First report of *Neocosmospora falciformis* causing wilt and root rot of Muskmelon in Spain

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'Cantaloupe' and 'Piel de Sapo' are melon (*Cucumis melo* L.) varieties cultivated in Spain. In 2018, during a pathogens survey in experimental fields of Valencia and Alicante provinces (SE Spain), wilt and root rot of melon plants were detected in grafted and ungrafted plants. Disease incidence ranged from 10% (Alicante) to 45% (Valencia). Symptoms included yellowing and wilting of leaves, rotting at the stem base and upper root and collapse of the entire plant. Samplings were conducted from severely decayed and dead plants. Fragments (0.5-1 cm) from rotted lower stems and roots were surface disinfected for 1 min in 1.5% NaOCl, washed twice with sterilized distilled water and plated onto potato dextrose agar (PDA) with streptomycin sulphate (0.5 g L^{-1}). Plates were incubated at 25°C in the dark for 3-5 days. Mycelia resembling *Fusarium* were isolated and characterized by morphological and molecular methods. Based on their adpresed beige mycelia, growth in concentric rings and the absence of

sporodochia, colonies growing on PDA and Spezieller Nährstoffarmer Agar (SNA) were preliminary identified as belonging to the *Fusarium solani* species complex (*FSSC*). On PDA, colonies were white-greyish to pale-cream growing in concentric rings with beige reverse after 6 days. No sporodochia were observed. Macroconidia were slender, falcate, hyaline, 3-5 septate 43 (38-47) x 4.5 (3.8-5.2) µm; aerial microconidia were abundant, borne on short, undifferentiated monophialides, ellipsoidal to reniform, sometimes with truncate base, 0-1 septate 10 (9.2-11.4) x 3.5 (2.5-6) µm. Chlamydospores were globose, single or in chains, intercalary and thin to thick-walled. Sequencing of the ITS region, a fragment of translation elongation factor-1α (TEF-1α) and RNA Polymerase II (RPB2) partial genes was done using ITS1/ITS4 (White et al., 1990), EF1/ EF2 (O'Donell et al., 1998) and fRPB2-7cF / fRPB2-11aR (Reeb et al., 2004) primers, respectively. After comparisons using BLASTn and Fusarium ID Database (http://www.westerdijkinstitute.nl/fusarium/), eight isolates were identified as *Neocosmospora falciformis*. The ITS, EF-1α and RPB2 sequences of isolate CRR 2-6 showed 99% homology with *Neocosmospora falciformis* EU329691 (ITS), AB817158 (EF-1α) and EU329650 (RPB2). Sequences were deposited in GenBank with accession numbers MN086327 (ITS), MN509809 (TEF-1α) and MN509810 (RPB2). For pathogenicity tests, isolate CRR 2-6 was grown in 250 ml flasks containing potato sucrose medium for 3 days at 25ºC in the dark with constant agitation. Roots of ten 15-day-old 'Piel de Sapo' seedlings grown 6 days in trays with sterilized substrate were submerged into a suspension of 5 x 10^6 conidia/ml for 2 min, and transferred to the plastic. Three plants submerged in sterile water served as controls. Plants were incubated in a growth chamber (25ºC; 16/8 h photoperiod). Scarce development, wilting and yellowing, followed by plant death were observed 15 days post-inoculation. Non-inoculated controls remained asymptomatic. The fungus was re-isolated from all the

inoculated plants and identified using ITS, TEF-1α and RPB2. *Neocosmospora falciformis* belongs to the *Neocosmospora* (*Fusarium*) *solani* species complex (O'Donnell et al., 2008). To our knowledge, this is the first report of *N. falciformis* causing wilt and root rot of melon in Spain. The adoption of molecular-based identification methods should lead to a more precise determination on incidence of the pathogen in this Mediterranean area.

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