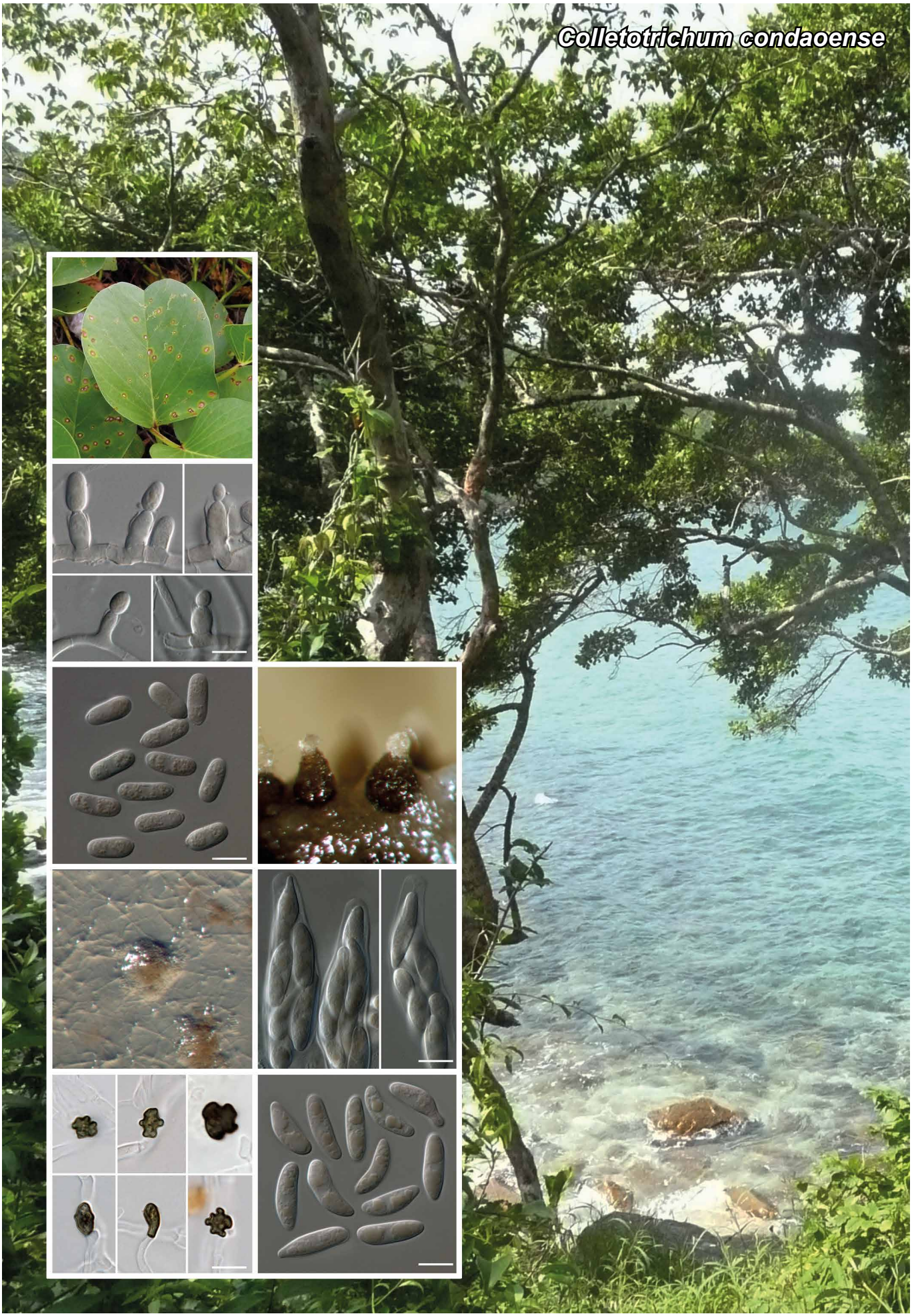
Colletotrichum condaoense

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Colletotrichum condaoense Damm, *sp. nov.*

Etymology. The species epithet is derived from the locality where it was collected, Côn Đảo Islands, Vietnam.

Classification — *Glomerellaceae*, *Glomerellales*, *Sordariomycetes.*

Sexual morph on *SNA*. *Ascomata* ovoidal to obpyriform, medium to dark brown, glabrous, 170–260 × 150–180 µm, ostiolate, wall 10–14 µm (4–6 cells) thick, outer layer composed of flattened pale brown angular cells, 5–17.5 µm diam. *Interascal tissue* composed of paraphyses, hyaline, septate, branched at the base, disintegrating quickly, 35–70 µm long, base 3–5 µm diam, apically free, the apex rounded. *Asci* cylindrical to clavate, 55–72 × 11–15.5 µm, 8-spored. *Ascospores* biseriately arranged, hyaline, smooth-walled, aseptate, fusoid, usually more tapering towards one end than to the other, straight or slightly curved, both ends rounded or one end rounded and other end ± acute, (12.5–)15–18.5(–21.5) × (4.5–)5.5–7(–9) µm, mean ± SD = 16.6 ± 1.7 × 6.2 ± 0.8 µm, L/W ratio = 2.7. *Asexual morph on SNA. Vegetative hyphae* 1–8 µm diam, hyaline, smooth-walled, septate, branched. *Chlamydospores* not observed. *Conidiomata* consisting of conidiophores and setae formed directly on hyphae. *Setae* (few observed) pale brown, smooth-walled, 14–50 µm long, 3–4-septate, base cylindrical, 5–5.5 µm diam, tip ± rounded. *Conidiophores* hyaline, smooth-walled, septate, branched, to 20 µm long. *Conidiogenous cells* hyaline, smooth-walled, ovoid to doliiform, with a double gelatinous layer, sometimes integrated, 7–19 × 5–6 µm, opening 1.5–2 µm diam, collarette ≤ 0.5 µm long, periclinal thickening distinct. *Conidia* hyaline, smooth-walled, aseptate, straight, sometimes very slightly curved, apex and base rounded, hilum sometimes visible, 12.5–14(–15) × 5–5.5(–6) µm, av. ± SD = 13.4 ± 0.8 × 5.4 ± 0.3 µm, L/W ratio = 2.5. *Appressoria* single, pale to medium brown, smooth-walled, elliptical, clavate, subglobose or irregular outline, with an undulate or lobate margin, (4.5–)7.5–13(–15) × (3–)4.5–8.5(–12) µm, av. ± SD = 10.3 ± 2.6 × 6.4 ± 1.9 µm, L/W ratio = 1.6.

Culture characteristics — (near UV light with a 12 h photoperiod, 20 °C after 10 d): Colonies on SNA flat with entire margin, hyaline to cinnamon, agar medium, filter paper and *Anthriscus* stem partly covered with grey fruiting bodies (ascomata) and sparse whitish aerial mycelium, reverse same colours; growth 12.5–15 mm in 7 d (19–21.5 mm in 10 d). Colonies on OA flat with entire margin; buff, salmon, ochreous to isabelline, partly covered with grey ascomata, salmon to ochreous conidiomata and sparse whitish aerial mycelium, reverse olivaceous grey, growth 14–16 mm in 7 d (23–24.5 mm in 10 d). Conidia in mass rosy buff to pale salmon.

Typus. Vietnam, Côn Đảo Islands, Côn Sơn, sea shore, from leaf spots on *Ipomoea pes-caprae* (*Convolvulaceae*), 12 Dec. 2012, *U. Damm* (CBS H-21508 holotype, culture ex-holotype CBS 134299; ITS, *gapdh*, *tub2*, *chs-1*, *his3* and LSU sequences GenBank MH229914, MH229920, MH229923, MH229926, MH229927 and MH229917, MycoBank MB825023).

Colour illustrations. Sea shore of Côn Sơn (Vietnam); left: leaf of *Ipomoea pes-caprae* with leaf spots; conidiophores; conidia; conidiomata; appressoria; right: ascomata; asci; ascospores. Scale bars = 10 µm.

Additional material examined. Vietnam, Côn Đảo Islands, Côn Sơn, sea shore, from leaf spots on *Ipomoea pes-caprae*, 12 Dec. 2012, *U. Damm*, culture CBS 135823, ITS, *gapdh*, *tub2* and LSU sequences GenBank MH229915, MH229921, MH229924 and MH229918; idem, culture CBS 135989, ITS, *gapdh*, *tub2* and LSU sequences GenBank MH229916, MH229922, MH229925 and MH229919.

Notes — *Ipomoea pes-caprae*, called bayhops, beach morning glory or goat's foot, is a creeping vine that grows worldwide at tropical beaches; it is one of the most common and most widely distributed salt tolerant plants and one of the first colonisers of dunes (https://en.wikipedia.org/).

Two *Colletotrichum* species were described from *Ipomoea*, none from *I. pes-caprae*. *Colletotrichum ipomoeae* was described from stems of *I. batatas* in Portugal (De Sousa da Câmara 1931) with conidia that are larger than those of *C. condaoense* 16–25 × 3.5–5 µm, while *C. ipomoeicola* (Rao 1963) from leaves of *I. batatas* in India, has curved conidia. There are several *Colletotrichum* species on *Ipomoea* listed in Farr & Rossman (2018): *C. truncatum* (syn. *C. capsici*), *C. circinans*, *C. dematium*, *C. dematium* f. *ipomoaea*, *C. gloeosporioides*, *C. ipomoeicola* and *Colletotrichum* sp. However, there is no report from *Ipomoea pes-caprae*, and most of the species listed are species with curved conidia (Rao 1963, Damm et al. 2009), except for *C. gloeosporioides* (Weir et al. 2012). All reports were from disease indexes/lists or from references prior to the molecular era, and therefore most of the identifications are not reliable.

There is no sequence of a *Colletotrichum* species from *I. pes-caprae* in GenBank, but six sequences of five strains from other *Ipomoea* spp. Three of them (GenBank KT185055 and KT185056, Huang et al., unpubl. data, and JN672591, Hipol 2012) could be assigned to the *C. orchidearum and C. magnum* species complexes, respectively (Damm et al. 2019), while the other two strains (GenBank JN672598, Hipol 2012, and DQ117967/DQ119125, Steiner et al. 2006), belong to the *C. boninense* species complex but are not conspecific with *C. condaoense* (95 % and 98 % sequence identity). In contrast, the ITS of the ex-type strain of *C. condaoense* is 100 % identical with '*C. hippeastri*' strain TV-06 (GenBank KR704574) from a leaf of *Croton bonplandianus* (*Euphorbiaceae*) probably in India (U. Nagajyothi et al., unpubl. data). It is possible that this is also *C. condaoense*; however, sequences of more loci are necessary to confirm this.

The closest species in BLASTn searches with ITS, *gapdh*, *tub2*, *chs-1* and *his3* sequences of the ex-holotype of *C. condaoense*, CBS 134299, in NCBIs GenBank nucleotide database restricted to ex-type strains, is *C. parsonsiae* (*C. boninense* species complex) with four (99 %), seven (97 %), six (99 %), one (99 %) and four (99 %) nucleotides different, respectively. There are several morphological differences between *C. condaoense* and *C. parsonsiae.* For example, conidia of *C. condaoense* are shorter than those of *C. parsonsiae* (18.5 × 5.4 µm on average on SNA), and the shapes of appressoria and ascospores are different (Damm et al. 2012). Based on these results we regard the strains from *I. pes-caprae* as a new species belonging to the *C. boninense* species complex.

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