



<https://doi.org/10.11646/phytotaxa.597.3.6>

Erratum: Yang, K.L., Yang, Z.L., Zhang, M., Wang, G.S. & Liu, X. (2023) *Gautieria mianjin* (Gomphales, Basidiomycota), a new species of false truffle from China. *Phytotaxa* 594 (2): 119–129.

Introduction

When we were further studying several DNA loci of *Gautieria mianjin* Kun L. Yang, Xiao Liu & Zhu L. Yang (2023: 119–129) after the article *Gautieria mianjin* (Gomphales, Basidiomycota), a new species of false truffle from China (hereinafter referred to as “Yang *et al.* (2023)”) was published, we resequenced the internal transcribed spacer region (ITS) of its holotype HKAS126926, and found that the quality of the one used for phylogenetic analyses in Yang *et al.* (2023) was not good enough, as the completeness and accuracy of its ITS1 region were somewhat poor according to the newly generated sequence, which led to some imperfections within the results of the phylogenetic position of this species explained in Yang *et al.* (2023).

We apologize for this problem. Considering to give a stricter conclusion of the phylogenetic position of *G. mianjin*, we reran the phylogenetic analyses and wrote this erratum to further clarify its phylogenetic position based on our newly generated ITS sequence of its holotype HKAS126926.

Materials and methods

DNA extraction, PCR and resequencing of HKAS126926

The other steps were the same as described in Yang *et al.* (2023), except the forward primer to amplify the internal transcribed spacer region (ITS) was changed to ITS1-F following Liu *et al.* (2023). The newly generated ITS sequence of HKAS126926 was uploaded to GenBank (<https://www.ncbi.nlm.nih.gov/genbank>) under the accession No. OQ282702, replacing the previously used one in Yang *et al.* (2023).

Molecular phylogenetic analyses rerunning

Replacing the previously used ITS sequence of HKAS126926 in Yang *et al.* (2023) with the newly generated one, while the ITS sequences of other species were kept the same as listed in the Table 1 in Yang *et al.* (2023). The other steps were also the same as described in Yang *et al.* (2023).

Results and Discussion

The aligned ITS dataset contained 1211 nucleotides in length (Alignment E1, see Supplementary materials). The phylogenetic trees generated from Maximum Likelihood (ML) and Bayesian Inference (BI) analyses had almost identical topologies with minimal variation in statistical support values, so only the tree inferred from the former was displayed (Fig. E1).

The rerun phylogenetic tree shared the same topology with the one in the Fig. 1 of Yang *et al.* (2023). The main difference between them was the monophyletic lineage formed by *Gautieria mianjin* HKAS126926 and the “uncultured fungus” in the rerun one got shorter genetic distance separating from other specimens in Clade 1E than the one in Yang *et al.* (2023). More specifically, the ITS-based genetic distance between *G. mianjin* HKAS126926 and *G. xinjiangensis* HMJAU6009 reduced to 2.19%, while it’s still a relatively large distance. The ITS-based genetic distance between *G. mianjin* HKAS126926, vouchers 16988 labeled as *G. graveolens*, T4547 and HH222 labeled as *G. morchelliformis* reduced to $\leq 1.35\%$ each other, indicating that they were closely related. However, both *G. morchelliformis* and *G. graveolens* are significantly different from *G. mianjin* in their basidiospores characteristics according to the available references (Table E1), so it’s likely that only by ITS sequences could not distinguish them well, and more molecular markers, even the whole genome, are needed to refer in future study.

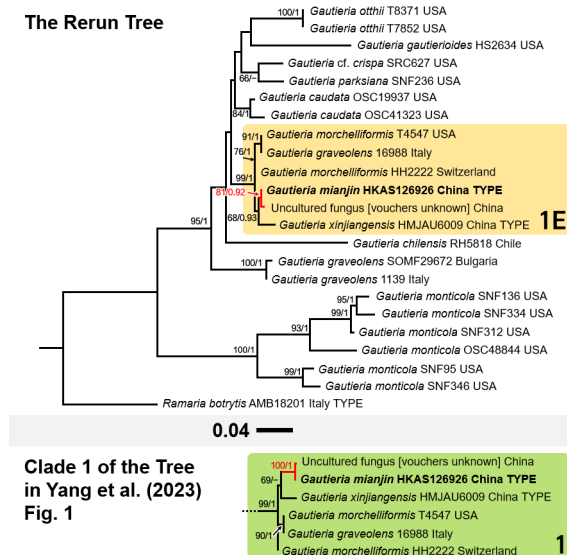


FIGURE E1. The top tree is the rerun phylogenetic tree of *Gautieria*. The bottom tree is the clade 1 in the Fig.1 of Yang *et al.* (2023), as the comparison to the clade 1E on the rerun tree. The two trees were adjusted in the same scale. The monophyletic lineages formed by *Gautieria mianjin* HKAS126926 and the “uncultured fungus” were traced in red. Nodes were annotated if supported by $\geq 50\%$ MLB (left) or ≥ 0.90 BPP (right).

TABLE E1. The basidiospores characteristics of *Gautieria mianjin*, *G. morchelliformis* and *G. graveolens*, extracted from Yang *et al.* (2023). Records from literature that published the certain taxon were marked with “(T)”. Text in square brackets was note added by the authors.

Taxa	Locality	Basidiospores characteristics				References
		Shape	Length (μm)	Width (μm)	Number of longitudinal ribs	
<i>Gautieria mianjin</i>	China	subglobose to broadly ellipsoid, Q = (1.00) 1.04–1.24 (1.26) and $Q_m = 1.12 \pm 0.07$ including ribs, Q = (1.05) 1.15–1.33 (1.43) and $Q_m = 1.23 \pm 0.10$ excluding ribs	(10) 11–14 (16) [12.24 \pm 1.20] including ribs, (9) 10–12 (15) [11.53 \pm 1.36] excluding ribs	(9.5) 10–12 (13) [10.96 \pm 0.77] including ribs, (8) 9–10 (11) [9.33 \pm 0.69] excluding ribs	10–14	This study (T)
<i>G. morchelliformis</i>	Italy	[described in Latin] fusiform to citriform oblong to limoniform	not mentioned 12–24 14–24	not mentioned 8–12.5 8–12	not mentioned 8–10 8–10	Vittadini 1831 (T) Zeller & Dodge 1918 Liu 1998
<i>G. graveolens</i>	Italy	[described in Latin] apex rounded [other shape characteristics not mentioned] broadly ellipsoid with a conical or rounded apiculus	not mentioned 18–19 14–19	not mentioned 11–12 8.5–10	not mentioned usually 10 [not mentioned, but approximately 10 as seen from the SEM photos in the article]	Vittadini 1831 (T) Zeller & Dodge 1918 Uzun <i>et al.</i> 2019

Supplementary materials

ALIGNMENT E1. The alignment of the rerun phylogenetic tree in Fig. E1 was deposited in Zenodo (<https://zenodo.org>) with doi 10.5281/zenodo.7883061. It contains 23 ITS sequences (22 of ingroup and 1 of outgroup), 1211 nucleotides in length.

Acknowledgements

The authors are grateful to the Phytotaxa editorial team for giving us this opportunity to remedy the imperfections in the article *Gautieria mianjin* (Gomphales, Basidiomycota), a new species of false truffle from China.

Availability of data and materials

The newly generated ITS sequence of the holotype HKAS126926 of *Gautieria mianjin* is available in NCBI GenBank (<https://www.ncbi.nlm.nih.gov/genbank>) under the accession No. OQ282702. The holotype HKAS126926 of *Gautieria mianjin* was deposited in the Herbarium of Cryptogams, Kunming Institute of Botany, Chinese Academy of Sciences (HKAS).

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