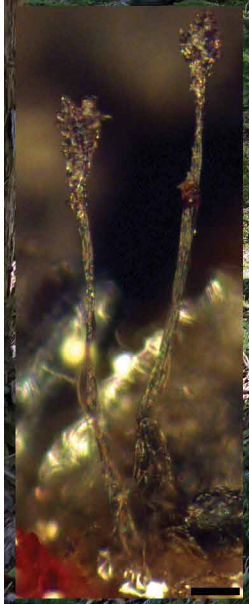


*Sorocybe oblongispora*



Fungal Planet 1032 – 18 December 2019

***Sorocybe oblongispora* Tanney & Seifert, sp. nov.**

*Etymology.* Refers to the oblong conidia that distinguish this species from the related *S. resiniae*.

*Classification* — *Herpotrichiellaceae*, *Chaetothyriales*, *Eurotiomycetes*.

*Ascomata* not observed. *Conidiomata* mononematous or synnematosus and arising from dark brown, well-developed subiculum. *Synnemata* scattered or gregarious, up to about 2 mm tall, dark brown to black, often splayed at the base but with a compact cylindrical stipe c. 60–80 µm wide, and a compact, dry, ellipsoidal conidial head c. 300 × 150 µm. Hyphae of stipe brown to dark brown, strictly parallel in the main part of the stipe, infrequently branched, with some anastomoses between adjacent hyphae, frequently septate, cells about 10–22 µm long, somewhat interwoven and rough-walled towards the base and (2.5–)3.5–5 µm wide, walls 0.5–1 µm thick, uneven in outline, smooth-walled and 2–3 µm wide in the main body of the stipe. *Conidiogenous cells* terminal or in pairs at the ends of the stipe hyphae, cylindrical and very similar in size to the conidia, but with a truncate base the same width as the stipe hyphae, 10–13 × 3.5–4.5 µm, or intercalary and arising as a lateral extension about 7–10.5 × 3.5 µm from a shorter stipe hyphal cell, lacking a basal septum. *Conidia* in sparingly branched acropetal chains, oblong-ellipsoidal to almost fusiform, (8.5–)11.5–15(–18.5) × (2.5–)3–4(–4.5) µm (length: n = 126, av. = 13.2 µm, SD = 1.9 µm, SE = 0.17 µm, 95 % CI = 0.33; width: n = 126, av. = 3.5 µm, SD = 0.4 µm, SE = 0.04 µm, 95 % CI = 0.07), brown, mostly aseptate, fewer than 5 % of the conidia with a ± central septum, with lateral walls 0.5–1 µm thick, with no visible secession scars, connection almost a point to a flat area about 1.5 µm wide, smooth-walled, sometimes adjacent conidia anastomosing; ramoconidia infrequent, 11–15.5 × 3.5–4 µm, usually with just two emerging chains, conidial chains appressed and more or less parallel.

*Culture characteristics* — Colonies after 4 wk at 20 °C on malt extract agar restricted, coal-black, brittle and wrinkled. *Synnemata* not produced.

*Typus.* CANADA, New Brunswick, Charlotte County, Campobello Island, Roosevelt Campobello International Park, Fox Farm Trail, 44.849288, -66.966173, on resin on self-pruned branch stub of *Picea rubens* (*Pinaceae*), 26 Sept. 2016, J.B. Tanney (holotype DAOM 867433, culture ex-type DAOMC 251618, culture ex-paratype DAOMC 241619; ITS and LSU sequences GenBank MN114116 and MN114118, MycoBank MB831660).

*Notes* — *Sorocybe oblongispora* differs from the type species, *S. resiniae*, by its longer, narrower conidia (mostly 11.5–15 × 3–4 µm vs 5.5–11 × 2.5–3.5 µm in *S. resiniae*) and ramoconidia (11–15.5 × 3.5–4 µm vs 7–12 × 4–7 µm). Both appear to be restricted to conifer resin, where they produce conspicuous synnemata and a less conspicuous mononematous morph. In North America, *S. oblongispora* occurs on the east coast of Canada on *Picea rubens*, and *S. resiniae* in the Pacific Northwest of Canada and the USA on *Abies*, *Picea*, and *Pseudotsuga* spp. *Sorocybe resiniae* was described from resin

*Colour illustrations.* Campobello Island, NB, Canada (photo R. Smith). From left to right (DAOM 867433: synnemata on *Picea rubens* resin, conidial head, mononematous conidiophore, conidia with examples of anastomosis. Scale bars = 100 µm (synnemata), 10 µm (all others).

of *Picea abies* in Sweden, and is also known from *Abies* and *Larix* elsewhere in Europe; it is unclear whether the morphologically identical western North American and European fungi are the same phylogenetic species (Seifert et al. 2007). The other two species, *S. indica* with slimy conidia (Pratibha et al. 2005) and the poorly-known *S. tenella* (Hughes 1958), seem unlikely to belong in *Sorocybe* as now circumscribed.

Phylogenetic analyses of ITS and LSU sequences confirm that *S. oblongispora* DAOMC 251618 and *S. resiniae* DAOM 239134 are congeneric (ITS: GenBank EU030275; Identities = 479/499 (96 %), 3 gaps (0 %); LSU: GenBank EU030277; Identities = 867/874 (99 %), 1 gap (0 %)). Our LSU phylogeny places *S. oblongispora* and *S. resiniae* in a strongly-supported clade sister to *Ceratosporella novae-zelandiae* (*incertae sedis*), potentially a long-branch attraction artefact, a sequence misidentified as *Lasallia pustulata* (*Umbilicariaceae*, *Umbilicariales*), and *Endococcus fusigera* (*incertae sedis*). This well-supported (PP = 0.97) clade is in turn sister to *Verrucaria* (*Verrucariaceae*, *Verrucariales*). Based on an NCBI GenBank BLASTn query of the *S. oblongispora* DAOMC 251618 ITS sequence, the closest related taxon after *S. resiniae* is *Endococcus fusigera* (GenBank FJ645262; Identities = 652/748 (87 %), 22 gaps (2 %)).

Seifert et al. (2007) placed *S. resiniae* sister to *Capronia villosa* (*Herpotrichiellaceae*, *Chaetothyriales*) from an ITS phylogeny (GenBank EU030275; Identities = 418/492 (85 %), 3 gaps (3 %)). We cannot confidently place *Sorocybe* in a family using the available reference sequences and Vu et al.'s (2019) rDNA taxonomic threshold values as a guide, but tentatively maintain this classification of *Sorocybe* within *Herpotrichiellaceae* pending further investigation.

*Sorocybe oblongispora* was commonly found in New Brunswick, Canada on *Picea rubens* resin flows associated with self-pruned branch stubs or wounds. The resin was older and blackish in colour from the proliferation of mycelia from *S. oblongispora* and an unidentified sooty mould (*Capnodiales*). *Sorocybe oblongispora* co-occurred with other resinicolous fungi including *Eustilbum aureum*, *Claussenomyces olivaceus*, *Lachnelula resinaria*, *Sarea difformis*, *S. resiniae*, and hysteriaceous species. Resiniculous fungi have been little studied in recent years and the known species are poorly represented by public DNA sequences. This recent discovery of *Chaenothecopsis claydenii* and now *S. oblongispora* highlights the undiscovered resinicolous fungal diversity of the Acadian forests of eastern Canada.

**Supplementary material**

**FP1032** Bayesian inference (BI) phylogenetic tree based on LSU sequences. The BI analysis was performed with MrBayes v. 3.2.6 using the best-fit nucleotide substitution model (GTR+G) estimated by the Akaike Information Criterion (AIC) using jModelTest v. 2.1.10, with a sampling frequency every 500 generations, three runs consisting of four chains (three heated, one cold), an automated stop value of 0.01, and the first 25 % of the trees discarded as burn-in. Posterior probabilities < 1 are presented in branch nodes. GenBank accession numbers follow the species name and sequences derived from ex-types are denoted with a superscript (\*). The novel species is indicated in **bold** and highlighted in an orange box.

Joey B. Tanney, Pacific Forestry Centre, Canadian Forest Service, Natural Resources Canada, 506 Burnside Road, Victoria, BC V8Z 1M5, Canada; e-mail: joey.tanney2@canada.ca  
Keith A. Seifert, Biodiversity (Mycology), Agriculture and Agri-Food Canada, 960 Carling Avenue, Ottawa, ON K1A 0C6, Canada; e-mail: keith.seifert@carleton.ca