Diseases Caused by Fungi and Fungus-Like Organisms

Occurrence of Powdery Mildew Caused by *Blumeria graminis* f. sp. *poae* on *Poa pratensis* in China

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Poa pratensis, known as bluegrass, is a perennial grass and one of the best varieties with highly valued pasture and turf grass uses. It is widely grown on golf courses and used for lawns in squares and parks (Luo et al. 2020). During April and May 2020, powdery mildew-like signs and symptoms were observed on leaves of *P. pratensis* in Muye Park, Xinxiang city (35.3°N; 113.9°E), Henan Province, China. White or grayish powdery masses in spots or coalesced lesions were abundant on the adaxial surfaces of leaves and covered up to 90% of the leaf area. Some of the mildew-infested leaves appeared chlorotic or began senescence. Mildew-infested leaves were collected to microscopically observe the morphological characteristics of this pathogen. Conidiophores were composed of foot cells, followed by one or two cells, and conidia. The ellipsoid-shaped conidia ($n = 50$) were 25 to 36 × 10 to 15 µm (length × width), on average 30 × 13 µm, with a length/width ratio of 2.3. Foot cells ($n = 15$) were 30 to 44 µm long and 7 to 15 µm wide. On leaf surfaces, germinated conidia produced a short primary germ tube and then a long secondary germ tube that finally differentiated into a hooked appressorium. Chasmothecia were not found. Based on these morphological characteristics, the pathogen was initially identified as *Blumeria graminis* f. sp. *poae*, the known *forma specialis* (f. sp.) of *B. graminis* on *P. pratensis* (Braun and Cook 2012;

Troch et al. 2014). Mycelia of the pathogen were scraped from infected leaves, and total genomic DNA was isolated using the method described previously (Zhu et al. 2019, 2020). The rDNA internal transcribed spacer (ITS) region was amplified applying primer pairs ITS1/ITS4 (White et al. 1990). The amplicon was cloned and sequenced by Invitrogen (Shanghai, China). The obtained sequence for the pathogen was deposited into GenBank under accession number MT892956 and was 100% identical (549/549 bp) to *B. graminis* on *P. pratensis* (AB273530) (Inuma et al. 2007). In addition, the phylogenetic analysis clearly showed that the identified fungus and *B. graminis* f. sp. *poae* were clustered in the same branch. To perform pathogenicity analysis, leaf surfaces of eight healthy plants were inoculated by dusting fungal conidia from diseased leaves. Eight noninoculated plants served as a control. The noninoculated and inoculated plants were separately maintained in two growth chambers (humidity, 60%; light/dark, 16 h/8 h; temperature, 18°C). Twelve to 14 days after inoculation, *B. graminis* signs were visible on inoculated leaves, whereas control plants remained healthy. The pathogenicity assays were repeated twice and showed the same results. Therefore, based on the morphological characteristics and molecular analysis, the pathogen was identified and confirmed as *B. graminis* f. sp. *poae*. This pathogen has been reported on *P. pratensis* in Switzerland and Japan (Inuma et al. 2007). This is, to our best knowledge, the first report of *B. graminis* on *P. pratensis* in China. Because the hybridization of *B. graminis formae speciales* allows the pathogens to adapt to new hosts, *P. pratensis* may serve as a primary inoculum reservoir of *B. graminis* to threaten other species, including cereal crops (Klingeman et al. 2018; Menardo et al. 2016). In addition, powdery mildew may negatively affect the yield and quality of grasses. Our report expands the knowledge of *B. graminis* f. sp. *poae* and provides fundamental information for future powdery mildew control.

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