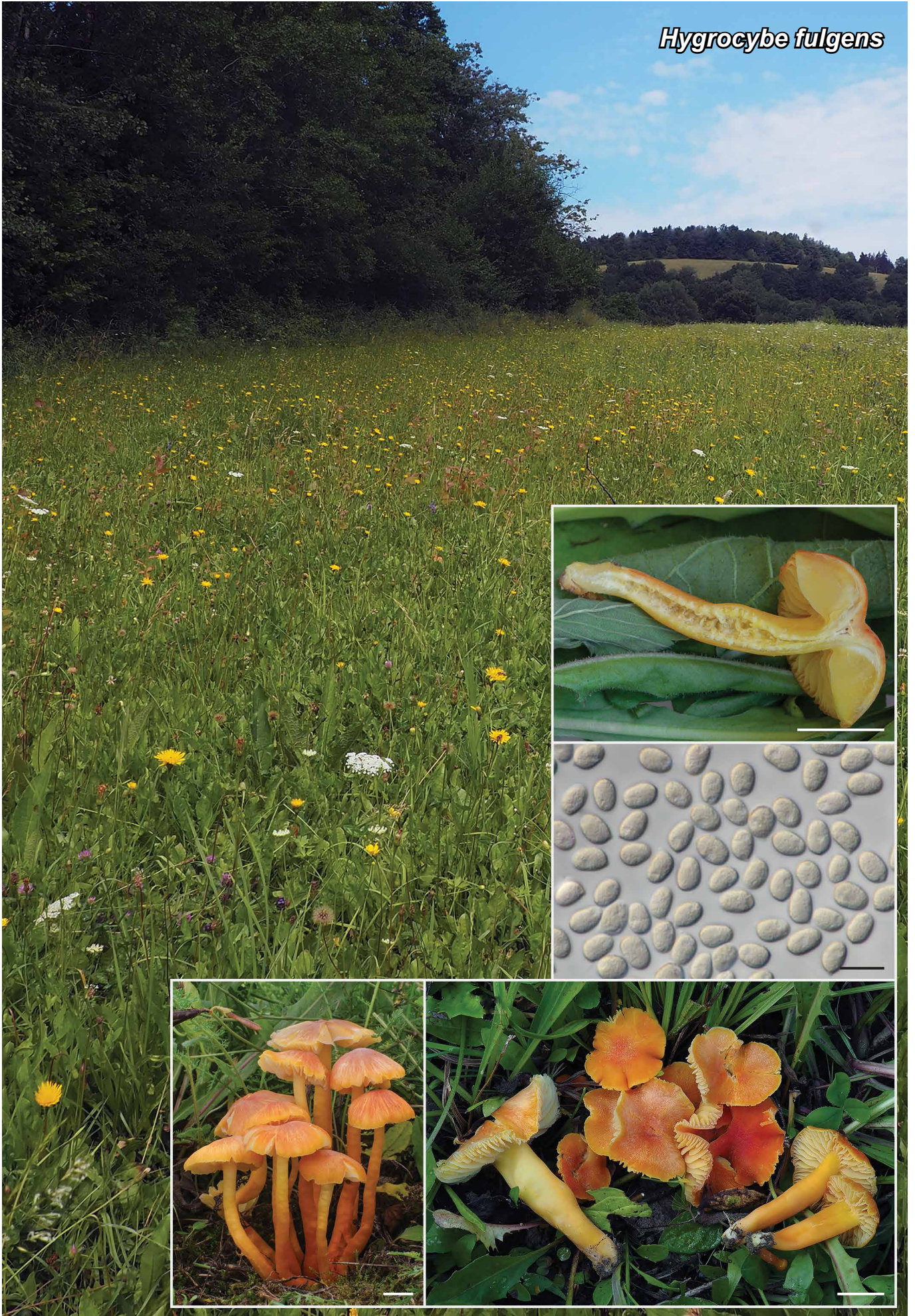


*Hygrocybe fulgens*



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***Hygrocybe fulgens* Fuljer, Kautmanová & Boertm., sp. nov.**

*Etymology.* The name reflects the shiny colour of the basidiomata.

Classification — *Hygrophoraceae*, *Agaricales*, *Agaricomycetes*.

*Pileus* 14–65 mm diam, at first hemispherical, broadly convex, later more or less applanate with depressed centre, brittle; surface finely squamulose, squamules concolorous or paler, sometimes smooth, dry, orange, yellowish orange or reddish (Pantone 1505C, Pantone 2018C, Pantone 716C) (Pantone Color Finder 2021; <https://www.pantone.com/color-finder/2021-C>), often with a slightly scarlet red centre (Pantone 2028C). *Stipe* 25–60 × 2.5–18 mm, terete or compressed, often attenuated downwards, brittle, hollow; surface smooth, sometimes finely fibrillose, dry, matt or silky sheen, golden yellow, yellow, yellowish orange, orange (Pantone 7406C to Pantone 7414C), sometimes paler at the top (Pantone 130C). *Lamellae* broadly adnate, ventricose, brittle, distant; surface smooth, paler than pileus and stipe, almost whitish at first, becoming yellowish or pale orange (Pantone 127C to Pantone 130C), sometimes with salmon hue; edges often paler. *Context* yellowish white (Pantone 127C to Pantone 130C), sometimes more orange or orange red in pileus and base of stem (Pantone Orange 021C), unchanging when cut. *Smell* and *taste* insignificant. *Spore print* white. *Basidiospores* smooth, non-amyloid, sometimes with one big vacuole, ellipsoid to oblong, (6.6–)7.1–9.9(–10.2) × (4.5–)4.8–6.3(–6.9) μm, Q = 1.3–1.9 (Lm = 8; Wm = 5.55; Qm = 1.54), 130 spores from three basidiomata measured from the holotype (BRACR 32958). *Basidia* 38–55 × 5–8 μm (excluding sterigmata), clavate, predominately 4-spored, relatively long with long attenuated base, *sterigmata* elongate, 4–7 μm long. *Cystidia* absent. *Pileipellis* as a trichoderm, with more or less clavate (inflated) terminal elements, hyphae sometimes septate and connected with a clamp, predominately short, (29–)32–103(–145) × (5.2–)6.3–13.1(–15) μm. *Stipitipellis* as a cutis, hyphae sometimes septate and clamped, predominately short, (28–)32–110(–111) × (3.8–)4.2–8.7(–9.1) μm. *Gill trama* sub-regular, with cells (42–)46–120(–145) × (8.5–)9.7–18(–19) μm.

*Distribution & Habitat* — Known from Slovakia, probably more widespread but overlooked and misidentified. Growing gregarious, solitary or scattered in mowed grasslands, mowed parks, on neutral to slightly calcareous soils. From July to September (–October).

*Typus.* SLOVAKIA, Javorníky Mts, Sádky, Petrovice, N49°15'21.73" E18°32'7.77", alt. 359 m, mowed grassland (south-facing, fertilised in the past), in association with *Leontodon hispidus*, *Trifolium pratense*, *Agrostis capillaris*, *Fragaria vesca*, *Daucus carota*, *Agrimonia eupatoria*, *Symphytum officinale*, *Plantago major*, *Trisetum flavescens*, *Trifolium repens*, etc., on bare soil, 30 Aug. 2019, F. Fuljer & I. Fuljer (holotype BRACR 32958, ITS and LSU sequences GenBank MW471672 and MW471670, BOLD ITS sequence FULGE001-20, MycoBank MB 839238).

*Colour illustrations.* Mowed grassland in Petrovice village (Javorníky Mts, Slovakia), where the typus (holotype) was collected. Type specimens *in situ*, cross section of the sporocarp (Photo credit F. Fuljer); basidiospores. Scale bars = 10 mm (fruitbodies), 10 μm (spores).

*Additional materials examined.* SLOVAKIA, Javorníky Mts, Sádky, Petrovice, N49°15'21.73" E18°32'7.77", alt. 359 m, mowed meadow (south-facing), in association of *Leontodon hispidus*, *Trifolium pratense*, *Agrostis capillaris*, *Fragaria vesca*, *Daucus carota*, *Agrimonia eupatoria*, *Symphytum officinale*, *Plantago major*, *Trisetum flavescens*, *Trifolium repens*, etc., on bare soil, 8 Sept. 2020, F. Fuljer, BRACR 32959; Beskydske predhorie Basin, Snina town, city park near the Vihorlat hotel, N48°59'21.4" E22°09'39.1", alt. 220 m, in moss and grass, 10 Sept. 2020, J. Pavlík, BRACR 33659, ITS and LSU sequences GenBank MW471671 and MW471669, BOLD ITS sequence FULGE002-20.

*Notes* — *Hygrocybe fulgens* is characterised by a dry, squamulose applanate pileus, dry, smooth and broad stipe, pileipellis a trichoderm, ellipsoid to oblong spores, and by a size and colour of whole sporocarps, which are usually orange yellow, often with golden yellow stipe and darker (almost scarlet red) central part of pileus. Due to these features, this species fits well with the concept of the subgenus *Pseudohygrocybe* section *Coccineae* and subsection *Squamulosae* (Lodge et al. 2014). Based on macromorphological features, the most similar species to *Hygrocybe fulgens* are *H. calciphila*, *H. miniata*, *H. reidii* and *H. substrangulata*. *Hygrocybe calciphila*, differs by typical subglobose to broadly ellipsoid spores and smaller basidiomata. Macroscopically, *H. fulgens* and *H. calciphila* are very similar, but sporocarps of *H. fulgens* are mostly much larger and robust. *Hygrocybe miniata* is characterised by triangular or pear-shaped spores, pileus without darker central part and also by a thinner stipe (usually to 5 mm broad). *Hygrocybe reidii* is another macroscopically similar species to *H. fulgens*, differing by a honey-like smell and smooth, orange-red coloured pileus. *Hygrocybe substrangulata* differs from other mentioned *Hygrocybe* species by much larger spores (up to 14.5 μm) and sometimes decurrent lamellae (Boertmann 2010). All above mentioned species grow in central Europe in the unimproved, sometimes grazed or mowed grasslands with *Nardus stricta* or *Agrostis* spp., but *H. fulgens* was found in a different type of grassland, where *Leontodon hispidus* was a dominant plant.

In the maximum likelihood tree based on the ITS sequences *H. fulgens* is positioned on a separate branch close to the clade of subsection *Squamulosae*, which is consistent with the results of macro- and micro-character observations.

**Supplementary material**

**FP1254** Subtree of the maximum likelihood tree obtained from the analysis of ITS sequences of *Hygrocybe* subgenera *Hygrocybe* and *Pseudohygrocybe*. The alignment was performed with ClustalW and the Tamura-Nei model was used for the phylogenetic analysis (Tamura & Nei 1993). Bootstrap support values are indicated at the nodes. The original analysis involved 66 nucleotide sequences, 21 of them are implemented in the subtree. There were a total of 700 positions in the final dataset. Evolutionary analyses were conducted in MEGA X (Kumar et al. 2018a).

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