First report of tomato early blight caused by Alternaria grandis in Algeria

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Résumé en anglais	Tomatoes (Solanum lycopersicum) are widely cultivated in Algeria throughout the year. In northwestern growing areas, characterized by temperate humid climates, severe early blight symptoms (i.e., black lesions surrounded by a yellow halo) on tomato leaves are regularly observed. In 2013, diseased samples were collected from various cultivars in five farms of the Mostaganem region where average disease incidence reached 50%. Plant material was cut into ~2-mm pieces, surface sterilized in 0.1% (v/v) Na hypochlorite for 2 min, transferred into potato agar medium, and incubated for 48 h at 25°C. Fungal mycelium developing from the lesion margins was transferred to potato carrot agar medium and further incubated for 7 days alternating darkness and cool-white fluorescent light to induce sporulation. Both small- and large-spored Alternaria isolates were obtained. While most of the large-spored isolates had morphological characteristics of A. linariae (syn. A. tomatophila) (Woudenberg et al. 2014), large-spored isolates from one location (Mamache) produced ovoid conidia whose length and width were 149.8 ± 8.9 µm and 16.4 ± 1.3 µm, respectively, ended by a single beak measuring up to 120 µm. Based on these morphological characteristics and host origin, these isolates were initially described as A. solani (Simmons 2000). To confirm the identification at the species level, DNA was extracted from mycelium of four representative isolates. As polymorphism in the ITS regions of rDNA is too low to delineate species within the Alternaria section Porri (Woudenberg et al. 2014), partial regions of the glyceraldehyde-3-phosphate dehydrogenase (gpd) and of the calmodulin (cal) genes were amplified using published primer sets (Gannibal et al. 2014; Woudenberg et al. 2014). For two isolates (NB250 and NB252), the sequences of the amplified products (GenBank Accession Nos. KR911747, KR911752 KR911765, and KR911767) were 100% identical to corresponding sequences of A. solani isolate CBS 109157 (GQ180080 and KJ397981). The gpd and cal sequences of the remaining isolates (NB248 and NB249, GenBank Accession Nos. KR911748, KR911754, KR911763, and KR911764) shared 100% sequence homology to A. grandis isolate CBS109158 (JQ646341 and JQ646249) and they were therefore assigned to this species. To confirm pathogenicity on tomato, the four isolates were spray inoculated (104 conidia/ml) on leaves of 3-week-old tomato plants (cv. Saint Pierre) in the greenhouse. Three replicates were performed for each test. Plants were rated for disease symptoms up to 21 days post inoculation (dpi). No symptom was observed on control plants treated with distilled water. All plants inoculated with A. solani and A. grandis isolates produced extending lesions on leaves albeit with variable virulence (affected leaf area from 50 to 80% at 21 dpi for NB249 and NB250, respectively). To our knowledge, this is the first report of A. grandis infecting tomato in Algeria and in Africa. Moreover, A. grandis has been reported on potato crops in North and South America (Simmons 2000; Rodrigues et al. 2010), but never on tomato. The fact that potato and tomato fields often coexist in close proximity in northwestern Algeria even with farmers using potato in rotation with tomato may favor the development of A. grandis on the latter plant species.
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