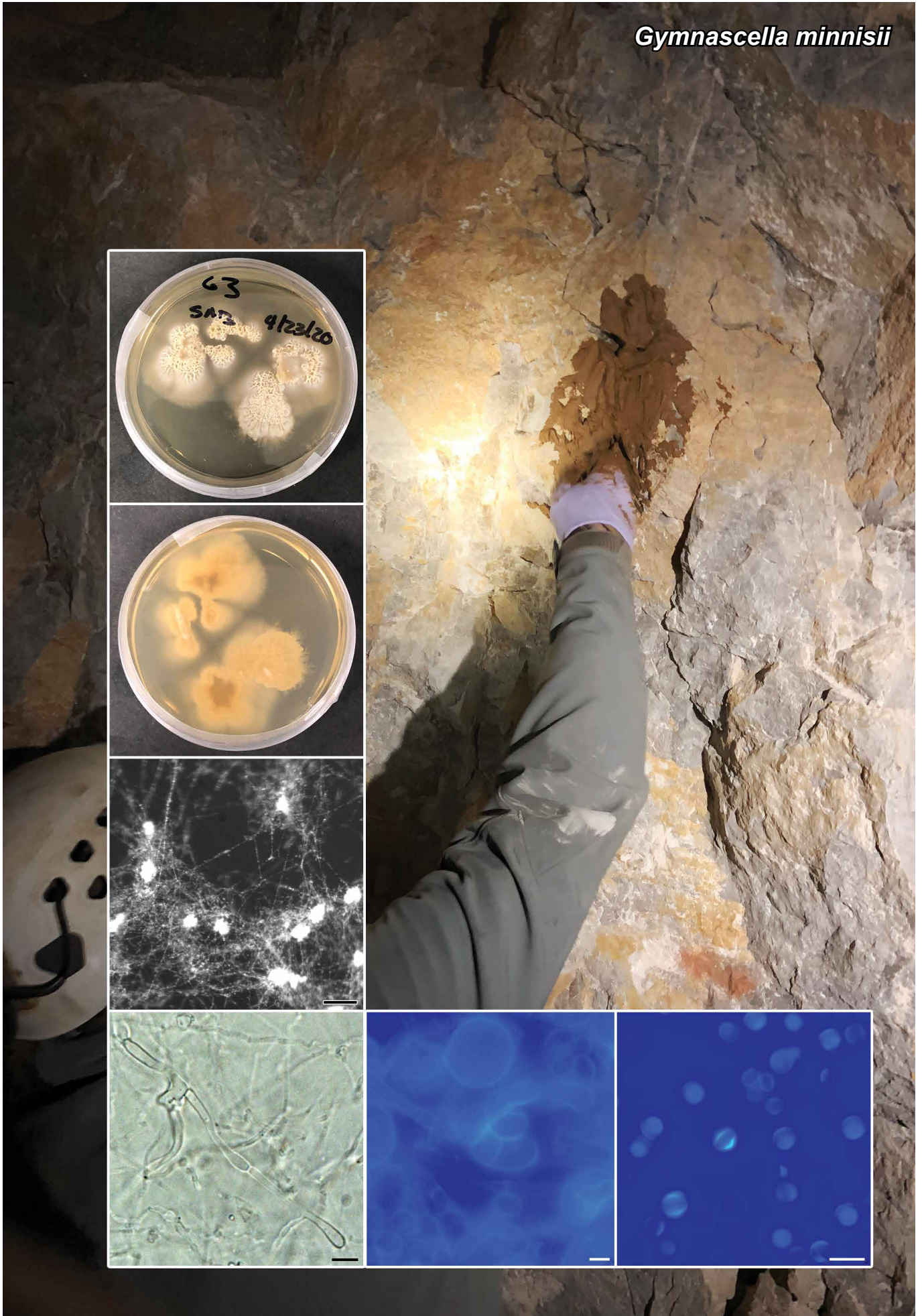


Gymnascella minnisii



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Gymnascella minnisii Adam, Rea-Ireland, Smyth & Overton, *sp. nov.*

Etymology. Named after Andrew Minnis who first mentioned the specimen as 24MN30 (GenBank JX270629) in a survey of Eastern United States bat hibernacula in 2013 after the initial outbreak of White-nose syndrome of bats.

Classification — *Gymnoascaceae*, *Onygenales*, *Eurotiomycetes*.

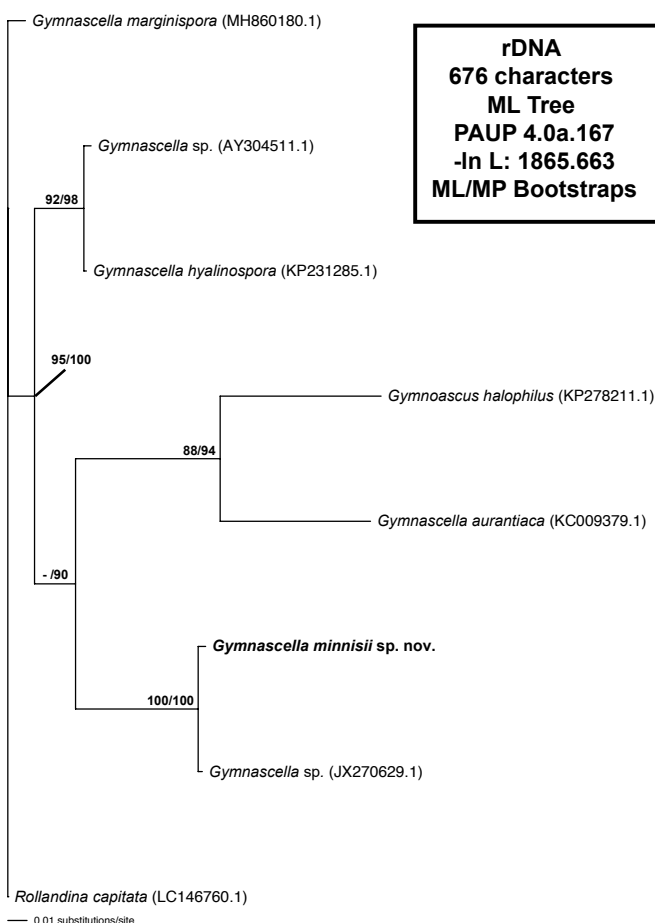
On oatmeal salt sediment agar: *Ascomata* gymnothecial-like, more hyphal than peridial, solitary, globose, measuring 28–118.5 (av. = 56.80, n = 40) µm diam; yellow grey (3B6; Korerup & Wanscher 1978); developing slowly and ripening within 90 d at 25 °C (12 h white fluorescing light / 12 h dark). *Ascomatal* initials clavate with thin curled hyphae; peridial hyphae light orange to gold yellow (5A4–5B7), smooth and septate with distinct appendages measuring 3.8–31 (av. = 14.86, n = 11) × 1.7–4. (av. = 1.93, n = 11) µm. *Asci* globose to ovoid, 8-spored, 6.8–10 (av. = 8.5, n = 11) µm diam. *Ascospores* globose to hat- or saturn-shaped, measuring 2.6–4 (av. = 3.34, n = 19) × 2.8–3.5 (av. = 3.13, n = 13) µm.

Culture characteristics — On Sabouraud dextrose agar (SAB) acidified with 120 µL 85 % lactic acid for optimal pigment production, (12 h white fluorescent light / 12 h dark at 25 °C): Colony yeast-like, at first yellow-grey (3A3–3B6), in age darkening slightly after 90 d. On synthetic nutrient-poor agar (SNA), colony filamentous, at first white to pale yellow-white on SNA (2A1–2A2).

Typus. USA, Pennsylvania, Blair County, Canoe Creek State Park, Canoe Creek Hartman Mine, from bat guano, 15 Mar. 2012, *B. Overton* LHU G3 (dried, non-metabolically active holotype CUP-70725, in Cornell University Plant Pathology Fungarium, metabolically active culture CBS 147160, ITS sequence GenBank MT988379, MycoBank MB836835).

Colour illustrations. Background photo of Canoe Creek Hartman Mine. Colony front colour on SAB at 90 d; colony back colour on SAB at 90 d; dissecting scope image of ascomata on SNA; DIC racket hyphae; fluorescence image of claw-like initials in calcofluor white; ascospores displaying hat- or saturn-shape in calcofluor white. Scale bar = 100 µm (ascomata), 2 µm (ascomatal initial), 5 µm (all others)

Notes — *Gymnascella minnisii* can be differentiated from other species of *Gymnascella* due to the absence of conidial development. The ascomata of *G. minnisii* are more hyphal and less developed than the peridial ascomata described in *Pseudogymnoascus* species. Additionally, the hat- or saturn-shaped ascospores place this species in the *Onygenales*. Genetic analysis of the ITS gene of *G. minnisii* suggests that the new species described here is identical to the ITS gene sequence of isolate 24MN30 (Lorch et al. 2013) deposited in GenBank (accession number JX270629). Isolate 24MN30 has remained an undescribed species since the publication of their work. This work is the first to unite 24MN30 and LHU G3 under one name through morphological and molecular data. This species forms racket hyphae similar to that observed by Peck (1985).



Phylogenetic placement of *Gymnascella minnisii* compared to close relatives on a maximum likelihood tree with maximum likelihood/maximum parsimony bootstrap support values. *Gymnascella minnisii* is highlighted in **bold**. This analysis was based on a single gene alignment, utilising nrDNA sequences (ITS1, ITS4 primers; White et al. 1990) only. PAUP v. 4.0a build 167 (Swoford 2003) was utilised to conduct the 1 000 bootstrap maximum parsimony analysis and maximum likelihood analysis. The maximum likelihood analysis utilised the General Time Reversible (GTR) nucleotide model with rate matrix set to estimate, and variable sites set to gamma distribution. Bootstrap support values greater than 70 % are shown on nodes in the following order: maximum likelihood/maximum parsimony. The alignment was deposited in TreeBASE (submission S26902).

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