wide (average 5.6 µm) in size (n = 50). No microconidia were observed. The translation elongation factor 1-α (*TEF*) gene sequences were amplified with EF1 and EF2 primer pair (O'Donnell *et al.*, 1998) and sequenced. The sequences were all identical and a representative sequence of isolate YPR-5 was submitted to GenBank (Accession no. MK160497). BLAST analysis showed that the *TEF* consensus sequences showed the highest identity (99%) with the sequence of *Fusarium lateritium* (MF521454). Based on the above, the isolates were identified as *F. lateritium*.

Pathogenicity was confirmed by inoculating surface-sterilised healthy fruit

of yellow peach (cv. Jinxiu) as described by Alam *et al.* (2017). After ten days, all inoculated fruit became infected and displayed the same symptoms as seen for naturally infected fruit while control fruit remained symptomless. The pathogen was re-isolated from symptomatic rotten fruit by the above-mentioned methods and identified as *F. lateritium* on the basis of morphological characteristics and *TEF* gene sequences, thus fulfilling Koch's postulates.

*Fusarium lateritium* has been reported causing fruit rot of walnut and olive, and causing grey necrosis on hazelnut fruit in Italy (Vitale *et al.*, 2011). To our knowledge, this is the first report of *F. lateritium* causing fruit rot on yellow peach; the pathogen may seriously affect the quality and yield of yellow peach and result in significant economic losses, so the disease needs to be properly managed.

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Figure 1

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