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NEW DISEASE REPORT

First report of *Fusarium solani* causing root rot of cucumber in Kosovo

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KEYWORDS

epidemiology, pathogenicity

FIGURE 1 Foliar wilting and stem disintegration symptoms on cucumber plants caused by *Fusarium solani* in a greenhouse in the municipality of Mamusha, Kosovo.

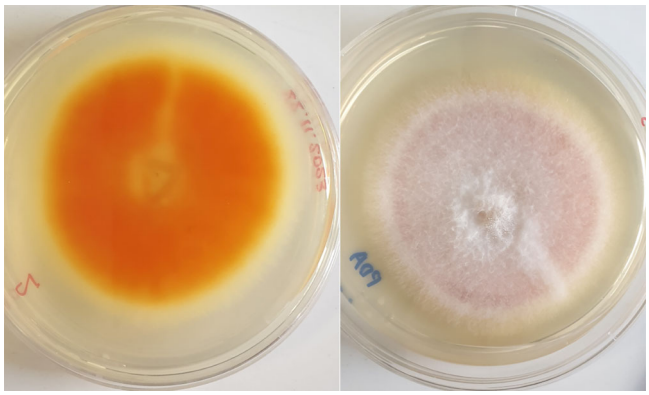

FIGURE 2 *Fusarium solani* colony morphology on potato dextrose agar.

In July 2023, symptoms of foliar wilting and yellowing, and cortical rot of stems were observed on cucumber (*Cucumis sativus* cv. Ekol) in a commercial greenhouse located in Mamusha, Kosovo (Figure 1). The disease incidence was estimated to be approximately 30%. Diseased material (stem and root fragments) was collected from affected plants. Samples were surface sterilised using 75% ethanol for one minute and rinsed in sterile distilled water. The sterilised fragments were then placed on potato dextrose agar (PDA) and incubated at 27°C in the dark for seven days. Colonies had white mycelial growth with an orange to purple pigmentation in the centre (Figure 2). Macroconidia were slightly curved with three to five septa (Figure 3). The morphology of two representative isolates, DLS2081 (stem) and DLS2082 (root), was consistent with *Fusarium solani* (Li et al., 2010).

Single spore isolates of DLS2081 and DLS2082 were used for DNA extraction using a CTAB-based method. The internal transcribed spacer (ITS) region, translation elongation factor (*TEF1α*) and second largest subunit of nuclear RNA polymerase II (*RPB2*) from both isolates were amplified and sequenced with primer pairs ITS1/ITS4 (White et al., 1990), EF-1/EF-2 (Karlsson *et al.*, 2016) and 5F2/7cR (Liu et al., 1999), respectively. Sequences were deposited

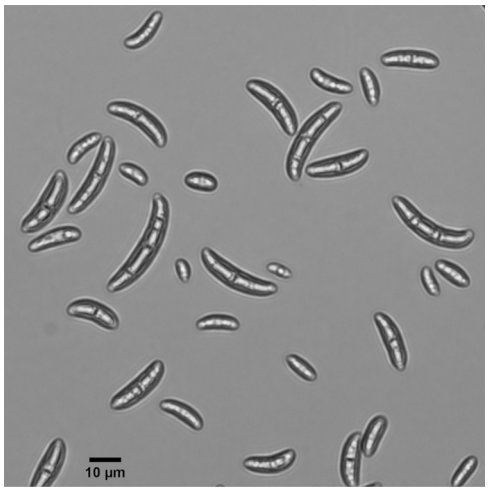

FIGURE 3 Macroconidia and microconidia of the isolated *Fusarium solani*. The size of macroconidia averaged 26–36 × 5–8 µm. Microconidia, with 0–1 septum, measured 8–22 × 2.5–5 µm on average.

in GenBank under Accession Nos. PP940094 and PP940095 (ITS), PP963514 and PP963515 (*TEF1α*), PQ119501 and PQ119502 (*RPB2*) for DLS2081 and DLS2082 isolates, respectively. A BLAST analysis of ITS sequences showed 100% identity with *F. solani* (MT371374.1, HQ384397.1), *TEF1α* sequences showed 99–100% identity with *F. solani* (HQ731056.1, MT305228.1), and *RPB2* sequences showed 100% identity with *F. solani* (MF276966.1, MF276931.1). Phylogenetic analysis revealed that both DLS2081 and DLS2082 isolates clustered with *F. solani* strains (Figure 4).

To fulfil Koch's postulates, two-week-old cucumber (cv. Ekol) plantlets (twelve per isolate) were inoculated with DLS2081 and DLS208 isolates. Plant roots were cleaned by removing soil and washing with sterile water, then a portion of the roots were excised using sterile scissors to wound them. Plantlets were inoculated by dipping their roots in a conidial suspension (1×10^6 conidia ml^{-1}), while control plants were mock inoculated with sterile water. Plants were then potted in a sterile compost mix and grown in an environmentally controlled greenhouse (25 ±2°C). Twenty-one days later, all inoculated plants developed wilting and yellowed leaves, similar to those observed initially. No symptoms occurred on the control plants. *F. solani* was re-isolated from symptomatic plants and identified through sequencing of the ITS gene amplicons.

F.solani has been described as the causal agent of root rot disease affecting cucumber in China (Li et al., 2010), India (Shanmugam et al., 2016) and Taiwan (Sritongkam *et al.*, 2022). To our knowledge, this is the first report of the *Fusarium solani* affecting cucumber crops in Kosovo.

ACKNOWLEDGEMENTS

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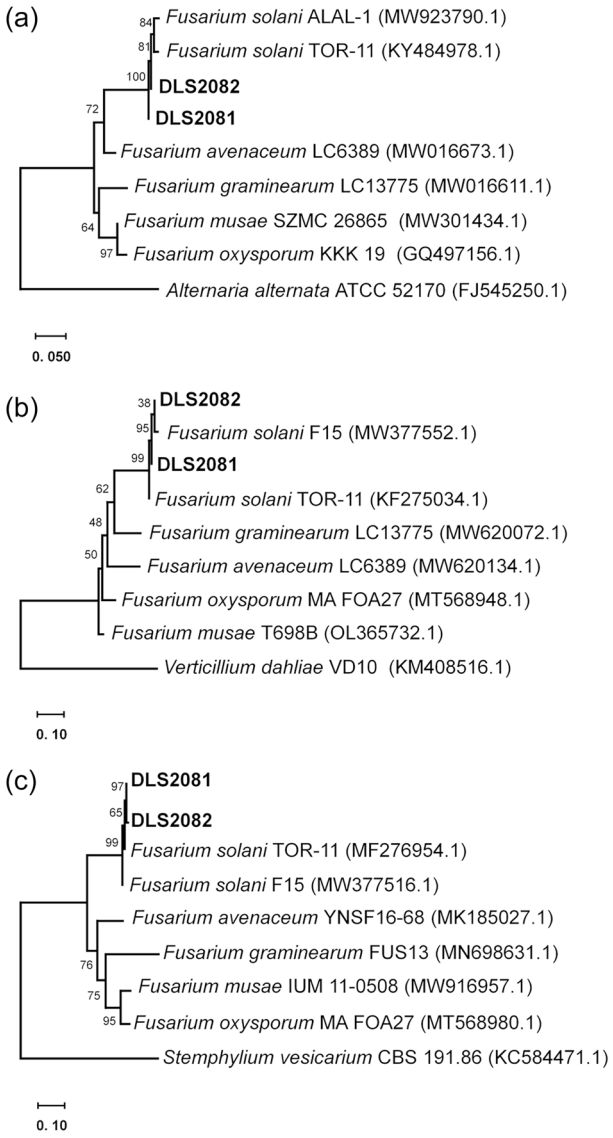

FIGURE 4 Maximum likelihood phylogenetic trees generated with MEGA 11 by applying 1,000 bootstrap replications based on the alignment of (A) ITS; (B) *TEF1α* and (C) *RPB2* sequences. The numbers in brackets represent the accession numbers in GenBank. The values from 1000 replicates are indicated at the branch nodes as the percentages supported by bootstrap. The phylogenetic trees A, B and C are rooted to the outgroups *Alternaria alternata* strain ATCC52170, *Verticillium dahliae* strain VD10 and *Stemphylium vesicarium* strain CBS 191.86 respectively. Scale bars represent a genetic distance of 0.050, 0.10 and 0.10 substitutions per nucleotide position for ITS, *TEF1α* and *RPB2* respectively. The *Fusarium solani* isolates obtained in this study are highlighted.

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