Diseases Caused by Oomycetes

First Report of Late Blight Caused by *Phytophthora infestans* in Potato in Tibet, China

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Late blight caused by *Phytophthora infestans* (Mont.) De Bary is one of the most destructive diseases in potato fields. Although it has been studied worldwide, it has not been reported in Tibet Autonomous Region of China, one of the highest areas on Earth with an elevation around 4,000 m. To investigate whether the disease caused by *P. infestans* occurred in this region, a survey on potato disease was conducted in the summer in 2020. In August, potato (*Solanum tuberosum*) of the cultivar Longshu 7 with diseased leaves was observed in a potato field in Shigatse city in Tibet (29.3°N, 88.8°E). The necrotic brown lesions were round or irregularly shaped with whitish growth of sporangium-producing structures on the underleaf surface, similar to typical late blight symptoms. Affected leaves were collected for pathogen isolation. The abaxial side of the decayed leaves showed gray zones of sporulation. Upon isolation, three isolates were used for further investigation. The mycelium grew at an average linear rate of 4.35 mm per day at 19°C on Rye B agar (RBA, containing 50 g/liter rye and 12 g/liter agar), forming a white colony. The opaque and lemon-shaped spores with a papilla at the distal end had an average size of 36.2 × 20.3 μm, the shape and size consistent with *P. infestans* (Cárdenas et al. 2011; Winton et al. 2007). The ribosomal ITS1-5.8S-ITS2 region was amplified from genomic DNA obtained from mycelium using primers ITS1 and ITS4 (Glass and Donaldson 1995). The

829-bp sequences obtained from three isolates were identical, among which one of the sequences from Tibet, isolate RKZ_27, was submitted to GenBank with accession no. MW559423. A BLAST search in NCBI revealed that MW559423 had the highest similarity (100%) to *P. infestans* sequences (GenBank accession nos. MK507866, MH401206, and KU992300). In addition, a partial nucleus DNA sequence from elongation factor 1-α (EF1-α) was amplified using primer set EF_F/EF_R (EF_F: 5'-GGCCTTGACGAC ATCCAGAA-3'; EF_R: 5'-TAGCAGCTCAACCCGAAGTG-3'), and a partial mitochondria DNA sequence (P2 region) including partial ATP synthase F1 subunit α gene (atp1), tRNA-Glu gene, and partial NADH dehydrogenase subunit 4 (ND4) was amplified using primer set P2F/P2R (P2F: 5'-TTCCCT TTGTCCTCTACCGAT-3'; P2R: 5'-TTACGGCGGTTTAGCACATACA-3') (Vargas et al. 2009). The EF1-α and P2 region for three isolates were all identical and one of each sequence was submitted to GenBank with accession nos. MZ189257 and MZ399710, respectively, which had 99.78% (XM_002998924.1) and 100% (MG869098) similarity with *P. infestans*. Phylogenetic analyses showed that RKZ_27 was close to *P. infestans*. Pathogenicity was confirmed by inoculating 10 potato leaves cv. Favorita for each isolate with a 5 mm diameter mycelium plug on each leaf. After 3 days of incubation at 19°C in airtight plastic bags, the inoculated leaves developed typical symptoms of late blight. All control leaves treated with distilled water remained healthy. The pathogenicity of three isolates were also confirmed by inoculating 'Favorita' potato seedlings with sporangia suspension. The pathogen reisolation on inoculated symptomatic leaves and seedlings was confirmed to be *P. infestans* by morphological characteristics, fulfilling Koch's postulates. The pathogenicity tests on leaves and seedlings were conducted twice. To our knowledge, this is the first report of *P. infestans* in potato fields in Tibet, China. The finding of potato late blight in this region has important epidemiological implications for the growers, especially under favorable environmental conditions.

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