Cyanodermella banksiæ
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**Cyanodermella banksiae** Crous, *sp. nov.*

**Etymology.** Name refers to *Banksia*, the host genus from which this fungus was collected.

**Classification.** Stictidaceae, Ostropales, Lecanoromycetes.

Mycelium consisting of hyaline, smooth, branched, septate, 2–3 µm diam hyphae, immersed, forming a hyaline stroma that gives rise to brown, erect, cylindrical to slightly obpyriform ascomata (circular in outline), brown, with single locule, 150–300 x 250–300 µm; wall of crustose, medium brown cells with dark brown exudate. Asci intermingled among hyaline, smooth, septate hypha-like paraphyses, 1.5 µm diam. **Asci** unitunicate, cylindrical with apical mechanism, stipitate, 130–150 x 8–10 µm.

Asciospores parallel in ascus, twisted, number undetermined, hyaline to olivaceous, smooth, guttulate, cylindrical, ends obtuse to subobtuse, multiseptate, and breaking into part-spores, each section (12–16 x 2.5–3 µm) containing 3 septa, with age disarticulating into aseptate phragmospores, 5–6 x 3 µm. Sterile in culture.

Culture characteristics — Colonies erumpent, spreading, with sparse aerial mycelium and even, smooth margin, reaching 15 mm diam after 2 wk at 25 °C. On MEA, PDA and OA surface pale luteous to buff, and reverse sienna.


Notes — The sexual morph of *Cyanodermella* (based on *C. viridula*) forms erumpent, subconical ascosporas, the upper parts of which are covered in a grainy white-mealy substance. Asci are numerous, thin-walled, cylindrical, gradually tapering towards base. Ascosporas are parallel, spirally twisted, filiform, multiseptate, c. 1 µm diam, and paraphyses are sparse (Eriksson 1967). The present collection clusters basal to species identified as *Cyanodermella*, and is consequently placed in this genus, as it is also morphologically similar to other taxa presently accommodated in *Cyanodermella*. Based on Van Nieuwenuijzen et al. (2016), *Cyanodermella* could have phoma-like asexual morphs, although cultures of *C. banksiae* were sterile and this could not be confirmed.

Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hits using the ITS sequence had highest similarity to *Cyanodermella asteris* (GenBank KT758843.1; Identities = 492/587 (84 %), 23 gaps (3 %)), *Cyanodermella oleoligni* (GenBank NR_153930.1; Identities = 346/406 (85 %), 11 gaps (2 %)) and *Xylographa septentrionalis* (GenBank KJ462316.1; Identities = 307/356 (86 %), 13 gaps (3 %)).

Closest hits using the LSU sequence are *Cyanodermella asteris* (GenBank KT758843.1; Identities = 799/846 (94 %), 4 gaps (0 %)), *Cyanodermella oleoligni* (GenBank KX950461.1; Identities = 763/833 (92 %), 10 gaps (1 %)) and *Micropeltis zingiberacicola* (GenBank JQ036227.1; Identities = 749/825 (91 %), 6 gaps (0 %)). No significant hits were obtained when the *rpb2* sequence was used in a megablast search; however, a BLASTn search yielded as best hits *Cyanodermella asteris* (GenBank KU934214.1; Identities = 635/872 (73 %), 10 gaps (1 %)) and *Cyanodermella viridula* (GenBank HM244792.1; Identities = 626/877 (71 %), 29 gaps (3 %)).

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