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**First Report of Leaf Spot Caused by *Colletotrichum fioriniae* on Mexican bush Sage (*Salvia leucantha*) in Italy.** A. Garibaldi, G. Gilardi, S. Franco-Ortega, M.L. Gullino, Centre of Competence for the Innovation in the Agro-Environmental Sector, AGROINNOVA and DI.SAFA, University of Torino, Largo P. Braccini 2, 10095 Grugliasco, Italy.

*Salvia leucantha*, common name Mexican bush sage, is a herbaceous perennial belonging to the Lamiaceae family. Native to subtropical and tropical conifer forests in central and eastern Mexico, due to its white flowers emerging from colored bracts and its rusticity, this species is used in gardens in mix borders at warm latitudes. The plant is also appreciated for the production of essential oils. During the summer-fall of 2014, in a mountain garden located near Biella (northern Italy, 45.6121660 latitude and 8.0562970 longitude) at an altitude of 850 m, a previously unreported leaf spot was observed on 6 to 8 month-old plants. At temperatures between 15 and 25°C, 80% of plants grown in the garden were affected, though at different level. The first symptoms consisted in small necrotic spots, measuring 10 to 30 mm, interesting a large percentage of the leaf, which eventually wilted. The disease started from basal leaves on plants grown in shadow and at higher RH. At the final stage, plants were almost completely defoliated. In several isolations carried out during six months on potato dextrose agar amended with 25 mg/l of streptomycin sulphate from infected tissues, *Colletotrichum* sp. was consistently recovered from infected tissues (Bailey and Jeger 1992). Hyaline, elliptical to cylindrical aseptate and thin walled conidia (10.7 to 17.1 x 4.6 to 6.9, average 14.6 x 5.6 µm size) were abundantly produced in acervuli (85 to 197, 136 µm average) in a gray mycelium. Genomic DNA was extracted with E.Z.N.A. Plant DNA Kit (Omega Bio-Tek) from 7 days old pure culture. PCR reaction was performed using primers ITS1/ITS4 to amplify the Internal Transcribed Spacer, the intergenic region between 28 S and 18 S sequences of the ribosomal RNA, including the 5.8 S sequence. PCR product was purified and sent to sequencing to BMR Genomics (Padova, Italy). Blastn analysis of 455 bp sequence showed a 100% homology with *Colletotrichum fioriniae* (Genbank accession number KR003979.1). Sequence has been deposited to GenBank with Accession number KT354920. To confirm the result, beta-tubulin 2 gene (TUB2) between exons 2 and 6 was performed with the primers T1 (O'Donnell and Cigelink 1997) and βt2b (Glass and Donaldson 1995). The PCR product was purified and sequenced in both direction by BMR Genomics. Blastn analysis (Altschul et al. 1997) of the 458 bp product produced a 100% homology with *Colletotrichum fioriniae* (Genbank accession number KR149828.1). The sequence has been deposited to the Genbank with accession number KT354919. Pathogenicity tests were performed on healthy *S. leucantha* plants 6 to 8 month-old. Plants were inoculated by spraying leaves with a conidial suspension prepared from PDA plates of one representative isolate of the pathogen, at 1x10<sup>5</sup> CFU/ml. Control plants were sprayed with sterile water. Three plants/treatment were used. After the artificial inoculation, plants were covered for 5 days with plastic bags in order to maintain very high RH conditions and kept under greenhouse at temperatures ranging between 19 and 26°C. Seven days after the artificial inoculation, the first symptoms were observed on all inoculated plants, while not inoculated plants remained healthy. *C. fioriniae* was consistently reisolated only from inoculated plants. The pathogenicity test was repeated once. This is to our knowledge the first report of *C. fioriniae* on *S. leucantha* in Italy as well as worldwide.

#### References:

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- (2) Bailey, J.A., and Jeger, M.J. 1992. Page 315 In: *Colletotrichum*. Biology, Pathology and Control, CAB International, UK.
- (3) Glass, N.L., and Donaldson, G.C. 1995. Applied and Environmental Microbiology 61:1323–1330.

(4) O'Donnell, K., and Cigelnik, E. 1997. *Molecular Phylogenetics and Evolution* 7:103–116.