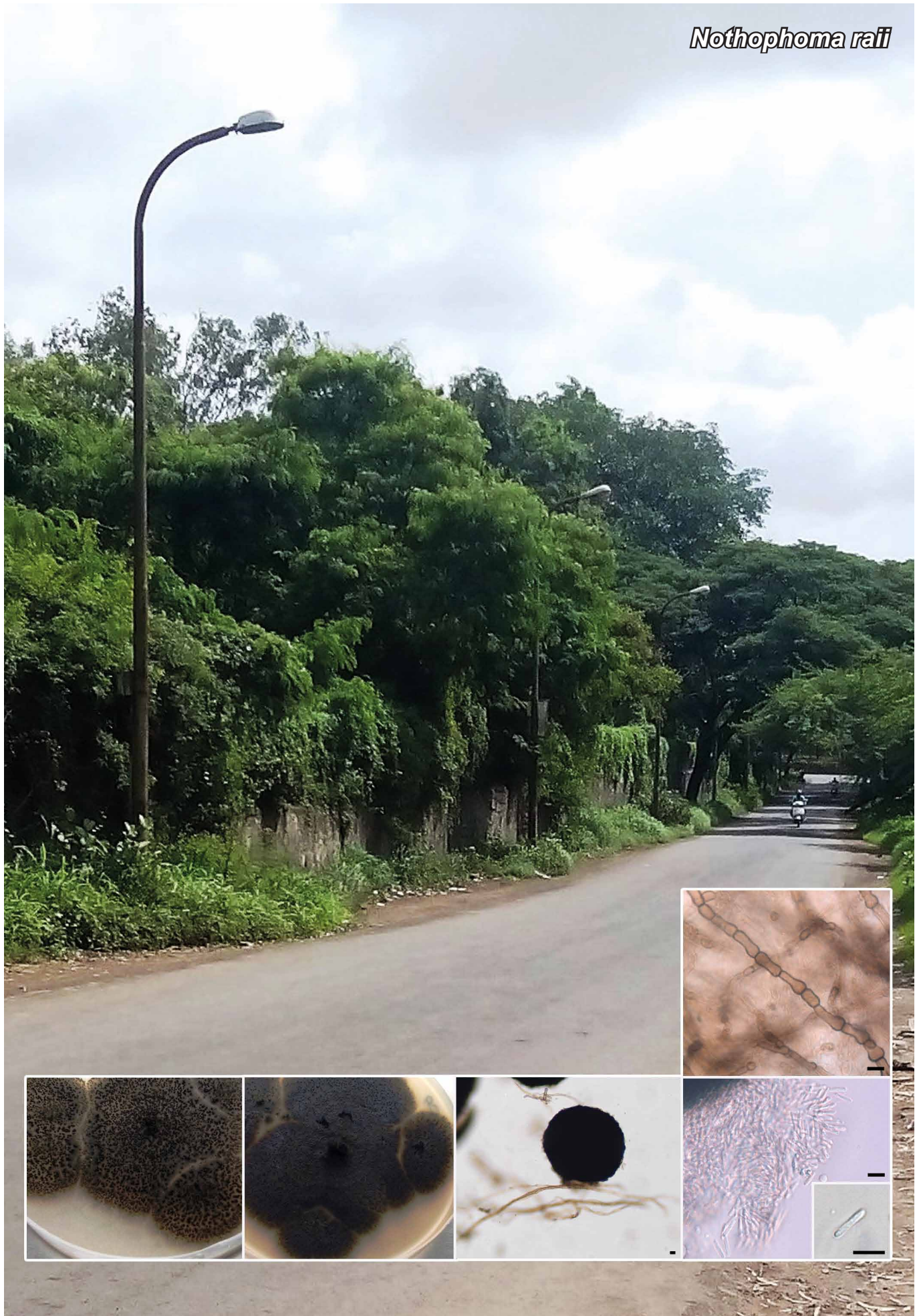


*Nothophoma raii*



Fungal Planet 643 – 20 December 2017

***Nothophoma raii* Rohit Sharma, sp. nov.**

**Etymology.** The species is named in the honour of Prof. Mahendra K. Rai, SGB Amaravati University, India, for his contribution to the systematics of the genus *Phoma*.

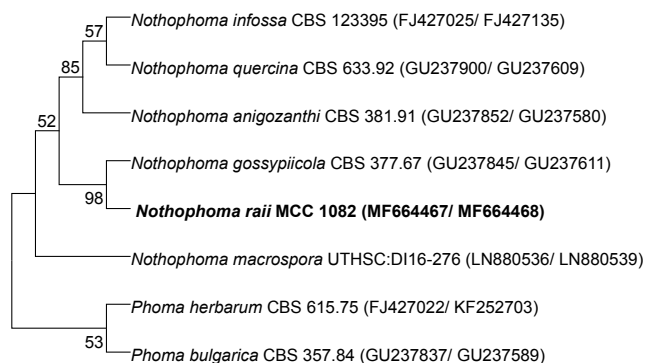
**Classification** — *Didymellaceae*, *Pleosporales*, *Pleosporomycetidae*, *Dothideomycetes*.

**Conidiomata** pycnidial, 194.3–315.5 × 195.6–411.3 µm, globose to subglobose, solitary or confluent, scattered across the Petri dish, glabrous, with or without non-papillate ostiole, sometimes projections around the ostiolium, initially brown, later brownish black; peridium 3–5-layered, 15–25 µm thick, cells of pycnidial wall composed of angular dark brown cells, 9.7–14.4 µm diam, thick-walled, *Conidiogenous cells* hyaline, thin-walled, bottle-shaped. *Conidia* aseptate, 11–14.5 × 1.5–2.5 µm, ellipsoidal, with several small, scattered guttules. *Chlamydospores* present, elongated barrel-shaped, in chains, olivaceous brown, 11–21.5 µm × 4.5–8.5 µm diam. *Hyphae* pale to dark brown, thin- to thick-walled, smooth, septate, anastomosing. *Sexual morph* not observed.

**Culture characteristics** — The fungus was isolated from soil on customized HK Medium 30A (sucrose 1 g, casein enzymic hydrolysate 0.75 g, yeast extract 0.25 g, pancreatic digest of casein 0.154 g, papaic digest of soybean meal 0.027 g, sodium chloride 0.045 g, dipotassium hydrogen phosphate 0.022 g, agar 15.0 g) (Hi-Media, India) reaching 60 mm diam in 7 d at 28 °C; moist, flattened, irregular margin, indefinite shape, did not produce pycnidia, front and reverse are black coloured. Colonies on CA attaining 50 mm in 7 d at 25 °C, brownish black, flattened or effused, compact, reverse concolorous, and margins regular with mycelia embedded in the medium. Colonies on OA attaining 60 mm in 7 d at 25 °C, brown olivaceous, flattened or effused, compact, reverse concolorous, and margins thread like with mycelia embedded in the medium. Black dot-like pycnidia formed in OA and CA after 1 mo of incubation that are darker than the mycelia. Pycnidia are larger and more abundant on OA.

**Habitat** — Soil.

**Distribution** — India (Pimpri, Pune, Maharashtra).



**Colour illustrations.** India, Maharashtra, Pune, Pimpri industrial area near antibiotic producing industry; colony on OA and CA after 30 d at 25 °C, conidiomata under microscope, hyaline conidia, thick-walled elongated and barrel-shaped chlamydospores. Scale bars = 10 µm.

**Typus.** INDIA, Pune (Pimpri), Maharashtra, soil from industrial area, 1 Aug. 2012, R. Sharma (holotype preserved in metabolically inactive state MCC 1082, ITS and  $\beta$ -*tub* sequences GenBank MF664467 and MF664468, MycoBank MB822354).

**Notes** — The genus *Nothophoma* (*Didymellaceae*, *Pleosporales*) was established by transferring five species of *Phoma* section macrospora with *Nothophoma infossa* as type species (Chen et al. 2015). *Nothophoma* is a close relative of *Phoma* characterized by aseptate, ovoid, oblong to ellipsoidal conidia, and its distinct phylogenetic position (Chen et al. 2015). It now comprises six species viz., *N. anigozanthi*, *N. arachidishypogaeae*, *N. gossypicola*, *N. infossa* and *N. quercina*. The MP phylogenetic tree constructed by using the ITS and  $\beta$ -*tub* sequences showed that MCC 1082 represents a new species of the genus *Nothophoma* clustering together with *N. gossypicola* with a bootstrap value of 98 %. *Nothophoma raii* differs from *N. gossypicola* by its higher growth rate on OA, larger pycnidia (194.3–315.5 × 195.6–411.3 µm vs 100–250 µm) and slightly longer but narrower conidia (11–14.5 × 1.7–2.5 µm vs 10–12.5 × 2.5–3.5 µm). The chlamydospores of *N. raii* are also larger than *N. gossypicola* (11–21.5 × 4.5–8.5 vs 8–12 µm).

**Phylogenetic Analysis** — Two phylogenetic trees of ITS and  $\beta$ -*tub* regions were prepared using sequences of *N. raii* and other *Nothophoma* species from GenBank and Crous et al. (2016b) showing the phylogenetic position of the new species. The BLASTn results of ITS sequence of *N. raii* (GenBank MF664467) with fungal ex-type sequences showed closest similarity with *N. anigozanthi* CBS 381.91 (GenBank NR\_135992.1; Identities = 426/434 (98 %), Gaps = 2/434 (0 %)) and *N. infossa* CBS 123395 (GenBank NR\_135968; Identities = 423/434 (97 %), Gaps = 2/434 (0 %)). A phylogenetic tree showed that it clustered with *N. gossypicola* CBS 377.67. The BLASTn results of  $\beta$ -*tub* sequence of *N. raii* MCC 1082 (GenBank MF664468) with ex-type sequences showed maximum similarity with *Dothiora bupleuricola* strain CBS 112.75 (GenBank KU728618; Identities = 489/497 (98 %), Gaps = 0/497 (0 %)), *Verrucoconiothyrium eucalyptigenum* CBS 142535 (GenBank KY979935; Identities = 456/497 (92 %), Gaps = 1/497 (0 %)) and *N. anigozanthi* strain CBS 381.91 (GenBank GU237580; Identities = 313/335 (93 %), Gaps = 1/335 (0 %)). A phylogenetic tree of  $\beta$ -*tub* sequences including *N. raii* MCC 1082 shows that it clusters with *N. gossypicola* CBS 377.67.

Maximum parsimony phylogram of ITS and  $\beta$ -*tub* sequence analysis; species of *Phoma* are used as outgroup. The phylogenetic position of *N. raii* is indicated in bold. Branches with bootstrap support (BS)  $\geq$  50 % (based on 1 000 replicates) are shown.