Funbolia dimorpha
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**Funbolia** Crous & Seifert, *gen. nov.*

Spadicoidis morphologicae similes, sed conidiis dimorphis, sine septis fusciatibus.

*Etymology.* Named after the Fungal Barcode of Life group that convened at Front Royal, Virginia (USA) in 2007 to initiate the CBOL Fungal Working Group.

Associated with bark of a living tree. *Mycelium* of pale brown to hyaline, branched hyphae, giving rise to conidiophores. *Conidiophores* solitary, erect, straight to flexuous, cylindrical, unbranched, or branched below, brown, finely verruculose, multi-euseptate. *Conidigenous cells* terminal and lateral, pale to medium brown, finely verruculose, subcylindrical to somewhat swollen, clavate to irregular; loci aggregated in a rachis, at times subdenticulate with minute collarette; scars thickened along the rim, erumpent, but not darkened nor refractive. Conidia dimorphic, medium brown, finely verruculose, ellipsoidal when 1-septate, becoming subcylindrical when multisepate, apex obtusely rounded, tapering from basal septum to an obconically truncate hilum, not thickened, nor darkened (at times appearing to have a marginal frill); transversely euseptate.

*Type species.* *Funbolia dimorpha.*

MycoBank MB560161.

*Notes.* *Funbolia* resembles genera such as *Spadicoides* (but conidia lack the darkened septa), *Neta* (but lacks setae), *Thysanorea* (but has dimorphic conidia), and *Catenulisubulospora* (which lacks dimorphic conidia and has beaked conidia) (Seifert et al. 2011). Because it could not be accommodated in any of the genera listed here and its DNA sequences did not match any fungi currently deposited in GenBank, we introduce a new genus here to accommodate it.

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**Funbolia dimorpha** Crous & Seifert, *sp. nov.*


*Etymology.* Named after its dimorphic conidia.

*Mycelium* consisting of pale brown to hyaline, smooth, branched hyphae, 2–3 µm diam, becoming somewhat verruculose at fertile regions, giving rise to conidiophores. *Conidiophores* solitary, erect, straight to flexuous, cylindrical, unbranched, or branched below (branched conidiophores developing with age), 50–100 × 3–4 µm, brown, finely verruculose, multi-euseptate, septa 5–17 µm apart, becoming somewhat darkened, but not thickened. *Conidigenous cells* terminal and lateral, pale to medium brown, finely verruculose, subcylindrical to somewhat swollen, clavate to irregular, 7–20 × 2.5–5 µm; conidigenous loci dispersed on conidiogenous cells in young cultures, aggregated in a rachis on conidigenous cells in older cultures, at times subdenticulate with minute collarette, up to 1 µm tall, and 1 µm diam; scars thickened along the rim, erumpent, but neither darkened nor refractive. Conidia dimorphic, medium brown, finely verruculose, ellipsoidal when 1-septate, (6–)8–11–(20) × (4–)5 µm, becoming subcylindrical when multisepate, apex obtusely rounded, tapering from basal septum to an obconically truncate hilum, 1 µm diam, not thickened, nor darkened (at times appearing to have a marginal frill); (2–)3–(7)-euseptate, becoming darkened in older conidia, and also constricted at septa, (15–)20–35–(45) × (4–)5 µm; microcyclic conidiation observed in culture.

*Culture characteristics.* — (in the dark, 25 °C, after 1 mo): Colonies flat, spreading, with sparse to moderate aerial mycelium and even, lobate margins, reaching 8–10 mm diam. On potato-dextrose agar surface isabelline; reverse olivaceous; on oatmeal agar surface isabelline; on malt extract agar surface isabelline, reverse chestnut, with diffuse isabelline pigment surrounding colony.


*Notes.* Based on a megablast search of NCBI’s GenBank nucleotide database, the closest hit using the ITS sequence is *Didymosphaeria futilis* (GenBank EU552123; Identities = 471/552 (85 %), Gaps = 28/552 (5 %)) followed by species of *Cladonia* with shorter homology, e.g. *Cladonia subtenuis* (GenBank DQ482701; Identities = 242/271 (89 %), Gaps = 8/271 (3 %)). Closest hits using the LSU sequence yielded highest similarity to *Heleiospora barbatula* (GU479787; Identities = 834/891 (94 %), Gaps = 8/891 (1 %)), *Caloplaca sublobulata* (EF489950; Identities = 859/947 (91 %), Gaps = 24/947 (3 %)) and *Caloplaca regalis* (EU161240; Identities = 850/938 (91 %), Gaps = 24/938 (3 %)).