Diseases Caused by Fungi and Fungus-Like Organisms

First Report of Downy Mildew on Sweet Basil Caused by *Peronospora belbahrii* in India

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Sweet basil (*Ocimum basilicum* L.; family Lamiaceae) is an annual aromatic and medicinal plant grown in tropical and subtropical regions of the world. In India, it is cultivated as a commercial crop on ~8,000 ha. Aerial plant parts and essential oil of sweet basil are used in pharmaceutical, perfumery, and food industries and in different formulations of traditional Ayurvedic and Unani medicines (Shahrajabian et al. 2020). The leaves have the highest concentrations of secondary metabolites such as terpenes and phenylpropanoids, which provide the distinctive aroma (Viuda-Martos et al. 2011). During October 2020, severe foliar disease was observed in experimental fields of sweet basil at Council of Scientific and Industrial Research–Central Institute of Medicinal and Aromatic Plants in Lucknow, India. Initial symptoms included large, interveinal chlorotic lesions on the adaxial surface of the leaves and black sporulation on the abaxial surface. Within a few days, the abaxial side of leaves turned necrotic, and leaf senescence and defoliation occurred on plants with severe symptoms. Disease incidence was 20 to 30% of plants. The pathogen was characterized morphologically using a light microscope. Sporangiophores were hyaline, dichotomously branched, 186.9 to 423.07 × 6.85 to 9.06 µm, and branched three to five times with each branch, terminating in two slightly curved branchlets, the longer one 7.05 to 25.31 µm and the shorter one 4.98 to 15.92 µm. Each branchlet had a single sporangium at the tip. Conidia were ellipsoidal to subglobose, olive-brown in color, and typically measured 25.21 to 33.86 × 17.92 to 26.24 µm, each, without a pedicel. Based on these morphological characteristics, the foliar disease was identified as downy mildew caused by *Peronospora belbahrii* (Thines et al. 2009). Eight symptomatic and two asymptomatic plant samples were collected

from different locations in the field, and genomic DNA was extracted from the conidia of the eight naturally infected tissues of sweet basil samples as well as leaf tissues from two asymptomatic plants, using the CTAB method. The internal transcribed spacer (ITS) region was amplified using ITS1 and ITS4 primers. Only eight infected samples amplified products of the expected size (~700 bp), and two asymptomatic samples showed no amplification. Only five amplified PCR products were sequenced (White et al. 1990). All five sequences were identical and were a 98.1% match with five *P. belbahrii* isolates (MN450330.1, MN308051.1, MH620351.1, KJ960193, and MF693898). The consensus sequence was deposited into the NCBI database (GenBank accession no. MW689257). Downy mildew caused by *P. belbahrii* previously has been reported on sweet basil from several countries (Wyenandt et al. 2015). To confirm the pathogenicity of these isolates on sweet basil (cv. CIM-Saumya), 25-day-old sweet basil plants were sprayed with a suspension (1 × 10⁵ sporangia/ml) of *P. belbahrii*. All plants were kept in a growth chamber with a 23/18°C diurnal cycle with 65 to 85% relative humidity for 24 h. Noninoculated plants treated with sterile water served as a control treatment. After 8 days, typical symptoms of downy mildew appeared on all the inoculated plants, whereas noninoculated plants remained asymptomatic. Inoculated leaves with symptoms consistent with downy mildew were collected and the causal agent again identified as *P. belbahrii* on the basis of microscopic examination and ITS rDNA sequence data. To our knowledge, this is the first report of downy mildew caused by *P. belbahrii* on sweet basil in India. The pathogen has a broad host range and may pose a serious threat to the cultivation of this valuable crop in India. Thus, it is pertinent to develop effective control measures to avoid further spread and mitigate economic loss.

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