



Fungal Planet 1098 – 29 June 2020

***Neosetophoma hnaniceana* Spetik, Eichmeier & Berraf-Tebbal, sp. nov.**

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

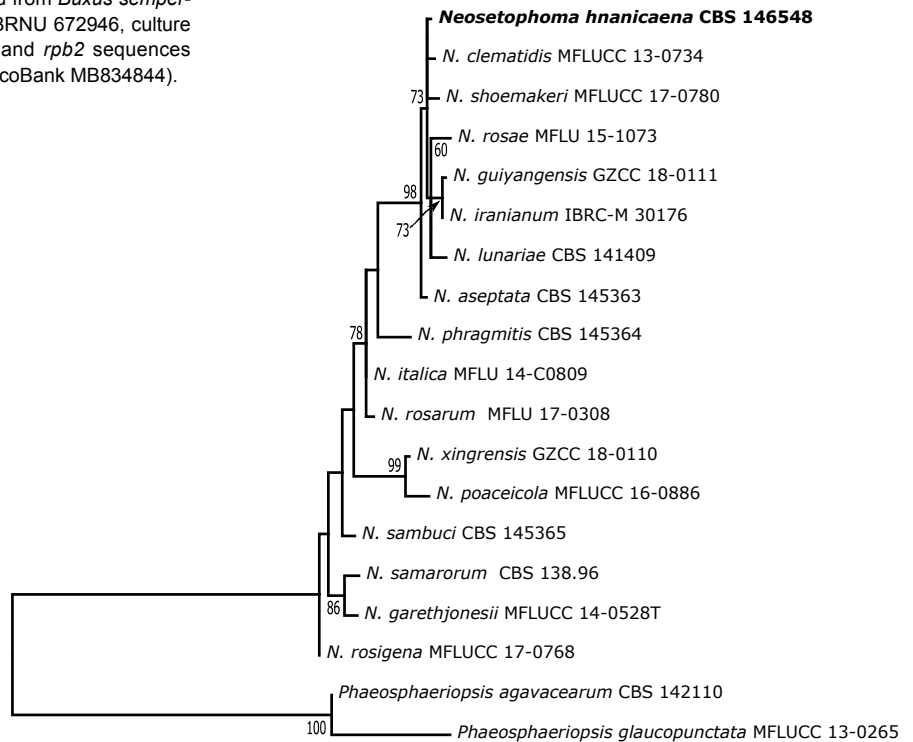
**Classification** — *Phaeosphaeriaceae*, *Pleosporales*, *Dothi-deomycetes*.

Saprobic on dead leaves and wood of *Buxus sempervirens*. Sexual morph: Undetermined. Asexual morph: Coelomycetous. *Conidiomata* pycnidial, separate, dark to pale brown, globose, subepidermal, unilocular, thin-walled, papillate, 80–120 µm high, 85–130 µm diam. *Conidiophores* reduced to conidiogenous cells. *Conidiogenous cells* enteroblastic, phialidic, dolii-form to ampulliform, determinate, hyaline, smooth-walled. *Conidia* subcylindrical, fusoid or ellipsoid to fusoid, individually hyaline, olivaceous green at maturity, with transverse septum, thin- and smooth-walled, (6.96–)8.14–8.79(–10.41) × (2.94–)3.3–3.64(–4.46) µm, mean ± S.D. 8.46 ± 0.9 × 3.47 ± 0.47 µm, L/W ratio = 2.5.

**Culture characteristics** — Colonies on malt extract agar (MEA) reaching 3–4 cm diam in the dark, at 25 °C, after 3 wk, slow growing, white to dirty white in the first week, becoming yellow-green with pale irregular margin after 3 wk, moderate aerial mycelium, reverse iron-grey to umber, with age.

**Typus.** CZECH REPUBLIC, Znojmo, Hnanice, isolated from *Buxus sempervirens* (*Buxaceae*), Feb. 2019, M. Spetik (holotype BRNU 672946, culture ex-type CBS 146548 = MEND-F-0083; ITS, LSU and *rpb2* sequences GenBank MT119769, MT119767 and MT119768, MycoBank MB834844).

**Notes** — Based on a megablast search of NCBI nucleotide database, the closest hits using the **ITS** sequence had the highest similarity to *Neosetophoma aseptata* (GenBank NR\_164449.1; Identities = 538/542 (99 %), no gaps), *Neosetophoma lunariae* (GenBank NR\_154242.1; Identities = 535/543 (99 %), no gaps) and *Neosetophoma shoemakeri* (GenBank NR\_161044.1; Identities = 524/530 (99 %), 1 gap (0 %)). The closest hits using the **LSU** sequence had the highest similarity to *Loratospora aestuarii* (GenBank GU301838.1; Identities = 1117/1124 (99 %), no gaps), *Ophiosphaerella herpotricha* (GenBank DQ767656.1; Identities = 1114/1125 (99 %), 1 gap (0 %)) and *Phoma cladoniicola* (GenBank JQ238625.1; Identities = 1112/1124 (99 %), no gaps); closest hits using the **rpb2** sequence are *Brunneomurispora lonicerae* (GenBank MK359079.1; Identities = 571/657 (87 %), no gaps), *Ophiosphaerella herpotricha* (GenBank DQ677958.1; Identities = 587/696 (94 %), 2 gaps (0 %)) and *Phaeo-poacea festucae* (GenBank KY824768.1; Identities = 590/705 (84 %), no gaps).



Sequences of all known *Neosetophoma* species were retrieved from GenBank and aligned with sequences of the isolate obtained in this study. Alignments were done with ClustalX v. 1.83 (Thompson et al. 1997). Kimura's two parameter model with Gamma distribution (K2+G) was used as the best nucleotide substitution model. The Maximum Likelihood (ML) analysis was performed using MEGA v. 7 software (Kumar et al. 2016). The robustness of the ML tree was evaluated by 1000 bootstrap replications. Maximum likelihood tree obtained from the ITS and LSU gene sequences of *Neosetophoma* species of our isolates and sequences retrieved from GenBank. The tree was built using MEGA v. 7.0. Bootstrap support values above 70 % are shown at the nodes. The species described here is highlighted in bold. The alignment and tree are available in TreeBASE (study S25862).

**Colour illustrations.** *Buxus sempervirens* growing in Hnanice. Conidiomata on MEA; conidiogenous cells and conidia. Scale bars = 10 µm.