Lecanicillium restrictum
**Lecanicillium restrictum** Hubka, Kubátová, Nonaka, Čmoková & Řehulka, *sp. nov.*

*Etymology. restrictum* (res.tric’tum. L. neut. part. adj.); limited, restricted, referring to the slow growth at room temperature (25 °C).

*Classification. — Cordycipitaceae, Hypocreales, Sordariomycetes.*

On PCA: Phialides produced on aerial hyphae, solitary or aggregated in whorls of 2–5 phialides, tapering toward the tip, (12–)17–30–(36) μm long (mean ± standard deviation; 22.4 ± 4.8), basal part 0.5–1.5 (1.1 ± 0.2) μm wide, 0.3–0.5 μm wide on the tip. Conidia dimorphic, macroconidia with pointed ends, fusiform or slightly falcate, smooth-walled, 1-celled, (5–)6–10–(12) × 1–1.5 μm (7.5 ± 1.3 × 1.1 ± 0.1), microconidia usually without sharply pointed ends, ovate, ellipsoidal, obovate or fusoid, frequently slightly curved, smooth-walled, 1-celled, 2.5–3 × 1–1.5 μm (3 ± 0.4 × 1 ± 0.1). No microscopic crystals observed.

Culture characteristics. — (in the dark, at 20 °C after 14 d): Colonies on PCA 20–23 mm diam (10–12 mm after 7 d), white, cottony, centrally raised, margin entire, no exudate and soluble pigments, reverse yellowish white (4A2; Komeru & Wanscher 1967). Colonies on MEA 19–22 mm diam (10–12 mm after 7 d), yellowish white (4A2), waxy, delicately funiculose, umbonate, radially wrinkled, margin entire, no exudate and soluble pigments, reverse pale yellow (4A3). Colonies on PDA 21–25 mm diam (11–13 mm after 7 d), yellowish white (4A2), floccose to delicately funiculose, umbonate, radially wrinkled, margin entire, no exudate and soluble pigments, reverse yellowish white (4A2) to pale yellow (4A3). Growth rates at 15 °C on PCA/MEA/ PDA: 8–10/8–10/9 mm after 7 d and 17–21/17–20/18–21 mm after 14 d, respectively. Growth rates at 25 °C on PCA/MEA/PDA: 1–3/2–4/2–4 mm after 7 d and 2–4/4–5/3–6 mm after 14 d, respectively. No growth to microcolonies on PCA and MEA at 27 °C; no growth at 30 °C.


Notes. — BLAST analysis with the ITS rDNA region sequence gave closest hits to *L. testudineum* CCF 5201T (99 %, 497/499 bp, GenBank LT548278), *L. kalimantanense* NBRC 105406T (94 %, 465/494 bp, GenBank AB360356), *L. wallacei* CBS 101237T (93 %, 448/484 bp, GenBank EF641891) and *Verticillium indonesiacum* BTCC-F36T (93 %, 462/495 bp, GenBank AB376516). LSU rDNA showed 99 % similarity to *L. testudineum* (99 %, 589/592 bp, GenBank LT548278) and *L. wallacei* (541/548 bp, GenBank AY184967), and 98 % similarity to *L. kalimantanense* (580/589 bp, GenBank AB360356) and *V. indonesiacum* (580/589 bp, GenBank AB376516). The tub2 sequence showed 91 % similarity to *L. testudineum* (1225/1348 bp, GenBank LT548284) and the tef1-α sequence 94 % similarity to *L. testudineum* (936/992 bp, GenBank LT626942).

*Lecanicillium restrictum* is characteristic by having slow growth at 25 °C, optimum temperature for growth around 20 °C and the production of dimorphic conidia. *Lecanicillium testudineum* has an optimum temperature for growth around 25 °C and smaller macroconidia than *L. restrictum*. Microconidia of *L. restrictum* are smaller than conidia produced by *L. kalimantanense* (3.5–12 × 1–2 μm) (Sukarno et al. 2009). Phialides of *V. indonesiacum* are most frequently produced in a single whorl at the end of erect hyphae (Sukarno et al. 2009). *Lecanicillium wallacei* grows more rapidly than *L. restrictum* on PCA at 20 and 25 °C (Zare & Gams 2001).

The best scoring maximum likelihood tree calculated from ITS rDNA and tef1-α sequences shows the species relationships within the genus *Lecanicillium*. The optimal partitioning scheme (PartitionFinder v. 1.1.1; Lanfear et al. 2012) divided the dataset into four partitions with the following substitution models: the GTR+G substitution model was used for ITS1 and ITS2 regions, JC+I model for the 5.8S nrDNA region and the 2nd codon positions of tef1-α, F81+H+G model for the 1st codon positions of tef1-α, and HKY+G model for the 3rd codon positions of tef1-α. The tree was constructed with IQ-TREE v. 1.4.0 (Nguyen et al. 2015). The dataset contained 30 taxa and a total of 1583 characters of which 478 were variable and 357 parsimony-informative. Bootstrap support values at branches were obtained by generating 1000 bootstrap replicates. Only bootstrap support values ≥ 70 % are shown; ex-type strains are indicated by a superscript †. The tree is rooted with *Simplisicum lanosoniveum* CBS 704.86 and *S. obclavatum* CBS 311.74†.

For phylogenetic tree see Fungal Planet 735.

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