

Nomenclatural novelties: K.L. Yang, G. Wu, J.X. Pan, J.Y. Lin & Z.L. Yang

Mycoamaranthus lasagniformis Kun L. Yang, G. Wu, Jia-Xi Pan, Jia Y. Lin & Zhu L. Yang, sp. nov.

IF 903154

Holotype: KUN-HKAS 144615

Etymology: Referring to the gleba of this fungus that resemble lasagne.

Diagnosis: Basidiomata small, sequestrate, irregularly subglobose, 29–34 mm wide, 24–28 mm high, rubbery, without any special odor. Peridium very thin, 0.3–0.5 mm thick; background sun orange (#FCD742), with tulip orange (#EDB345) felty squamules. Gleba spongy, with a radial texture and irregularly shaped locules, merino white (#F9F5EC) when young, becoming dark pepper red (#764840) to blackcurrant purple (#422F45). Columella indistinct. Stipe rudimental, very short, 4–6 mm long, tapering downwards, 4 mm wide at the widest part, sun orange (#FCD742). Rhizomorphs well-developed, sun orange (#FCD742) to darker. Basidiospores colorless or slightly yellowish to brownish, obovoid, broadly ellipsoid, ellipsoid to slightly ovoid, with a slightly thick to thick wall, smooth to slightly ornamented when young, becoming yellowish to darkly brownish, fully ovoid, with reticulate to verrucose ornamentation on a thick wall, 14–20 (–21) [average 17.16 ± 1.69] × (8.5–) 9–12.5 [average 10.71 ± 1.08] μm, length/width ratio (1.33–) 1.36–2.05 (–2.06) [average 1.61 ± 0.17] including ornamentation, (11–) 12–15 (–16) [average 13.73 ± 1.20] × (6–) 6.5–8.5 (–9) [average 7.45 ± 0.77] μm, length/width ratio 1.53–2.42 [average 1.87 ± 0.28] excluding ornamentation; ornamentation more or less dissolved at full maturity. Basidia 35–45 × 10–14 μm, clavate, mostly four-spored, rarely two- or three-spored, thin-walled, nearly colorless, yellowish to brownish, darker at the upper part, with sterigmata up to 5 μm long. Gleba trama subregular to irregular, composed of 3–4 μm wide, thin-walled, moderately to frequently branching, slightly gelatinous, nearly colorless hyphae. Pleurocystidia not recognized. Peridium composed of 2–4 (–5) μm wide, thin-walled, moderately to frequently branching hyphae parallelly arranged in the peridial trama, becoming interwoven and forming some squamule masses towards the peridial surface; nearly colorless to yellowish in the peridial trama, becoming yellowish to brownish towards the peridial surface. Clamp connections absent.

Ecology and distribution: Gregarious, scattered on soil, emergent or subhypogeous, in subtropical forests dominated by plants of Fagaceae. Currently known from China (southwest China).

Comments: During the microscopic observation, Kun L. Yang found that the cellular pigments of this fungus dissolved into the 5% KOH solution very quickly (Figure 1), so the colors of microscopic structures were not recorded in detail as the description may be inaccurate. The macroscopic colors were confirmed and described following Yang et al. (2024).

The genus *Mycoamaranthus* currently contains only two species, namely *M. cambodgensis* (Pat.) Trappe, Lumyong, P. Lumyong, Sanmee & Zhu L. Yang, reported from Cambodia and Thailand (Patouillard 1923; Lumyong et al. 2003), and *M. congolensis* (Dissing & M. Lange) Castellano & Walley, reported from Congo, Malawi and Zimbabwe (Dissing & Lange 1962; Castellano et al. 2000). Another member reported from Australia, namely *M. auriorbis* Castellano, Trappe & Malajczuk (Castellano et al. 1992), was considered as a synonym of *M. cambodgensis* by Lumyong et al. (2003). Our new species shows the typical morphological characteristics of *Mycoamaranthus* in the thin, brightly orangish peridium and the ovoid, darkly brownish and verrucosely ornamented basidiospores, but also differs from the two known species by the distinct peridial squamules, long basidia, relatively longer basidiospores, and the unique ITS sequence.

In the phylogenomic analyses by Wu et al. (2023), *Mycoamaranthus* has been confirmed to be a sequestrate genus belonging to the subfamily Zangioideae of Boletaceae. Thus, Kun L. Yang constructed three phylogenies based on different datasets (hereinafter referred to as Phylogenies 1–3, for original alignment files see doi: 10.5281/zenodo.14558373) regarding Zangioideae to explore the position of this new species (Table 1 & Figure 2), with *Hemileccinum* as the outgroup (referred to the phylogeny of Boletaceae in Wu et al. (2023)), each through a Maximum Likelihood analysis following the methodology described in Yang et al. (2024). Phylogeny 1 was inferred from the concatenated nrLSU-rpb1-rpb2-tef-1 α alignment of this species and the other representatives of the Zangioideae genera. Note that the specimens of other *Mycoamaranthus* species complete in these loci were unavailable, so no other samples of this genus were included (but see Phylogeny 3). In the result, our new species represented by KUN-HKAS144615 formed a distinct clade, sister to *Wakefieldia striispora* represented by NY1193852 but without significant support. Note that *W. striispora* is currently the only member of *Wakefieldia*, another sequestrate genus of Zangioideae as inferred by the phylogenomic analyses in Tremble et al. (2023). Phylogeny 2 was inferred from the ITS alignment of this species and the other *Mycoamaranthus* species. Note that the specimens of other Zangioideae genera generally do not have available ITS data, so they were not included. In the result, our new species represented by KUN-HKAS144615 formed a distinct clade separating from specimens of the two known species and an unclassified, possibly undescribed species. Moreover, our new species seemed to be sister to *M. cambodgensis* as the corresponding node received significant support. Phylogeny 3 was inferred from the combined data of Phylogenies 1 and 2 (ITS-nrLSU-rpb1-rpb2-tef-1 α). In the result, our new species represented by KUN-HKAS144615 still formed a distinct clade but the genus *Mycoamaranthus* became polyphyletic. However, it was probably caused by the inconsistent data completeness of different loci.

Collection examined: China, Guizhou Province, Qiannan Buyi-Miao Autonomous Prefecture, Duyun City, in a forest dominated by plants of Fagaceae, on soil, 26°20'12"N, 107°29'26"E, elevation 1,000 m, June 5, 2023, Jia-Xi Pan & Kun L. Yang, S2397 (KUN-HKAS 144615, holotype, deposited in the Herbarium of Cryptogams, Kunming Institute of Botany, Chinese Academy of Sciences (GenBank sequences: ITS PQ636467; nrLSU PQ632441; rpb1 PQ634673; rpb2 PQ634674; tef-1 α PQ634675); HTBM0340, isotype, deposited in Kun L. Yang's private fungarium).

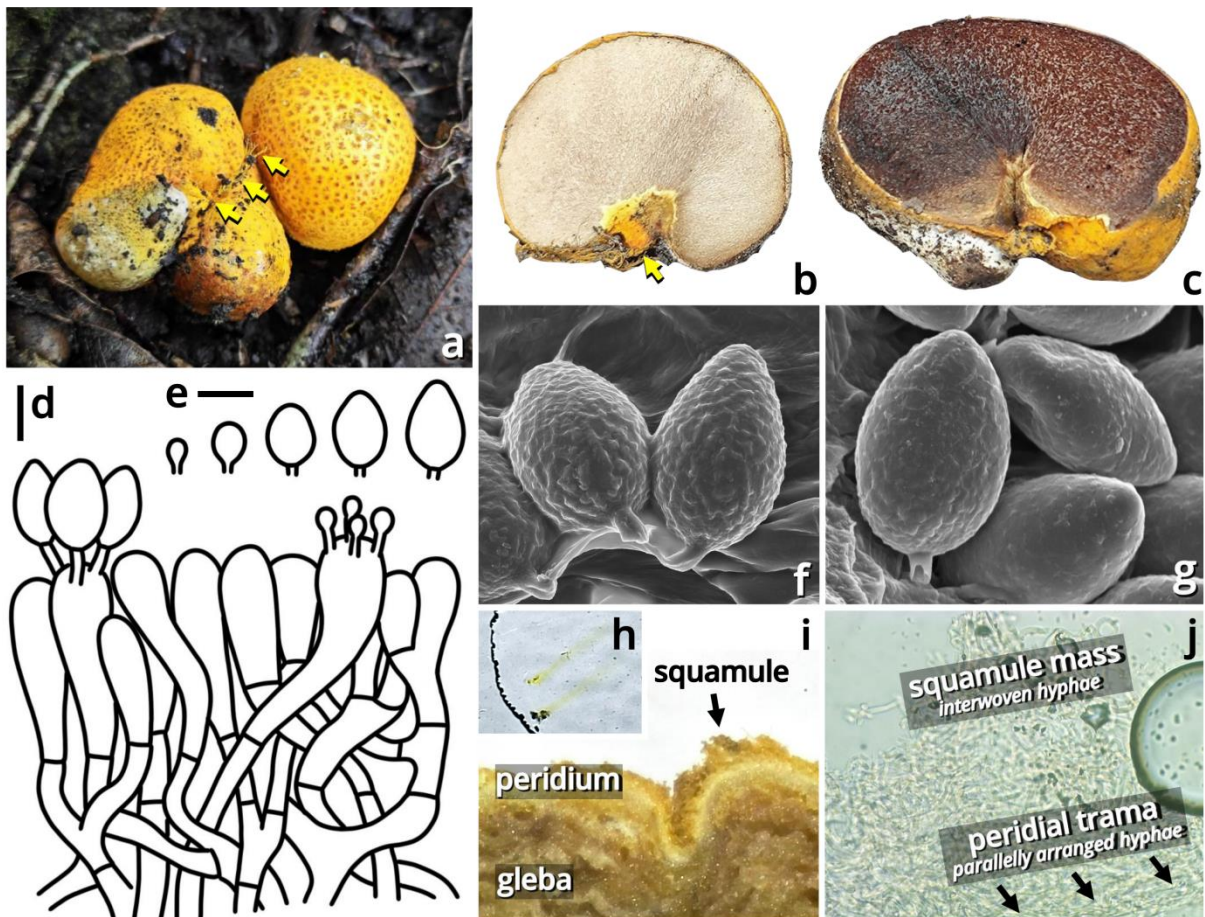


Figure 1. *Mycoamaranthus lasagniformis* (photos by Kun L. Yang & Jia-Xi Pan; drawings by Kun L. Yang, from KUN-HKAS144615). (a–c) fresh basidiomata: (a) basidiomata in the habitat; yellow arrows trace a rhizomorph; (b) longitudinal section of a middle-aged basidioma; yellow arrow indicates the rudimental stipe; (c) longitudinal section of a mature basidioma. (d) hymenium and subhymenium. (e) development of basidiospore shape towards maturity. (f) nearly mature basidiospores with clear ornamentation. (g) fully mature basidiospores with slightly dissolved ornamentation. (h) pigments of a peridial fragment distinctly dissolved in a drop of 5% KOH solution in just five seconds. (i) longitudinal section of the peridium and gleba. (j) microscopic longitudinal section of the peridium; the transition from parallel arranged hyphae in the peridial trama to interwoven hyphae towards the surface and squamules can be recognized. Bars: d–e = 10 μ m.

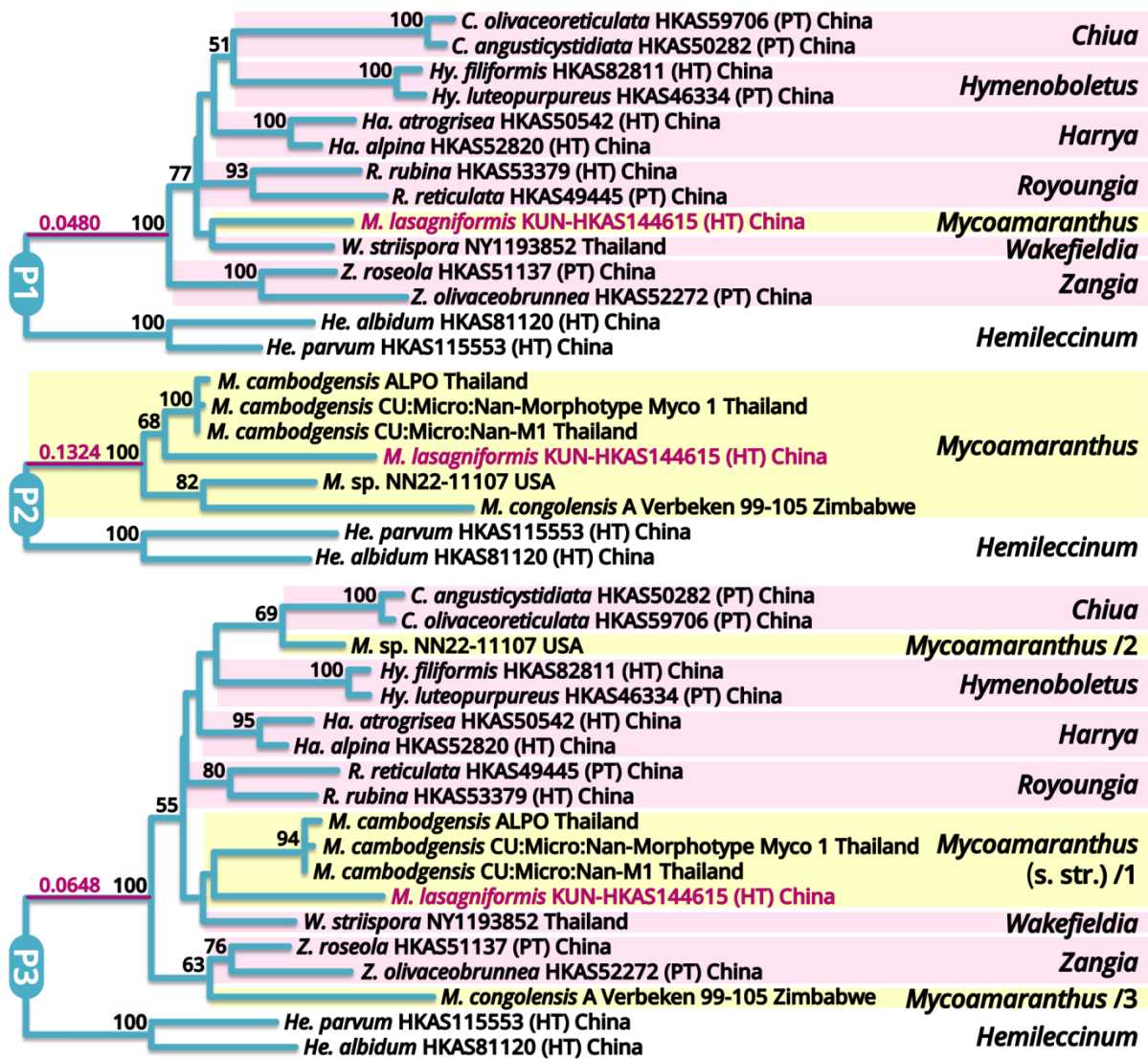


Figure 2. Phylogenies 1–3 (P1–P3) of Zangioideae inferred from three different alignments. Nodes are annotated if supported by $\geq 50\%$ maximum likelihood bootstrap. Each genus is highlighted with a colored box. Holotypes and paratypes are indicated by HT and PT, respectively; note that the paratypes of a species are only indicated when its holotype is not present. In each phylogeny, a selected branch is annotated with the length value as the scale.

Table 1. Information of the specimens used in the phylogenetic analyses. The collection sequenced in this study is in bold. For Phylogeny 1, all specimens without * are included; for Phylogeny 2, the specimen KUN-HKAS144615, two Hemileccinum specimens as the outgroup, and those specimens with * are included; for Phylogeny 3, all specimens are included. Unavailable sequences are indicated with -. Sequences extracted from genomic data are indicated with †. Holotypes and paratypes are indicated by HT and PT, respectively; note that the paratypes of a species are only indicated when its holotype is not present.

Genera	Species	Specimen Nos.	Origins	GenBank Accession Nos.					References
				ITS	nrLSU	rpb1	rpb2	tef-1 α	
Ingroup									
<i>Chiuia</i>	<i>C. angusticystiata</i>	KUN-HKAS50282 (PT)	China	-	KT990554	MT110408	KT990390	KT990754	Wu <i>et al.</i> (2016); Li & Yang (2021)
	<i>C. olivaceoreticulata</i>	KUN-HKAS59706 (PT)	China	-	KT990593	KT990941	KT990428	KT990787	Wu <i>et al.</i> (2016)

<i>Harrya</i>	<i>Ha. alpina</i>	KUN-HKAS52820 (HT)	China	-	KT990632	KT990977	KT990463	KT990826	Wu <i>et al.</i> (2016)
	<i>Ha. atrogrisea</i>	KUN-HKAS50542 (HT)	China	-	KT990694	KT991024	KT990499	KT990880	Wu <i>et al.</i> (2016)
<i>Hymenoboletus</i>	<i>Hy. luteopurpureus</i>	KUN-HKAS46334 (PT)	China	-	KF112471	KF112581	KF112795	KF112271	Wu <i>et al.</i> (2016)
	<i>Hy. filiformis</i>	KUN-HKAS82811 (HT)	China	-	MT154777	-	MT110446	MT110371	Li & Yang (2021)
<i>Mycoamaranthus</i>	<i>M. cambodgensis</i>	*ALPO	Thailand	MN203105	-	-	-	-	Yuwa-amornpitak & Yeunyaw (2020)
	<i>M. cambodgensis</i>	*CU:Micro:Na n-M1	Thailand	AB453031	-	-	-	-	Direct submission by Yomyart <i>et al.</i>
	<i>M. cambodgensis</i>	*CU:Micro:Na n-Morphotype Myco 1	Thailand	AB453043	-	-	-	-	Direct submission by Yomyart <i>et al.</i>
	<i>M. congolensis</i>	*A Verbeken 99-105	Zimbabwe	LC053665	LC053665	-	-	-	Smith <i>et al.</i> (2015)
	<i>M. lasagniformis</i>	KUN-HKAS144615 (HT)	China	PQ636467	PQ632441	PQ634673	PQ634674	PQ634675	This study
	<i>M. sp.</i>	*NN22-11107	USA	OR096286	-	-	OR099720	-	Direct submission by Gordon
<i>Royoungia</i>	<i>R. reticulata</i>	KUN-HKAS52253 (HT)	China	-	KT990592	KT990940	KT990427	KT990786	Wu <i>et al.</i> (2016)
	<i>R. rubina</i>	KUN-HKAS53379 (HT)	China	-	MT154776	-	KF112796	KF112274	Wu <i>et al.</i> (2016)
<i>Wakefieldia</i>	<i>W. striispora</i>	NY1193852	Thailand	-	†	†	†	†	Extracted from JBBPMU0000000-00; Tremble <i>et al.</i> (2023)
<i>Zangia</i>	<i>Z. olivaceobrunnea</i>	KUN-HKAS52272 (PT)	China	-	HQ326948	MW165279	MW165289	HQ326876	Li <i>et al.</i> (2011)
	<i>Z. roseola</i>	KUN-HKAS51137 (PT)	China	-	KF112414	KF112579	KF112791	KF112269	Li <i>et al.</i> (2011)
Outgroup									
<i>Hemileccinum</i>	<i>He. albidum</i>	KUN-HKAS81120 (HT)	China	MZ923782	MZ923766	MZ936339	MZ936320	MZ936352	Li <i>et al.</i> (2021)
	<i>He. parvum</i>	KUN-HKAS115553 (HT)	China	MZ923790	MZ923772	MZ936348	MZ936333	MZ973010	Li <i>et al.</i> (2021)

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