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First Report of Colletotrichum graminicola Causing Maize Anthracnose in Galicia, Northwestern Spain

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1 First Report of *Colletotrichum graminicola* Causing Maize Anthracnose in Galicia, 2 Northwestern Spain

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12 Maize (*Zea mays*) is one of the most important crops worldwide, and fungal diseases are
13 responsible for major losses in food production. Anthracnose caused by *Colletotrichum*
14 *graminicola* can infect all maize tissues, although stalk rot and seedling blight cause more
15 significant economic damage (Munkvold and White, 2016). Anthracnose stalk rot is
16 characterized by a distinctive external blackening of the lower stalks resulting in large black
17 streaks. Suspicious maize stems of variety *Tuy* (a locally grown, traditional variety that is used
18 for flour production for bread and other foods) exhibiting typical symptoms of anthracnose
19 stalk rot (black lesions and lodging) were collected from a field in Pontevedra, Galicia, Spain
20 (Geographical coordinates: 42°23'27.1" N - 8°30'46.3" W) between June and December of
21 2022. In this region, maize fields are typically small comprising a few thousand m² and are
22 planted at an approximate density of 60000 plants/ha. Approximately 200 m² in four fields
23 were sampled resulting in six symptomatic plants from one field, representing about 0.5%
24 incidence of disease. Stem samples, approximately 50 mm², were dissected and surface-
25 disinfected for 90 seconds in 20% sodium hypochlorite bleach (v/v) and rinsed three times in
26 sterile distilled water. The samples were transferred to one half-strength acidified potato
27 dextrose agar (PDA) supplemented with ampicillin (100 µg/mL) and lactic acid 90% (1.5
28 mL/L) and incubated for 5 days at 25 °C (Sukno *et al.* 2008). Single spores were transferred to
29 fresh PDA plates to obtain pure culture isolates. A total of six isolates were obtained, and
30 among them, two were selected for further characterization (SP-36820-1 and SP-36820-3).
31 Colonies grown on PDA have dark gray aerial mycelium with orange-colored spore masses.
32 Conidia are falcate, slightly curved, tapered toward the tips, and are produced in acervuli with
33 setae, measuring 37.65 to 24.84 x 8.02 to 4.67 µm, respectively (*n* = 100). These morphological
34 characteristics are in agreement with *C. graminicola* previously described by Bergstrom and
35 Nicholson (1999). Isolates were grown in potato dextrose broth (PDB) for 3 days at 25 °C and
36 total genomic DNA was extracted using a DNeasy Plant Mini Kit (Qiagen Inc., Valencia, CA,
37 USA). The internal transcribed spacer region of rDNA and the manganese-type superoxide
38 dismutase gene (*SOD2*) were amplified using primers ITS4/ITS5 (White *et al.* 1990) and
39 SOD625/SOD507 (Fang *et al.* 2002) and consequently sequenced. GenBank BLAST analysis
40 revealed that the sequences were 100% identical to each other and to strains of *C. graminicola*
41 in GenBank (including the epitype strain CBS 130836). All sequences were deposited in
42 GenBank (see e-Xtra 1 for accession numbers). To confirm Koch's postulates, plants of a
43 derivative of maize inbred line Mo940 (developmental stage V3) were placed horizontally in a
44 tray for inoculation and 20 droplets (7.5 µL) of a suspension of 3 x 10⁵ conidia per milliliter
45 were placed on the surface of the third leaf. The trays were closed to retain moisture and
46 incubated overnight at 23°C. The next day, the plants were returned to a vertical position and
47 incubated in a growth chamber at 25°C with 80% humidity and a light cycle of 16 h of light
48 and 8 h of dark (Vargas *et al.* 2012). After four days inoculated leaves presented brown
49 elongated lesions with necrotic centers consistent with *C. graminicola* infection, whereas
50 control plants remained asymptomatic. The strains reisolated from infected leaves were

morphologically identical to the original isolates. To our knowledge, this is the first report of *Colletotrichum graminicola* causing maize anthracnose in Spain. Recently, maize anthracnose was also reported in Bosnia and Herzegovina and China (Duan et al. 2019; Cuevas-Fernández et al. 2019), suggesting the pathogen's geographic range is increasing, which may be a threat to maize cultivation in locations with optimal humid conditions for disease development.

References

- Bergstrom, G. C., and Nicholson, R. L. 1999. Plant Disease. 83:596–608.
- Cuevas-Fernández, F. B., Robledo-Briones, A. M., Baroncelli, R., Trkulja, V., Thon, M. R., Buhinicek, I., et al. 2019. Plant Dis. 103:4–6.
- Duan, C. X., Guo, C., Yang, Z. H., Sun, S. L., Zhu, Z. D., Wang, X. M. 2019. Plant Dis. 103:1770.
- Fang, G. C., Hanau, R. M., Vaillancourt, L. J. 2002. Fungal Genet. Biol. 36:155–165.
- Munkvold, G.P. and White, D. 2016. Compendium of Corn diseases. 4th ed. APS Press, St Paul, MN.
- Sukno, S. A., García, V. M., Shaw, B. D., and Thon, M. R. 2008. Applied and Environmental Microbiology. 74:823–832.
- Vargas, W. A., Martín, J. M. S., Rech, G. E., Rivera, L. P., Benito, E. P., Díaz-Mínguez, J. M., et al. 2012. Plant Physiology. 158:1342–1358.
- White, T. J., Bruns, T., Lee, S., Taylor, J. 1990. Innis MA, Glefand JJ, White TJ PCR Protoc. a Guid. to methods Appl. Acad. Press. San Diego. 315–322.

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e-Xtra 1: Phylogenetic tree of the *C. graminicola* isolates and closely related sequences. Maximum Likelihood phylogenetic tree reconstructed using a multilocus concatenated alignment of ITS and *SOD2* genes of *Colletotrichum* strains used in this study and strains belonging to the *Colletotrichum graminicola* species complex. The phylogenetic tree confirmed the identity of strains isolated from maize as *C. graminicola*. GenBank accession numbers of *C. graminicola* sequences generated in this study: ITS - OQ708378, OQ708379,

96 OQ708380, OQ708381, OQ708382, OQ708383; *SOD2* - OQ716797, OQ716798, OQ716799,
97 OQ716800, OQ716801, OQ716802.

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99 **e-Xtra 2:** Leaves of inoculated maize plants.

100 Maize leaves 4 days post-inoculation with conidial suspension from *Colletotrichum*
101 *graminicola* isolates: M1.001 (A), SP-36820-1 (B), and SP-36820-3 (C), and mock-inoculated
102 control (C). The black dots indicate the inoculation points. The lesions display the typical
103 symptoms of anthracnose leaf blight.

104

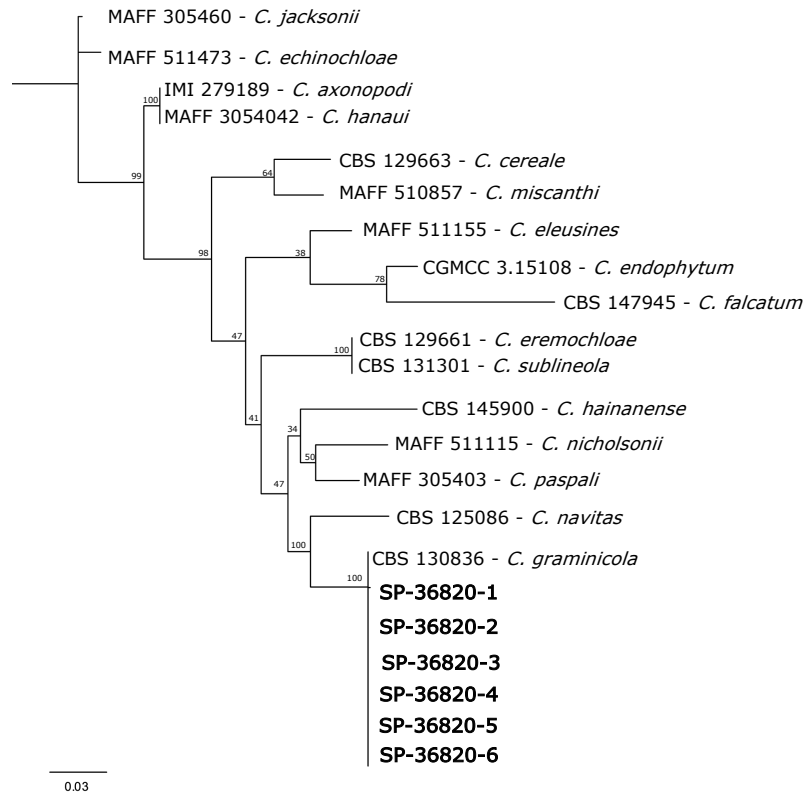


Figure S1. Maximum Likelihood phylogenetic tree reconstructed from a multilocus concatenated alignment of ITS and SOD2 genes of *Colletotrichum* strains used in this study and strains belonging to the *Colletotrichum graminicola* species complex. The phylogenetic tree confirmed the identity of strains isolated from maize as *C. graminicola*. GenBank accession numbers of *C. graminicola* sequences generated in this study: ITS - OQ708378, OQ708379, OQ708380, OQ708381, OQ708382, OQ708383; SOD2 - OQ716797, OQ716798, OQ716799, OQ716800, OQ716801, OQ716802.

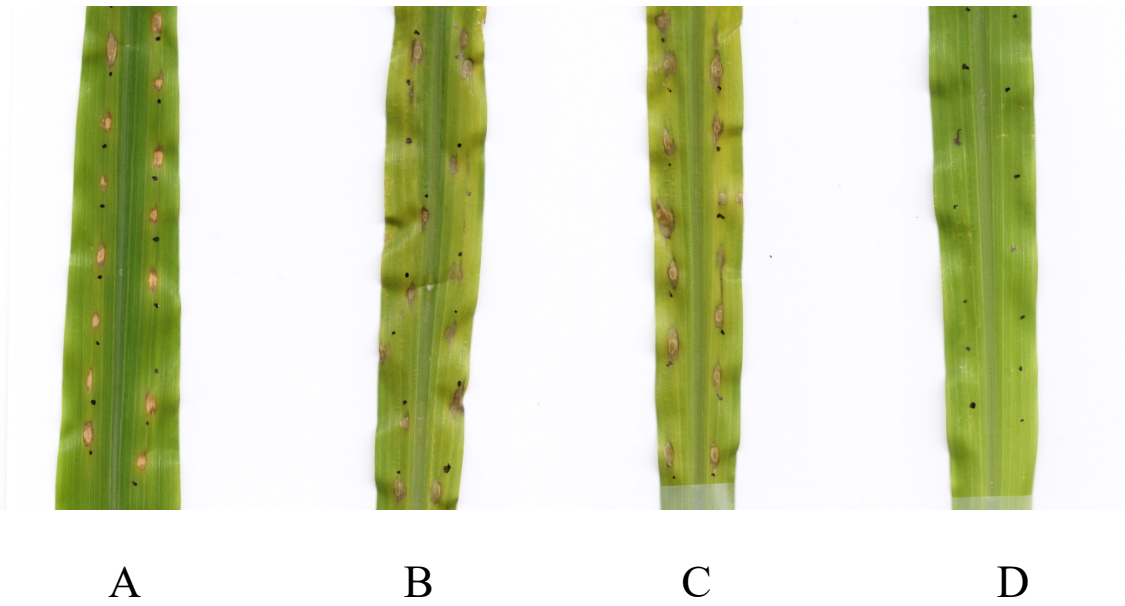


Figure S2. Maize leaves 4 days post-inoculation with conidial suspension from *Colletotrichum graminicola* isolates: (A) M1.001 - positive control, (B) SP-36820-1 and (C) SP-36820-3, and (D) mock-inoculated control. The black dots indicate the inoculation points. The lesions display the typical symptoms of anthracnose leaf blight.