Fig. 1 (A) Typical symptoms of ginger soft rot caused by Calonectria ilicicola in Guangxi Province, China. The disease is mainly identified by above ground symptoms such as wilting and yellowing. (B-C) Rhizomes from diseased plants appear brown, soft and rotten, and will decay gradually. (D) Perithecia which formed on 10% V8-juice agar. (E) The microscopic structures of the perithecia. Bar = 360μm. (F) The microscopic structures of the ascospore. Bar = 40μm. (G) Soft rot diseased rhizomes. (H) Healthy rhizomes.
First Report of Soft Rot of Ginger Caused by *Calonectria ilicicola* in Guangxi Province, China.

Qimeng Zhang¹, Dongmei Zhou¹, Wen Jiang², Hongli Zhu¹, Sheng Deng¹, Lihui Wei¹*

1. Institute of Plant Protection, Jiangsu Academy of Agricultural Sciences, Nanjing, 210014, China;
2. Institute of Biotechnology Research, Guangxi Academy of Agricultural Sciences, Nanning, 530007, China.

*Corresponding authors: Lihui Wei, weilihui@jaas.ac.cn

Ginger (*Zingiber officinale* Rosc.) is an important economic crop in China with a planting area of 293,207 hectares in 2018. In October 2018, leaf chlorosis symptoms were observed on ginger plants grown in the field in Guilin (24°36′N; 110°36′E), Guangxi Province. The rhizomes of the symptomatic plants were soft and rotted, which is different from dry rot caused by Fusarium (Li et al. 2014a). Eventually, whole plants wilted, but wilting occurred more slowly than is typical for *Pythium* infection (Li et al. 2014b; Stirling et al. 2009). In order to determine the causal agent of this disease, five infected root tissues from different individuals were sterilized in 2% Sodium hypochlorite solution for 1 min, and then thoroughly washed three times with sterile distilled water, followed by culturing on 10% V8-juice agar at 25°C. Three fungal isolates were obtained. All the fungal isolates on the plate had the same morphological phenotype and developed orange to reddish perithecia in culture after 10 days of growth. The perithecia were subglobose and measured 400 to 520 × 440 to 560 µm (avg. 425.5×481.8 µm) (n=21). A large number of ascospores were released from the pressed perithecia. Ascospores were hyaline and falcate with septum and were 17.5 to 50.3×4.4 to 8.6 µm (avg. 33.6×6.2 µm) (n=127). DNA was extracted from the fungal isolates and PCR amplicons of the internal transcribed spacer (ITS) rDNA region (Primer pairs ITS1/ITS4), TUB (partial β-tubulin gene, T1/Bt2b) (Glass and Donaldson 1995; ODonnell and Cigelnik 1997), HIS (partial histone 3 gene, CYLH3F/CYLH3R) (Crous et al. 2004) were sequenced and BLAST was used to identify the cultured fungi. The sequence of the ITS and TUB regions (GenBank accession no. MK564748 and MK580968) exhibited 100% (498/498 bp and 599/599
bp) identity to sequences corresponding to *Calonectria ilicicola* accession MF785081.1 and GU073284.1. In addition, the histone H3 sequence (GenBank MK580969) matched 100% (405/405 bp) with that of *C. ilicicola* accession JQ973141.1, GQ267256.1, AY725693.1, AY725676.1. These morphological and molecular characters allowed identification of the pathogen as *C. ilicicola*. In order to fulfil Koch’s postulates, 3-month-old ginger plants were inoculated with a suspension of 10 ml perithecia (100 perithecia/ml) by the root irrigation method (Fei et al. 2018). Control plants were treated with the same volume of sterile water. All ginger plants were incubated at 25°C. At 30 days post inoculation, the inoculated plants exhibited severe wilt and rhizome rot, while the control plants appeared healthy. The fungus was re-isolated from infected plants. It has been reported that this fungus is able to infect *Medicago sativa*, blueberry and peanut in China (Fei et al. 2018; Gai et al. 2012; Pei et al. 2015). As far as we know, this is the first report of *C. ilicicola* that infected ginger and caused rhizome rot in China.

References:


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