Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Nigrospora oryzae* Causing Leaf Spot on Ginger in China

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Ginger (*Zingiber officinale* Rosc.) is an herbal crop widely grown in China for its medicinal and savory qualities of rhizomes. In August 2018, leaf spot symptoms were observed on ginger plants grown in a field in Nanning, Guangxi Province (E108°3'54", N23°14'48"). Disease incidence was above 50%, and in a Nanning field, rhizome yield loss was almost 30%. Early symptoms appeared as circular, necrotic areas that later developed into circular or irregular spots. The centers of the lesions were white and often surrounded by chlorotic halos. In severe infections, the spots frequently coalesced, causing the entire leaf to become withered and curved. Small pieces (3 to 4 mm²) from the margin of infected lesions were surface sterilized in 75% ethanol for 40 s followed by 1% NaOCl for 90 s, placed on potato dextrose agar (PDA), and incubated at 28°C in the dark for 4 days. Hyphal tips from the leading edge of colonies were transferred to fresh PDA plates to obtain pure cultures. Fungal colonies were initially white, then turned black/grayish brown when maintained in the dark at 28°C after 5 days. Conidia were single-celled, brown, or black, smooth, spherical, or sub-spherical with diameters varying from 9.5 to 15 µm (mean = 13.5 ± 0.72 µm, *n* = 50). Based on these morphological characteristics, the isolates were provisionally identified as *Nigrospora oryzae* (Ellis 1971; Hudson 1963). Genomic

DNA was extracted from representative isolate Sjb-2. The internal transcribed spacer (ITS) region, beta-tubulin (TUB2), and the translation elongation factor 1-alpha (TEF1-α) were amplified using primer pairs including ITS1/ITS4 (White et al. 1990), Bt-2a/Bt-2b (Glass and Donaldson 1995), and EF1-728F/EF1-986R (Carbone and Kohn 1999), respectively. The obtained ITS sequence (GenBank accession no. MW555242), TUB2 sequence (MZ048644), and TEF1-α sequence (MZ048645) showed >99% similarity with several GenBank sequences of *N. oryzae* (KF516962 for ITS; MK550707 for TUB2; and KY019425 for TEF1-α, respectively). Based on the combined sequences of ITS, TUB2, and TEF1-α sequences, a phylogenetic tree was constructed using the maximum likelihood method and confirmed that the isolates were *N. oryzae*. Pathogenicity of the isolate was confirmed by fulfilling Koch's postulates. Agar blocks (3 mm diameter) containing a fungal mycelium were placed on detached healthy leaves of ginger. The leaves were then wrapped with sterile polyethylene and incubated in a greenhouse at 25°C with 60% relative humidity. Within 7 days, symptoms appeared on inoculated leaves similar to spots observed in the field, whereas controls remained symptomless. The same pathogen was reisolated from the spots. Pathogenicity tests were performed twice with three replications, indicating that *N. oryzae* is responsible for leaf spot disease on ginger. The disease in ginger caused by *N. oryzae* had been reported in southern Africa (Grech et al. 1989). To our knowledge, this is the first report of *N. oryzae* causing leaf spot of ginger in China. In the field, this pathogen can substantially affect ginger's health and rhizome yield if no effective control measures are implemented. Therefore, management of the disease should be further investigated to avoid major economic losses.

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The author(s) declare no conflict of interest.

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