

*Geoglossum jirinae*



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***Geoglossum jirinae*** V. Kučera, Ševčíková, Slovák, *sp. nov.*

**Etymology.** The name 'jirinae' honours the collector of the holotype, Jiřina Hrabáková.

**Classification** — *Geoglossaceae*, *Geoglossales*, *Geoglossomycetes*.

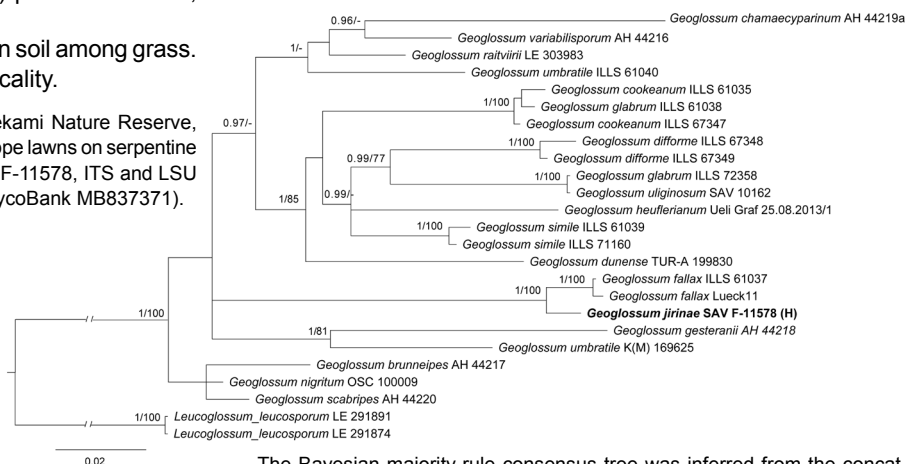
**Ascomata** solitary, scattered, clavate, stipitate, 18–36 × 2–4 mm, dry, black. **Ascigerous part** lanceolate or broadly clavate, 1/3–2/3 of the total ascomata length, black, compressed in cross section, clearly delimited from the stipe, smooth both in fresh and dry conditions. **Stipe** cylindrical, oval in cross section, 9–15 × 1.5–2.5 mm, robust, with black squamules, slightly thickened upward. **Asci** cylindrical to clavate, (123–)135–145(–166) × 14–17 μm (all measurements of microscopic characters refer to material examined in 3 % KOH), Q = 7.8–9.7, unitunicate, inoperculate, 8-spored, with euamyloid ascoapical apparatus and inamyloid wall in MLZ and IKI. **Ascospores** elongated clavate to ellipsoid baculiform, usually slightly curved, (39–)45–57(–60) × 5–6(–6.5) μm, Q = 7–10(–12), first hyaline, finally becoming brown in water, blackish in 5 % KOH, 1–4(–7)-septate when mature, most often with three septa, smooth. **Ascoconidia** not observed. **Paraphyses** numerous, longer than asci, straight, sparsely or moderately septate, 2–3 μm wide, hyaline, agglutinated by light brown amorphous matter in apical part. **Apical cells of paraphyses** variable, cylindrical, clavate to capitate, curved, contorted, sometimes bifurcate, or proliferating, mostly 22–47 × 2–3 μm, some cells inflated up to 10 μm. **Stipe surface** squamulose. Hyphae of the squamules straight, moderately septate, formed by chains of several (4–7) pale brown cells, apical cells clavate.

**Habit, Habitat & Distribution** — Solitary, on soil among grass. The species is known only from the type locality.

**Typus.** CZECH REPUBLIC, Hrubšice village, Nad řekami Nature Reserve, N49°05'35" E16°17'33", elev. 257 m, on soil in dry steppe lawns on serpentine slopes, 16 Nov. 2019, *J. Hrabáková*, (holotype SAV F-11578, ITS and LSU sequences GenBank MT940893 and MT940893, MycoBank MB837371).

**Colour illustrations.** Steppe lawns on serpentine slopes near Hrubšice village in the Czech Republic. Macro- and microscopic structures of holotype: ascomata; ascospores (in KOH); amyloid reaction of the ascoapical apparatus (in IKI); paraphyses (in 3 % KOH); stipe surface (in 3 % KOH). Scale bars = 1 cm (ascomata), 10 μm (microscopic structures).

**Notes** — The combination of characters involving short ascospores (45–55 × 5–6 μm) with predominantly three septa (occasionally 0–7) and stipe with scales, and long (22–45 × 2–3.5 μm) slightly curved last cell of paraphyses is unique for this *Geoglossum* species. Macromorphologically similar *G. fallax* differs in longer (65–105 × 5–7 μm) and more septate (7–12) spores (Durand 1908). The steppe habitat on calcareous soil could host also *G. cookeanum* which is different in chain-forming apical cells of paraphyses, almost smooth stipe and 7-septate ascospores (Minter & Cannon 2015). Very close in having a squamulose stipe, spores (50–60 × 4–6 μm) with 1–3 (5–7 when mature) septa is *G. vleugelianum*, but the difference is in the coloured and stout, upwardly clavulate paraphyses with pyriform or globose apical cells and easily removed tufts of hyphae on the stipe; *G. elongatum* has likewise elongate paraphyses and relatively short spores (50–60 × 5–7 μm) with 0–7 septa (Nannfeldt 1942), but has setose hairs on the stipe and therefore was relocated to *Hemileucoglossum* (Arauzo & Iglesias 2014). It was impossible to verify the type specimen of *G. elongatum* due to undergoing renovation of the fungarium building (S), but the presence of setose hairs on the stipe is the basic character of the genus *Hemileucoglossum*. Possibly similar could also be *G. fumosum* with a densely squamulose stipe, short spores (30–40 × 4.5–5.5 μm) and asci (100–125 × 12–17 μm), but the ascigerous part characteristically looks like it is impregnated by brown smoke (Hakeliev 1967).



The Bayesian majority-rule consensus tree was inferred from the concatenated dataset of ITS-LSU sequences. The dataset included *G. jirinae* (H: holotype), relevant *Geoglossum* species, and *Leucoglossum leucosporum* as an outgroup (TreeBASE study S26857). Bayesian inference was run in MrBayes v. 3.2.7a, using four independent chains, 10 M generations, and a sampling frequency of 1000 (Ronquist et al. 2012). The best-fit partitioning schemes and models were estimated for the concatenated tree, using the greedy search mode as implemented in the PartitionFinder v. 2.1.1 (Lanfear et al. 2016). The maximum likelihood analysis was computed in RAxML v. 8.2.12 (Stamatakis 2014). Analyses were computed in the CIPRES Science Gateway v. 3.3 (Miller et al. 2010). Numbers above branches indicate Bayesian posterior probabilities  $\geq 0.95$  and the maximum likelihood bootstrap support values  $\geq 85\%$ . The scale bar represents the number of nucleotide changes per site.

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