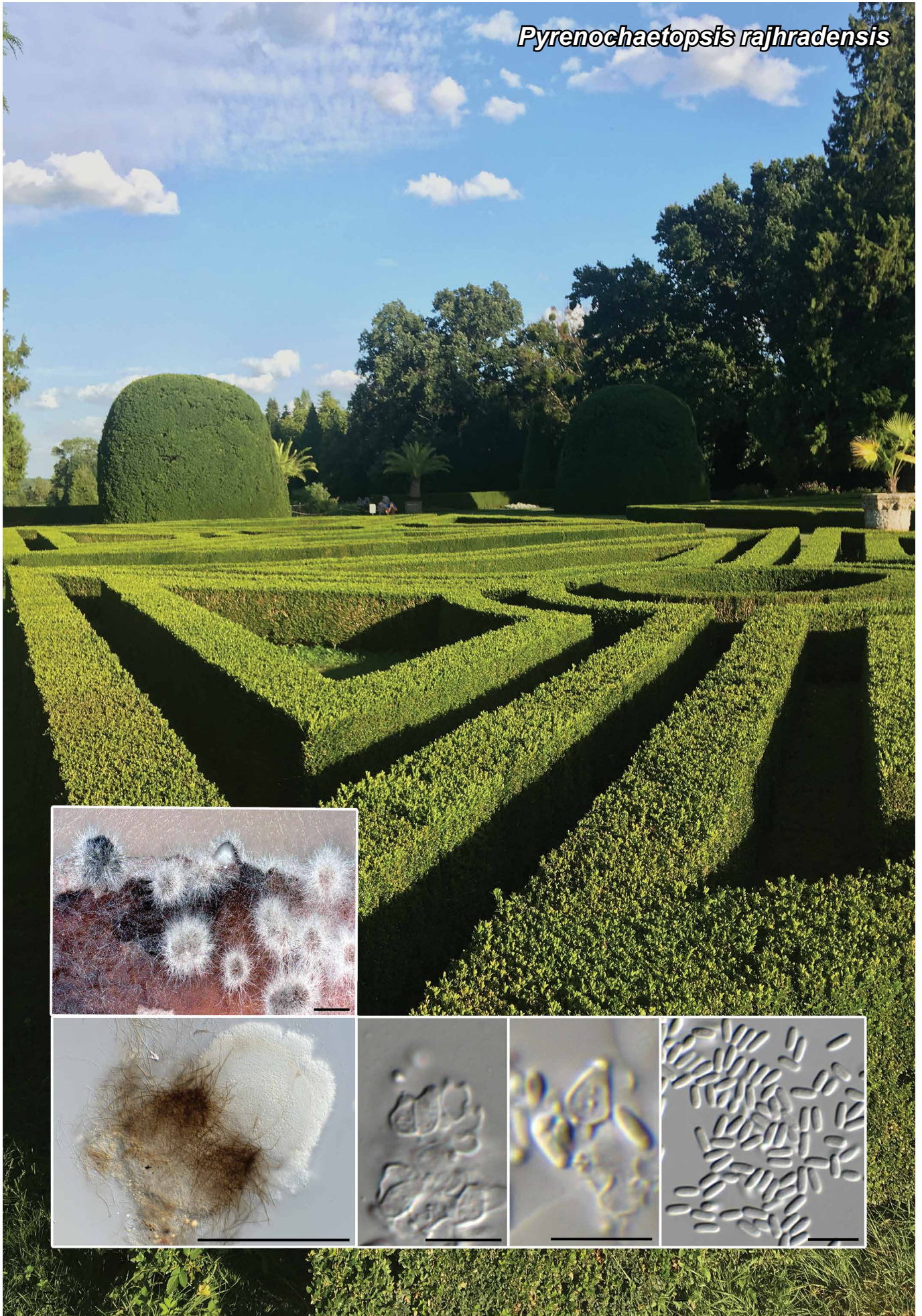


*Pyrenochaetopsis rajhradensis*



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***Pyrenochaetopsis rajhradensis* Spetik, Eichmeier & Berraf-Tebbal, sp. nov.**

*Etymology.* Named after Rajhrad (Czech Republic) where the fungus was collected.

*Classification* — *Pyrenochaetopsidaceae*, *Pleosporales*, *Dothideomycetes*.

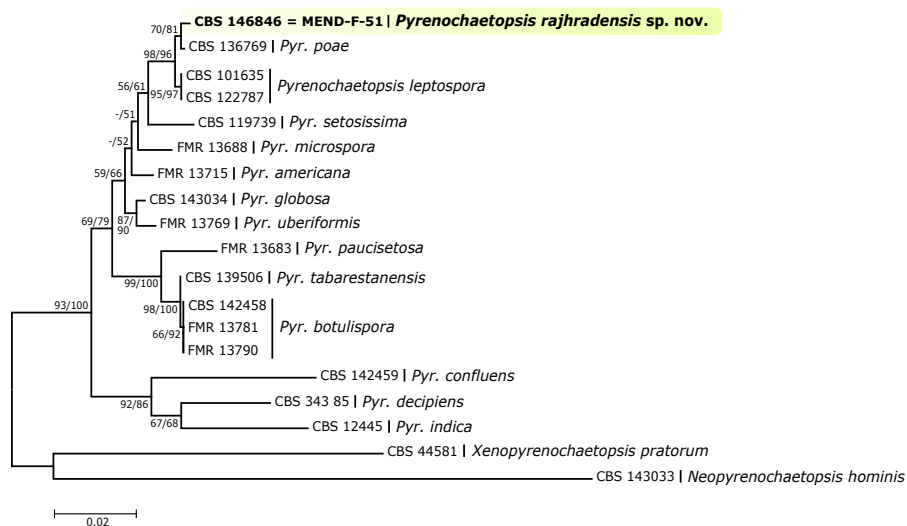
*Conidiomata* pycnidial, brown, solitary or aggregated, semi-immersed, globose to ovoid, setose, ostiolate, uniloculate. *Conidiogenous cells* phialidic, hyaline, discrete and integrated. *Conidia* hyaline, aseptate, cylindrical to allantoid, guttulate, (3.6–)4.1–4.9(–5.7) × (1.4–)1.6–2.2(–2.4) µm (av. ± S.D. 4.5 ± 0.4 × 1.8 ± 0.2 µm, L/W ratio = 2.5). *Sexual morph* unknown.

*Culture characteristics* — Colonies on potato dextrose agar (PDA) reaching 23.8 mm diam at 25 °C after 10 d, margin regular, floccose, dirty white; reverse white. On malt extract agar (MEA) reaching 22 mm diam after 10 d, margin regular, floccose, dirty white; reverse white. On oatmeal agar (OA) reaching 25.8 mm diam after 10 d, margin regular, floccose, white; reverse white.

*Typus.* CZECH REPUBLIC, Rajhrad, isolated as saprobe from dead wood of *Buxus sempervirens* (*Buxaceae*), July 2018, *M. Spetik* (holotype CBS H-24478, ex-type culture CBS 146846 = MEND-F-51, ITS, LSU, *rpb2*, *tef1* and *tub2* sequences GenBank MT853115, MT853182, MT857727, MT857725 and MT857726, MycoBank MB836856).

*Notes* — Based on a megablast search of NCBI nucleotide database, the closest hits using the ITS sequence had the highest similarity to *Pyrenochaetopsis leptospora* (GenBank

MT453283.1; Identities = 471/471 (100 %), no gaps), *Phoma* sp. (GenBank MN401018.1; Identities = 471/471 (100 %), no gaps) and *Pyrenochaetopsis leptospora* (GenBank LR216648.1; Identities = 471/471 (100 %), no gaps). The closest hits using the LSU sequence had the highest similarity to *Pyrenochaetopsis microspora* (GenBank NG\_069864.1; Identities = 937/939 (99 %), no gaps), *Pyrenochaetopsis leptospora* (GenBank NG\_069858.1; Identities = 937/939 (99 %), no gaps) and *Pyrenochaetopsis* sp. (GenBank KJ395496.1; Identities = 937/939 (99 %), no gaps); closest hits using the *rpb2* sequence are *Pyrenochaetopsis leptospora* (GenBank LT623283.1; Identities = 893/906 (99 %), no gaps and GenBank LT623282.1; Identities = 846/858 (99 %), no gaps), *Phaeoecocea festucae* (GenBank MF795835.1; Identities = 840/854 (98 %), 2/854 (0 %)) and *Pyrenochaetopsis poae* (GenBank LT623286.1; Identities = 864/906 (95 %), no gaps). The closest hits using the *tef1-α* sequence had the highest similarity to *Pyrenochaetopsis leptospora* (GenBank MF795881.1; Identities = 266/281 (95 %), 3/281 gaps (1 %)), *Parastagonospora novozelandica* (GenBank MK540151.1; Identities = 57/58 (98 %), no gaps) and *Parafenestella rosacearum* (GenBank MK357586.1; Identities = 186/245 (76 %), 27/245 gaps (11 %)). The closest hits using the *tub2* sequence had the highest similarity to *Pyrenochaetopsis poae* (GenBank KJ869243.1; Identities = 407/407 (100 %), no gaps), *Pyrenochaetopsis leptospora* (GenBank MF795917.1; Identities = 402/407 (99 %), no gaps and GenBank LT623242.1; Identities = 325/332 (98 %), no gaps).



Maximum likelihood tree obtained from the ITS, *tub2*, LSU and *rpb2* gene sequences of *Pyrenochaetopsis* species of our isolates and sequences retrieved from GenBank. The tree was built using MEGA v. 7.0 (Kumar et al. 2016). The combined LSU, ITS, *tub2* and *rpb2* sequence data set consisted of 17 *Pyrenochaetopsis* strains with *Xenopyrenochaetopsis pratorum* and *Neopyrenochaetopsis hominis* as the outgroup taxa and consisted of 2 195 characters. Of these 1 643 were constant, 188 were variable and parsimony-uninformative and 337 were parsimony-informative. A heuristic search

*Colour illustrations.* *Buxus sempervirens* growing in Lednice castle garden. Pycnidia forming on sterile poplar twig on WA; pycnidium in culture oozing conidia; conidiogenous cells; conidia. Scale bars = 200 µm (pycnidia), 10 µm (all others).

of these 337 parsimony-informative characters resulted in 1000 equally parsimonious trees of 467 steps with CI = 0.72, RI = 0.65 and HI = 0.28. The ML analysis yielded a best scoring tree with the final ML optimization likelihood value of –4554.41 (ln) and a gamma distribution shape parameter value of  $\alpha = 0.1411$ . All individual trees obtained from single gene datasets were essentially similar in topology and not substantially different from the tree generated from the concatenated dataset. One of the two ML trees obtained is presented with ML/MP bootstrap support values at the nodes. The alignment and tree are available in TreeBASE (Submission ID: 26835).

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