Cucurbits, plants belonging to the Cucurbitaceae family, have been cultivated for edible purposes or grow wild throughout the world. Several cucurbits, such as watermelon, cucumber, melon, and pumpkin, are economically important crops cultivated in Korea. In 2018, 29,508 ha were used for cucurbits production, occupying about 10% of the total area used for vegetable production in Korea [1]. Among cucurbits, melon (Cucumis melo L.) is one of the most popular tropical fruits and is cultivated for its juicy and sweet taste worldwide. The cultivated area of melon in Korea has fluctuated slightly each year; however, the average area over the last decade (2009–2018) was about 1530 ha [1].

In November 2016, circular leaf spots were observed on the leaves of melon in a greenhouse located in Gochang, Korea (35°21′02.6″N, 126°32′58.8″E) (Figure 1(A)). Initially, small pale brown spots with a yellow halo were observed on the leaves; later, they coalesced to form larger irregular dark brown lesions (Figure 1(B)). The centers of the lesions became grayish white. As the disease progressed, the diseased leaves finally wilted and dried (Figure 1(C)). About 80–90% of plants presented these symptoms. The identity of the disease-causing agent was determined based on morphological characteristics, molecular analyses, and a pathogenicity test.

Small sections of leaf tissue were excised from lesions and surface-sterilized by dipping in 70% ethanol for 3 min and 1% sodium hypochlorite for 1 min, after which they were rinsed in sterile distilled water. To isolate the causal agent, the leaf tissues were placed on potato dextrose agar (PDA) plates and incubated at 25°C. Mycelia growing out from the plant tissues were subcultured on fresh PDA plates. All cultures showed same colony morphology, and one representative fungal isolate (16–525) was selected for use in subsequent experiments. The culture was deposited in the Korean Agricultural Culture Collection as KACC 48922. Morphological features of fungal structures formed on fresh plant materials were examined and photographed using a Zeiss AXIO Zoom V16 and AXIO Imager A2 microscopes equipped with AxioCam 506 color (Carl Zeiss, Oberkochen, Germany). Colonies on the PDA were pale pinkish to light gray, with cottony aerial mycelium, and reached approximately 65 mm diameter at 25°C after 10-day incubation (Figure 2(D)). Morphologically, stromata were poorly developed, consisting of brown hyphal cells, and were 3–10 μm in size (Figure 2(A)). Conidiophores were fasciculate, olivaceous brown, paler toward the apex, straight to slightly curved, 3–15-septate, 50–250 × 3–5 μm (Figure 2(B)). Conidia were hyaline, acicular to cylindrical, truncate to subtruncate at the base, 3–17-septate, and 40–200 × 3–5 μm (Figure 2(C)). The morphological characteristics of the causal fungus were consistent with the description of Cercospora flagellaris Ellis & G. Martin [2–4].

Multi-gene sequence analysis was performed to identify the fungal species. An aerial mycelium...
Figure 1. Cercospora leaf spot disease caused by *Cercospora cf. flagellaris* on melon. (A) Occurrence of Cercospora leaf spot disease on melon plants cultivated in a farm. (B,C) Leaf spot lesions on upper (B) and lower (C) sides of leaves. (D) Melon seedlings with leaf spot symptoms seven days after inoculation. (E) Symptom appearing on inoculated plant. (F) Close-up of lesions formed on young leaves of melon plant.

Figure 2. Morphological and cultural features of *Cercospora cf. flagellaris* causing leaf spot on melon. (A) Stromata. (B) Conidiophores (arrows indicate conidiogenous loci). (C) Conidia. (D) Upper and reverse sides of colony grown on PDA after incubation for 10 days. Scale bars: A–C = 50 μm.
The pathogenicity of the present isolate from melon was tested in a glasshouse on melon seedlings, thus fulfilling Koch’s postulates. The fungus was re-isolated from the symptomatic tissues of inoculated plants. A pathogenicity test revealed that the present isolate was pathogenic to melon seedlings, thus fulfilling Koch’s postulates.

The genus *Cercospora* includes important phytopathogens that cause leaf spot diseases on many host plants worldwide [6,7]. Currently, polyphasic approaches based on ecology, morphology, cultural characteristics, and molecular phylogeny, are used to identify *Cercospora* species following the consolidated species concept [8]. Multi-gene phylogeny inferred from the sequence data of five genes (ITS rDNA, TEF, ACT, CAL, and HIS) has been used to identify and delimit *Cercospora* species [4,9–13]. More recently, three genes, glyceraldehyde-3-phosphate dehydrogenase (GAPDH), RNA polymerase II-β (RPB2), and β-tubulin (TUB), were found to be useful for improving the phylogenetic resolution of *Cercospora* species complexes, including *C. apii*, *C. armoricacae*, *C. beticola*, and *C. cf. flagellaris* [14]. Members of the *C. cf. flagellaris* species complex were phylogenetically separated into three distinct clades but were indistinguishable by morphology or host range [14].

*C. cf. flagellaris* remains an unresolved species complex. It has broad host ranges and has been associated with members of more than 20 plant families including Cucurbitaceae members [4,13,14]. *C. cf. flagellaris* has been identified around the world, except in European countries [4,14,15]. In Asian countries, the fungus has been reported as a plant pathogen from Korea, China, and Japan [15]. In Korea, seven plant hosts of *C. cf. flagellaris* have been found; *Amaranthus patulus* (Amaranthaceae), *Celosia argentea* var. *cristata* (Amaranthaceae), *Cichorium intybus* (Asteraceae), *Siegesbeckia pubescens* (Asteraceae), *Disphania ambrosioides* (Chenopodiaceae), *Phytolacca americana* and *P. esculenta* (Phytolaccaceae) [3,4,16]. However, there have been no previous records of leaf spot associated with *C. cf. flagellaris* on *Cucumis melo*.
(Cucurbitaceae) in Korea or other countries. As
cucurbitaceous plants, Citrullus lanatus, Cucurbita
maxima, Cucurbita pepo, and Ecballium elaterium
have been recorded as plant hosts infected by the
fungal pathogen in Iran [13,14]. Therefore, this is
the first report of Cercospora leaf spot on melon
caused by C. cf. flagellaris in Korea.

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Figure 3. A neighbor-joining tree based on the concatenated alignment of sequence data of five genes, ITS rDNA, translation
elongation factor 1-a, actin, calmodulin and histone H3, showing phylogenetic affinities of one isolate obtained from this study
with other members of Cercospora cf. flagellaris. Septoria provencialis was designated as outgroup. Isolate in boldface was
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