

Fungal Planet 1147 – 19 December 2020

***Colletotrichum cycadis* Andjic, Maxwell & Smith, sp. nov.**

Etymology. Named after the host genus, *Cycas*, from which it was isolated.

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

Sexual morph not observed. *Asexual morph on malt extract agar* (MEA) (microscopic preparations in lacto-glycerol, with at least 30 measurements per structure). *Hyphae* hyaline to pale brown, smooth-walled, septate, branched. *Mycelium* white, becoming olive grey with age. *Conidiomata* acervular, brown to black. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* hyaline to pale brown, smooth-walled, aseptate, occasionally septate, mostly cylindrical, gradually thinner towards the apex, (7.5–)11–12(–17.5) × (2–)2.5–3(–4.5) μm (av. ± SD = 11.5 ± 2.3 × 2.6 ± 0.6 μm, L/W ratio = 4.4). *Conidia* aseptate, hyaline, smooth-walled, cylindrical to fusoid with obtuse ends, sometimes tapering towards the apex, contents granular or guttulate, 9.5–13.5 × 3–4 μm (av. ± SD = 11.5 ± 0.65 × 3.5 ± 0.2 μm, L/W ratio = 3.3). *Appressoria* single or in small groups, pale to dark brown, smooth-walled, variable in shape, ovate to irregularly lobed, often tapering towards apex, 4.5–8 × 2–5.5 μm (av. ± SD = 6.1 ± 1.1 × 4.5 ± 0.9 μm, L/W ratio = 1.3).

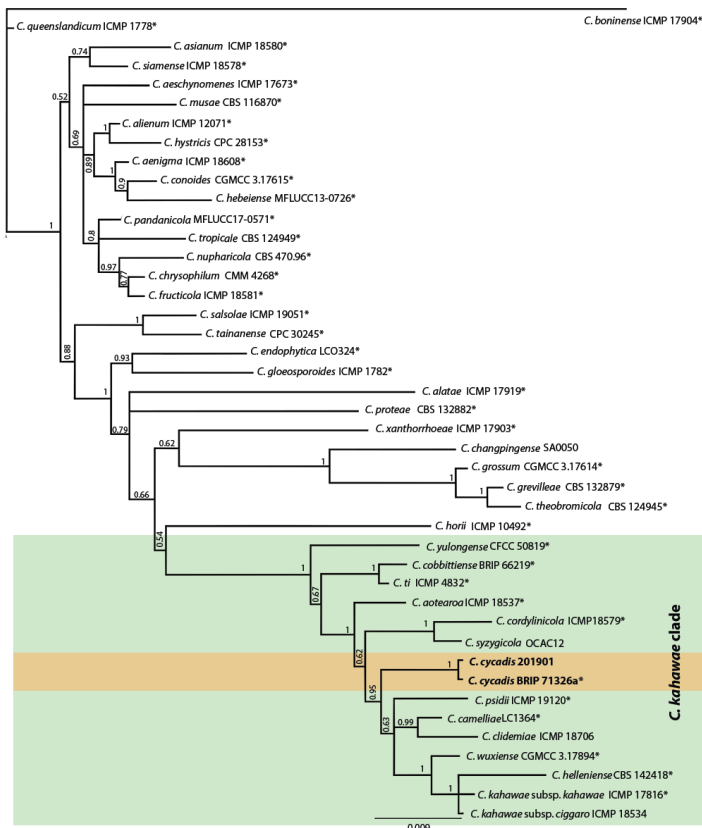
Culture characteristics — Colonies grown from single conidium on MEA reaching 70–80 mm diam after 10 d at 25 °C in the dark, light grey (5Y 7/1) to light olive grey (5Y 6/2) (Munsell & Munsell 2000); with orange conidial ooze on the surface of colony, aerial mycelium white, tufted near centre. Reverse dark olive grey (5Y 3/2), surrounded with white cottony mycelium.

Typus. CHINA, Fujian, Zhangzhou, on leaves of *Cycas revoluta*, intercepted at Australian border, July 2019, V. Andjic & A. Maxwell (holotype BRIP 71326a, includes holotype culture, LSU, ITS, *chs-1*, *gapdh* and *tub2* sequences GenBank MW136942, MT439915, MT439917, MT439919, and MT439921, MycoBank MB836054).

Additional material examined. CHINA, Fujian, Zhangzhou, on leaves of *Cycas revoluta*, intercepted at Australian border, July 2019, V. Andjic & A. Maxwell, AQISWA201901 (culture dead), LSU, ITS, *chs-1*, *gapdh* and *tub2* sequences GenBank MW136943, MT439916, MT439918, MT439920, and MT439922.

Notes — Leaf spots were observed on the young leaves of *Cycas revoluta* in a post entry quarantine greenhouse in Carabooda, Western Australia, Australia. Infected plants were destroyed and the pathogen remains absent from Australia (Australian Plant Pest Database 2020). The leaf symptoms were characterised by chlorosis starting from the tip of the leaf going towards the base where it becomes cream and then dark brown. Conidiomata occur in small, black, irregular shaped aggregates, sometimes clustered in concentric circles.

A phylogenetic tree obtained using Bayesian analysis as implemented in Geneious R10 (<https://www.geneious.com>) of separate and combined sequence data from four gene loci (*chs-1*, *gapdh*, ITS and *tub2*) placed the pathogenic fungus in the *Kahawae* clade in the *C. gloeosporioides* species complex (Weir et al. 2012). It is phylogenetically distinct from all other species of the *Kahawae* clade and can be distinguished with all loci studied, except LSU and *tub2*. Based on megablast searches on NCBI's GenBank nucleotide database, the closest match to *C. cycadis* using the LSU sequences was *C. lentis* (99.83 %), using ITS was *C. cobbtense* (98.92 % identity), using *chs-1* was *C. wuxiense* and *C. aotearoa* (98.62 % identity), and using *gapdh* was *C. aotearoa* (98.91 % identity).



Colour illustrations. *Cycas revoluta* plant. Symptomatic leaves; appressoria; conidiogenous cells; colony on MEA at 10 d; conidia. Scale bars = 10 μm.

Phylogenetic tree from Bayesian analysis based on combined gene sequences (*chs-1*, *gapdh*, ITS and *tub2*) showing the phylogenetic relationships amongst the newly described taxon *C. cycadis* (in bold) and known species in the *C. gloeosporioides* complex. Bayesian posterior probabilities (PP > 0.95) are shown at the nodes. The tree is rooted with *C. boninense* (ICMP 17904). Ex-type cultures are marked with an asterisk (*). The alignment and tree were deposited in TreeBASE (Submission ID S26714).