Diseases Caused by Fungi and Fungus-Like Organisms

First Report of *Colletotrichum aenigma* Causing Anthracnose of Grape (*Vitis vinifera*) in Korea

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Grape (cv. Kyoho) is one of the most popular dessert fruits in South Korea. Anthracnose caused by *Colletotrichum* species is a common and very destructive disease of grape in the country. In 2019, severe outbreaks of anthracnose were observed in different grape orchards in Gimcheon (36°09'N, 128°00'E), South Korea. The disease incidence on fruit was up to 50% in the orchards with most severe outbreaks, and infected fruit displayed typical anthracnose symptoms including sunken necrotic lesions with orangish conidial mass. For isolation of putative causal agents, nine diseased fruits were collected from three commercial orchards. A total of nine isolates were made from nine of the infected fruits by spreading spore masses (1×10^6 conidia/ml) from each fruit on water agar and collecting single germinated spores after incubation at 25°C overnight. The single germinated spores were transferred on to fresh potato dextrose agar (Difco, Becton Dickinson) and incubated at 25°C in the dark. Seven-day-old colonies were cottony white on the upper side and gray at the center on the reverse side. Conidia were cylindrical with round ends and measured 13.9 to 20.1×5.4 to 8.1 μm (mean = 16.5×6.6 μm , $n = 30$). Appressoria were brownish, subcylindrical with a few lobes, and 10.3 to 16.7×6.6 to 10.9 μm (mean = 13.1×8.1 μm , $n = 30$). The morphological characteristics of the isolates resembled those of *Colletotrichum* species within the *C. gloeosporioides* complex (Weir et al. 2012). DNA was amplified using the following primer pairs: ITS1/ITS4, GDF/GDR, ACT-512F/ACT-783R, Bt2a/Bt2b, and CHS79-F/CHS-354R (Weir et al. 2012). Accession numbers LC586811 to LC586825 were obtained after depositing all the resulting sequences in GenBank. A 50% majority rule phylogenetic tree (Bayesian

phylogenetic analysis) was constructed based on concatenated sequences of ITS, GAPDH, ACT, TUB, and CHS using MrBayes 3.2.10. The present isolates formed a single clade with the reference isolates of *Colletotrichum aenigma* (isolates ICMP 18608 and ICMP 18686). For a pathogenicity test, healthy grape fruits were collected from an orchard, surface sterilized by dipping in 1% sodium hypochlorite, rinsed with sterilized water, and dried by blotting. A conidial suspension (1×10^6 conidia/ml) in sterilized water was prepared from 1-week-old colonies of isolates GRAP10 and GRAP12. A small wound was made on sterilized detached fruits by punching with a sterile pin. A drop of the conidial suspension was placed on the wound, whereas the control fruits received a drop of sterile water. Similarly, unwounded fruits were also inoculated with a single droplet of conidial suspension. For each isolate and method (wounded and unwounded), 10 fruits were inoculated, and 10 noninoculated fruits were used as a control. All the treated fruits were kept in a plastic box containing moist tissue and incubated at 25°C in the dark. Typical anthracnose lesions appeared on all inoculated wounded fruits, whereas noninoculated and inoculated unwounded fruits remained asymptomatic. Koch's postulates were fulfilled by reisolating and reidentifying the causal agent from inoculated fruits. *C. aenigma* has been reported as the causal agent of anthracnose on *Juglans regia*, *Camellia sinensis*, and *Actinidia arguta* in China (Wang et al. 2016, 2019; Weir et al. 2012). Previous studies reported four *Colletotrichum* species (*C. acutatum*, *C. gloeosporioides*, *C. fructicola*, and *C. viniferum*) to cause this disease on grapes in South Korea (Lim et al. 2020; Oo and Oh 2017). To the best of our knowledge, this is the first report on grape anthracnose caused by *C. aenigma* in South Korea. This finding may help to take effective control measures for this disease.

References:

- Lim, Y. S., et al. 2020. Mycobiology 48:75.
- Oo, M. M., and Oh, S. K. 2017. Mycobiology 45:421.
- Wang, Y., et al. 2019. Plant Dis. 103:372.
- Wang, Y. C., et al. 2016. Sci. Rep. 6:35287.
- Weir, B. S., et al. 2012. Stud. Mycol. 73:115.

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