Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Powdery Mildew Caused by *Erysiphe viciae-unijugae* on *Vicia sativa* subsp. *nigra* in Korea

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Vicia sativa subsp. *nigra*, also known as narrow-leaved vetch, belongs to the family Fabaceae and is distributed in different countries. Vetch is one of the most important annual forage legumes in the world; it is used as hay, grain, silage, green manure, and livestock fodder. In Korea, this plant is often used as cattle feed. In early May of 2019 and 2020, a powdery mildew was observed on leaves of *V. sativa* subsp. *nigra* plants in a garden of Chonnam National University, Gwangju, Korea. The first symptom appeared on the upper surface of the leaves as a small white spot. Within 2 weeks, white spots of powdery mildew spread and covered the entire leaf. Voucher specimens were deposited at the Environmental Microbiology Laboratory Herbarium, Chonnam National University, Gwangju, Korea, under the accession numbers CNUFC PWV1 and CNUFC PWV2. The hyphal appressoria of the fungus were nipple-shaped, moderately lobed or multilobed, single or in opposite pairs. Measurements were made of 35 conidiophores and 55 conidia. Conidiophores arising from the upper part of mother cells, were cylindrical, 60.5 to 117.5 × 7.5 to 9.5 µm. The foot cells of the conidiophores were cylindrical, straight to slightly curved at the base, 23.5 to 38.7 × 7.3 to 9.2 µm, followed by two to three shorter cells. Conidia were formed singly, subcylindrical to oval, 32.5 to 48.7 × 13.5 to 19.7 µm. Conidia produced short to long germ tubes, terminating in lobed or unlobed appressoria. No chasmothecia were observed. The morphological characteristics of conidiophores and conidia were consistent with the description of *Erysiphe viciae-unijugae* in Shin (2000). However, it was not possible to identify the fungus only based on the asexual morph. In addition, the conidiophore and conidium shapes of *E. baeumleri* on the known host *V. sativa* were similar to those of *E. viciae-unijugae* (Braun and Cook 2012). Therefore, genomic DNA was extracted directly from

the mycelia and conidia using a DNA prep kit (Solgent, Daejeon, Korea). The internal transcribed spacer (ITS) regions of ribosomal DNA (rDNA) and 28S rDNA from the two specimens were amplified using the primers ITS5/PM6 (Takamatsu and Kano 2001) and LROR/LR3 (Vilgalys and Hester 1990), respectively. A BLASTn search with the ITS sequences indicated that CNUFC PWV1 (GenBank MT509395) and CNUFC PWV2 (MT509396) were 100% (503/503 bp) and 99.8% (502/503 bp) identical to those of *E. viciae-unijugae* (LC010086 and LC009962), respectively. The 28S sequences of CNUFC PWV1 (MT705629) and CNUFC PWV2 (MT705630) showed 99.8% (507/508 bp) and 99.4% (505/508 bp) identity values with *E. viciae-unijugae* (LC009976 and LC010029), respectively. Phylogenetic analyses based on the combined ITS and 28S rDNA sequences indicated that the two specimens, CNUFC PWV1 and CNUFC PWV2, formed a monophyletic clade together with sequences retrieved from *E. viciae-unijugae*. Therefore, the causal pathogen was identified as *E. viciae-unijugae* based on the results of morphological and molecular analyses. Pathogenicity tests were performed by gently pressing the infected leaves onto 10 young leaves of three healthy plants. A noninoculated plant was used as a control. The plants were maintained in a greenhouse at 22 to 25°C, with relative humidity around 75%, and natural light. Powdery mildew symptoms were observed on the inoculated leaves after 10 to 14 days, whereas no symptoms were observed on the leaves of the control. The fungi on the inoculated leaves were morphologically identical to the fungi on the original infected leaves. *E. viciae-unijugae* has been reported to occur on *Lathyrus* spp. and *Vicia* spp. (Farr and Rossman 2020). To our knowledge, this is the first report of powdery mildew caused by *E. viciae-unijugae* on *V. sativa* subsp. *nigra* in Korea. The weather conditions, especially during May, are favorable for disease outbreaks. This disease may be a potential threat to feed production in Korea.

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