8

9

10

11

12

13

14

15

16

17

18

19

20

21

22

23

24

25

26

27

- 1 First report of Colletotrichum cliviicola causing anthracnose disease of cowpea (Vigna unquiculata L.
- 2 Walp) in Nigeria
- Adenike O. Dada^{1,2,3}, Victor O. Dania², Olaniyi A. Oyatomi³, Michael Abberton³, Alejandro Ortega-Beltran³
- 4 ¹ Institute of Agricultural Research and Training, Obafemi Awolowo University, Ile-Ife, Nigeria
- 5 ² Department of Crop Protection and Environmental Biology, University of Ibadan, Ibadan, Nigeria
- 6 ³ International Institute of Tropical Agriculture, Ibadan, Nigeria
- 7 Corresponding author: A.Beltran@cgiar.org
 - Cowpea (Vigna unquiculata L. Walp) is a staple crop for millions of people in sub-Saharan Africa. However, its production is challenged by various abiotic and biotic constraints, including fungal diseases. In February 2020, around 10% of cowpea plants in IITA-Ibadan research plots (N7°29'49" E3°53'49") had symptoms of cowpea anthracnose disease (CAD). Symptoms included reddish brown spots, necrotic lesions, and vein streaks (Fig. 1). Diseased leaves were collected and taken to the laboratory, cut into small discs (3 mm in diameter) at advancing edges of lesions, and surface disinfected. Dry leaf discs were plated on PDA and incubated at 28°C for 5 days and sub-cultured in PDA for another 7 days. Isolates yielded phenotypes similar to Colletotrichum spp. (Fig. 2). DNA templates of four isolates (CC17 NG, CC19 NG, CC21 NG, and CC24 NG) were amplified using primers of the actin (ACT; ACT512F and ACT783R) (Carbone and Kohn, 1999) and glyceraldehyde-3-phosphate dehydrogenase (GAPDH; GDF and GFR) (Templeton et al., 1992) genes and sequenced. The sequences were deposited in GenBank (accession numbers OP716557 to OP716560 for ACT and OP716561 to OP716564 for GADPH). BLASTn results on NCBI showed 98-100% identity of the four isolates with C. cliviicola. A bi-locus phylogenetic tree revealed that the isolates belong to the species C. cliviicola (Fig. 3) when compared with existing sequences in the GenBank (Table 1). To fulfill Koch's postulates, pathogenicity of each of the four C. cliviicola isolates was confirmed on 2-week-old cowpea plants cv. Ife Brown in screenhouse assays. Inocula were prepared from 7-d-old cultures washed with sterile water containing 0.1% TWEEN®20. Fungal suspensions were adjusted to 10⁶ conidia/ml. Inoculations were carried out using the brush method. Leaves inoculated with sterile water containing 0.1% TWEEN®20 served as negative controls. Plants were kept in the screenhouse at room temperature for 21 days. All four C. cliviicola isolates produced CAD symptoms on inoculated leaves, while control leaves remained asymptomatic (Fig. 4). Each inoculated isolate was successfully re-isolated from symptomatic tissues and

- their identity confirmed. The fungus C. cliviicola is distributed in tropical and subtropical regions and has a
- wide host range, including several legumes (Damm et al. 2018). To our knowledge, this is the first report of
- 31 *C. cliviicola* causing CAD in Nigeria and the world. There is the need to conduct a comprehensive distribution
- 32 survey and develop appropriate control strategies in Nigeria. In addition, breeding for resistance to CAD in
- 33 Nigeria should gear the efforts to all causal agents of the disease that occur across the country because
- 34 historically CAD has been attributed to C. lindemuthianum and C. destructivum.

References

- 36 Templeton, M. D., Rikkerink, E. H., Solon, S. L., and Crowhurst, R. N. 1992. Cloning and molecular
- 37 characterization of the glyceraldehyde-3-phosphate dehydrogenase-encoding gene and cDNA from the
- plant pathogenic fungus *Glomerella cingulata*. Gene 122:225–230.
- Carbone, I., and Kohn, L. M. 1999. A method for designing primer sets for speciation studies in filamentous
- 40 ascomycetes. Mycologia 91:553–556.
- 41 Damm, U., Sato, T., Alizadeh, A., Groenewald, J. Z., and Crous, P. W. 2018. The Colletotrichum
- 42 dracaenophilum, C. magnum and C. orchidearum species complexes. Stud. Mycol. 90:71–118.

Table 1. GenBank information of reference sequences of actin and GADPH genes of the various *Colletotrichum* spp. and *Monilochaetes infuscans* used for phylogenic tree construction.

		Accession number		Country	
Reference species	Isolate	Actin	GADPH	of origin	Crop
C. lindemuthianum	CBS 130841	JX546627	JX546723	China	-
	CG2	MT424581	MT411505	India	Phaseolus vulgaris
C. cliviicola	I5H	MF940416	MG001923	Brazil	Glycine max
	YN8-2	MH622565	MH681366	China	Mangifera indica
	HN18	MW971912	MW971916	China	Rubber tree
	CMM3366	KY498353	KY498351	Brazil	P. lunatus
	AH1A2	KU251679	KU251946	China	Camellia sinensis
C. destructivum	CBS 119187	KM105430	KM105575	-	-
	IMI 387103	KM105431	KM105576	-	-
Monilochaetes	CBS 869.96	JQ005843	JX546612	-	-
infuscans					

1 Supplementary files.

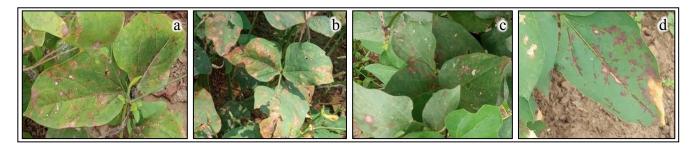


Fig. 1. Plants of cowpea cultivar Ife Brown showing symptoms of anthracnose disease (a-d).

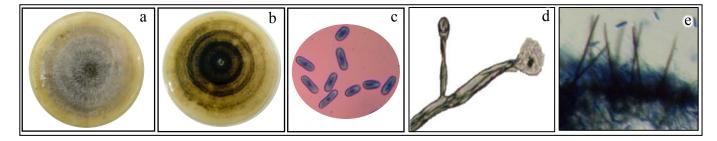


Fig. 2. Morphology of *Colletotrichum cliviicola* sp. Front (a) and back (b)view of the culture on PDA; conidia (c); appressorium (d); and setae (e).

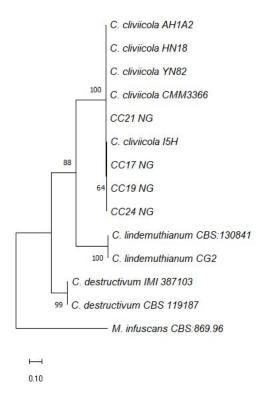


Fig. 3. Phylogenetic tree showing *Colletotrichum* spp. associated with cowpea plants in Nigeria and related spp. based on the Bayesian inference of combined sequences of portions of the glyceraldehyde-3-phosphate dehydrogenase (GAPDH) and actin (ACT) genes. The posterior probability is indicated near the branch nodes. *Monilochaetes infuscans* CBS 869.96 was used as an outgroup. Isolates with a NG legend represent those obtained from the cowpea plants from Nigeria.

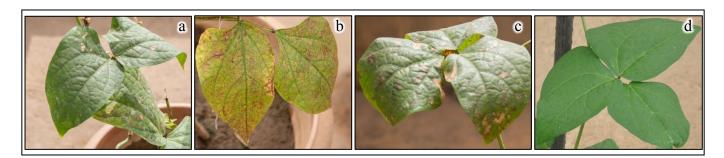


Fig. 4. Symptoms of anthracnose disease in artificially inoculated plants of Ife Brown cowpea cultivar (a-c) and water-uninoculated control plant (d).