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New species

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# 蜗孢属两个新种和一个中国新记录

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**摘　要：**蜗孢属隶属于子囊菌门 Ascomycota 毛筒壳科 Tubeufiaceae，它们形态特征独特，能够产生多种活性次级代谢产物，具有一定的应用前景。本研究从中国海南省采集的腐木标本上分离到 3 种卷旋型丝孢真菌，通过 ITS、LSU、RPB2 和 TEF1α 多基因系统发育分析证据结合形态学特征，确定了它们的分类地位。结果表明，其中 2 个物种为蜗孢属新种，1 个物种为中国新记录。为纪念李玉院士在中国菌物学界做出的贡献，本文特将其中一个新物种命名为李玉蜗孢菌。

**关键词：**卷旋型丝孢菌；毛筒壳科；腐生真菌；真菌分类学；分子系统学

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# Two novel species and one new record of *Helicoma* from tropical China

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**Abstract:** The fungal genus *Helicoma* has unique morphological characteristics and potential to produce a variety of active secondary metabolites. In this paper, two new species and one new Chinese record of *Helicoma* are introduced based on ITS, LSU, RPB2 and TEF1α multigene phylogenetic analyses and morphology. To commemorate the contribution of Prof. LI Yu, academician of the Chinese Academy of Engineering, to mycology, one new species is named as *Helicoma liyui*.

**Keywords:** helicosporous hyphomycetes; Tubeufiaceae; saprobic fungi; fungal taxonomy; molecular systematics

蜗孢属 *Helicoma* 是真菌界(kingdom of fungi) 子囊菌门 Ascomycota 座囊菌纲 Dothideomycetes 毛筒壳目 Tubeufiales 毛筒壳科 Tubeufiaceae 的一个类群，由 Corda (1837)于1837 年建立，模式种为 *Helicoma muelleri*，是真菌分类学家们最早发现并描述的卷旋型丝孢菌属之一(Linder 1929；Moore 1955；Goos 1986；Boonmee *et al*. 2014；Lu *et al*. 2018b)。该属真菌为木生腐生菌，生长环境包括陆生和水生，广泛分布于热带及亚热带地区(Zhao *et al*. 2007；Boonmee *et al*. 2011, 2014；Hyde *et al*. 2016；Lu *et al*. 2018b；Liu *et al*. 2019；卢永仲和康冀川 2020；Tian *et al*. 2022)，在我国海南、广西、广东、贵州、云南等南方地区均有分布(Zhao *et al*. 2007；Lu *et al*. 2018b；卢永仲和康冀川 2020)。

以往针对蜗孢属真菌的研究主要集中在分类学领域，且大多数已发表的物种只有形态学数据，缺乏 DNA 分子数据(Moore 1955；Goos 1986；Tsui *et al*. 2006；Zhao *et al*. 2007；Lu *et al*. 2018b)。21 世纪以来，随着分子生物学技术的快速发展，真菌 DNA 提取和测序成本大幅降低，近 20 年发表的蜗孢属真菌均提供了 DNA 部分片段的序列信息，使得该属物种的系统发育框架日趋完善。Boonmee *et al*. (2014)基于系统发育分析引入了 7 个有性型的蜗孢属新种，其中 4 个物种包含了无性型形态特征，即 *H. khunkornense*、*H. inthanonense*、*H. rugosum* 和 *H. siamense*。Hyde *et al*. (2016)基于系统发育分析发现了一个蜗孢属新种 *H. guttulatum*，其形态特征与该属模式种 *H. muelleri* 极为相似。Lu *et al*. (2018b) 发现蜗孢属物种中包含一类新的无性型，其分生孢子梗与典型的蜗孢属无性型特征极为相似，分生孢子同为卷旋型，但其卷旋的类别及孢子大小与典型的蜗孢属物种差距明显(图 1)。基于形态学和多基因系统发育分析，Lu *et al*. (2018b)重新定义了蜗孢属的形态特征，命名了 10 个该属新种，提出了 7 个新组合，并从该属中移除了 12 个物种。该研究显示，蜗孢属真菌的无性型形态特征分为两大类：第一类具备典型的蜗孢属特征，其分生孢子顶侧生，外形呈蜗牛外壳般卷旋状，

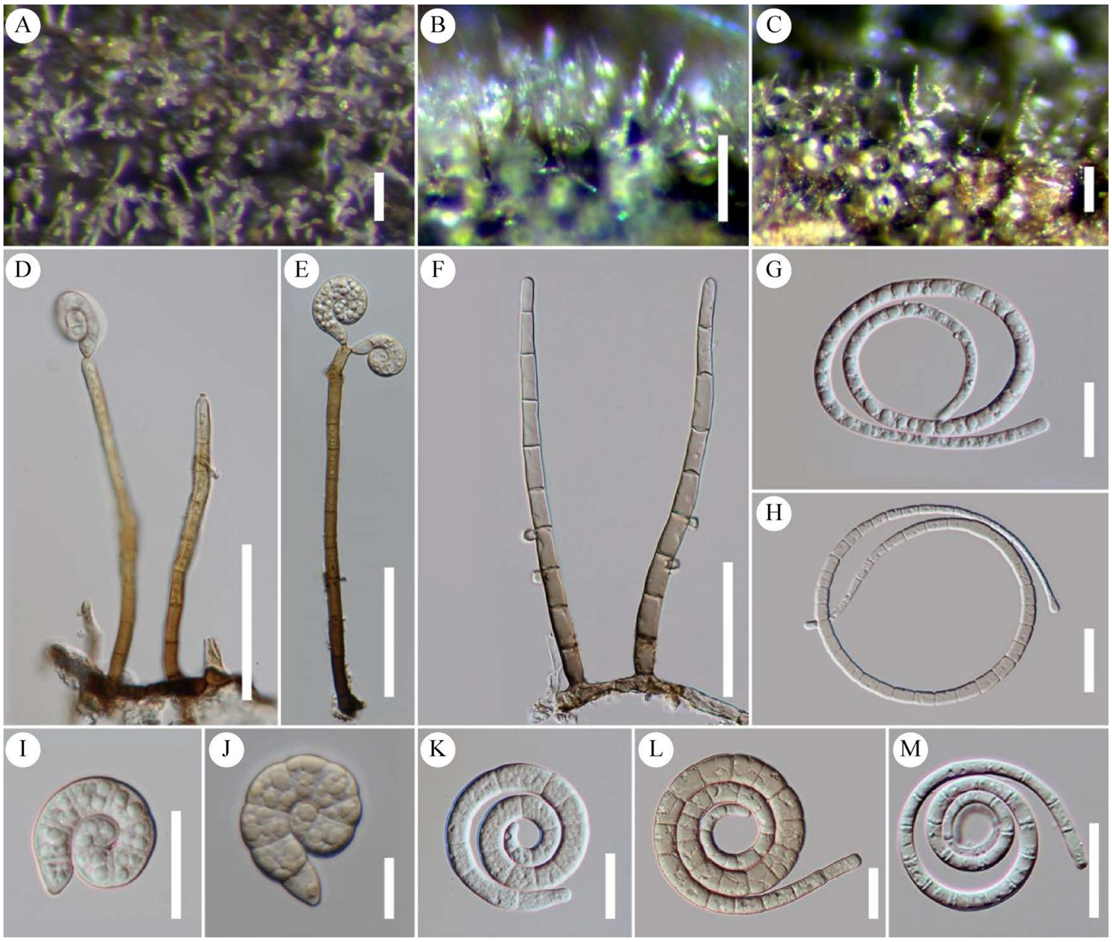

**图 1　蜗孢属真菌无性型形态特征**　A–C：自然基质上的菌落. D–F：分生孢子梗. G–M：分生孢子. 标尺：A–C=100 μm; D–F=50 μm; G–M=20 μm

Fig. 1　The asexual morph of *Helicoma*. A–C: Colonies on natural substrate. D–F: Conidiophores. G–M: Conidium. Scale bars: A–C=100 μm; D–F=50 μm; G–M=20 μm.

顶端渐窄，紧密卷曲 $1^1/_4$–$1^3/_4$ 圈，在水中不会松散(Lu *et al*. 2018b；Liu *et al*. 2019；Tian *et al*. 2022)；第二类分生孢子侧生，外形为卷旋型，紧密卷曲 $1^1/_2$–5 圈，在水中容易松散甚至全部展开，长度为第一类分生孢子长度的 4 倍以上(Lu *et al*. 2018b)。此外，蜗孢属真菌的有性型形态特征表现为子囊果表生，表面无刚毛，独居，近球形、椭圆形至倒卵形，顶部有乳突，乳突中心有一个孔口；子囊为双囊壁，具短柄，内含 8 个子囊孢子；子囊孢子为梭形或棍棒状，圆形末端逐渐变细，部分子囊孢子轻微弯曲，具多个分隔(Boonmee *et al*. 2014；Lu *et al*. 2018b)。

蜗孢属真菌具有产生多种活性次级代谢产物的潜力。Itazaki *et al*. (1990)从 *H. ambiens* (RF-1023)中获得了 2 个新的环四肽类化合物，并发现这 2 个化合物具有抑制组蛋白去乙酰化酶的活性。Hu *et al*. (2006)从 *H. viridis* 中分离得到 6 个醌类衍生物，其中 4 个化合物具有抗菌活性。范翠等(2019)发现 *H. multiseptatum* 发酵液的乙酸乙酯提取物对人宫颈癌细胞(HeLa 细胞株)有较好的体外抑制作用。

为挖掘更多具有生物活性的菌株，本课题组近年来一直致力于卷旋型丝孢真菌物种多样性的研究，丰富菌种资源库。本研究报道了 3 株

采自中国海南省的卷旋型丝孢真菌，并通过ITS、LSU、RPB2 和 TEF1α 多基因系统发育分析结合形态学特征，确定了它们的分类地位，其中，顶侧生蜗孢菌 *H. acropleurogenum* 和李玉蜗孢菌 *H. liyui* 为蜗孢属新物种，皱壁蜗孢菌 *H. rugosum* 为中国新记录。

## 1 材料与方法

### 1.1 标本采集

供试标本采自中国海南省。样品在野外随机采集后装入自封袋，记录采样信息后带回实验室，保湿培养 2 周后，使用体式显微镜(SMZ 745，尼康)检查供试标本表面菌落。模式标本保存在贵州省农业科学院标本馆(Herbarium of Guizhou Academy of Agricultural Sciences, GZAAS)和中国科学院昆明植物研究所隐花植物标本馆(Herbarium of Cryptogams Kunming Institute of Botany Academia Sinica, HKAS)。

### 1.2 方法

#### 1.2.1 菌株分离、纯化及保存

目标菌株的分离与纯化采用单孢分离的方法。在无菌操作下，将分生孢子制备成孢子悬浮液，分散到预先制备好的水琼脂培养基(WA)培养皿中，置于 25 ℃培养箱培养，8 h 后在显微镜下检查孢子萌发情况，将萌发后的分生孢子接种至预先制备好的马铃薯葡萄糖琼脂(PDA)培养基中，密封后置于 25 ℃培养箱中培养，并定期记录菌落形态特征，包括颜色、形状和菌落直径。模式菌株保存在贵州省农业科学院菌种库(Guizhou Culture Collection, GZCC)。

#### 1.2.2 真菌的形态学观察

用接种针从供试标本表面挑取少量生长完好的菌落置于载玻片上，制片后置于微分干涉显微系统(Nikon ECLIPSE 80i，尼康)下观察(显微镜配置 Canon EOS 70D 相机)，并拍照记录分生孢子梗、产孢细胞及分生孢子等形态特征。形态学描述中“$\overline{x}$”表示测量数据的平均值，“n”代表测量次数。

#### 1.2.3 菌株 DNA 提取和 PCR 扩增及测序

使用消毒灭菌后的手术刀从长好的菌落表面刮取新鲜菌丝，转移到 1.5 mL 离心管中备用。菌株 DNA 提取使用 Ezup 柱式真菌基因组 DNA 提取试剂盒，提取步骤参考试剂盒说明书。获得菌株 DNA 后，分别用 ITS5/ITS4、LR0R/LR5、fRPB2-5F/fRPB2-7cR 和 EF1-983F/EF1-2218R 作为引物扩增内转录间隔区(internal transcribed spacer, ITS)、核糖体大亚基(large ribosomal subunit, LSU)、RNA 聚合酶Ⅱ第二亚基(RNA polymerase Ⅱ second largest subunit, RPB2)和翻译延伸因子 1-α 基因(translation elongation factor 1-alpha gene, TEF1α)序列片段。聚合酶链式扩增反应(polymerase chain reaction, PCR)条件参考 Lu *et al*. (2017, 2018a)的报道。PCR 扩增体系为 50 μL，包括 25 μL 的 2× Bench Top™ *Taq* Master Mix，19 μL ddH$_2$O，正反向引物各 2 μL 以及 2 μL DNA 模板。PCR 扩增后以 1%琼脂糖凝胶电泳检测产物，引物设计和 PCR 产物测序均由北京擎科生物科技有限公司完成。

#### 1.2.4 系统发育分析

使用 BioEdit v 7.0.5.3 检查原始序列，通过 SeqMan v. 7.0.0 (DNASTAR, Madison)拼接正向和反向序列后提交 GenBank (GenBank 登录号见表 1)，并在 NCBI 数据库中进行 BLAST，下载同源性 90%以上及文献中蜗孢属真菌的参考序列和合适的外群，利用 LSU、ITS、RPB2 和 TEF1α 的联合基因片段以最大似然法(ML)和贝叶斯法(BI)构建系统发育树(Huelsenbeck & Ronquist 2001；Nylander *et al*. 2008；Daniel *et al*. 2010；Miller *et al*. 2010；Stamatakis 2014)。多基因片段数据矩阵通过 MAFFT v.7.473 校准(Hall 1999；Katoh & Standley 2013)。数据的修整采用 trimal.v1.2rev59 软件进行。通过 IQ Tree v.2 软件基于贝叶斯信息准则(BIC)构建最大似然树(ML)。通过 MrMTgui 软件中的 ModelTest 选择

**表 1** 构建系统发育树的蜗孢属真菌及其 **GenBank** 登录号

Table 1 Taxa used in this study and their GenBank accession numbers for ITS, LSU, RPB2, and TEF1α DNA sequence data

| Taxa | Strain/Voucher No. | GenBank accession No. | | | |
|---|---|---|---|---|---|
| | | ITS | LSU | TEF1α | RPB2 |
| *Acanthohelicospora aurea* | GZCC 16-0060 | KY321323 | KY321326 | KY792600 | MF589911 |
| *Acanthohelicospora pinicola* | MFLUCC 10-0116 | KF301526 | KF301534 | KF301555 | – |
| ***Helicoma acropleurogenum*** | **GZCC 22-2035** | **OP806857** | **OP806854** | **OP821894** | **OP821897** |
| *Helicoma ambiens* | UAMH 10533 | AY916451 | AY856916 | – | – |
| *Helicoma ambiens* | UAMH 10534 | AY916450 | AY856869 | – | – |
| *Helicoma aquaticum* | MFLUCC 17-2025 | MH558713 | MH558841 | MH550904 | MH551030 |
| *Helicoma brunneisporum* | MFLUCC 17-1983 | MH558714 | MH558842 | MH550905 | MH551031 |
| *Helicoma dennisii* | NBRC 30667 | AY916455 | AY856897 | – | – |
| *Helicoma freycinetiae* | MFLUCC 16-0363 | MH275062 | MH260295 | MH412770 | – |
| *Helicoma fusiforme* | MFLUCC 17-1981 | MH558715 | – | MH550906 | – |
| *Helicoma guttulatum* | GZCC 22-2004 | OP508739 | OP508779 | OP698090 | OP698079 |
| *Helicoma guttulatum* | GZCC 22-2024 | OP508733 | OP508773 | OP698084 | OP698073 |
| *Helicoma guttulatum* | GZCC 22-2025 | OP508737 | OP508777 | OP698088 | OP698077 |
| *Helicoma guttulatum* | MFLUCC 16-0022 | KX454171 | KX454172 | MF535254 | – |
| *Helicoma guttulatum* | MFLUCC 21-0152 | OL545456 | OL606150 | OL964521 | OL964527 |
| *Helicoma wuzhishanense* | GZCC 22-2003 | OP508732 | OP508772 | OP698083 | OP698072 |
| *Helicoma hongkongense* | MFLUCC 17-2005 | MH558716 | MH558843 | MH550907 | MH551033 |
| *Helicoma hydei* | MFLUCC 18-1270 | MH747116 | MH747101 | MH747100 | – |
| *Helicoma inthanonense* | MFLUCC 11-0003 | JN865211 | JN865199 | – | – |
| *Helicoma khunkornensis* | MFLUCC 10-0119 | JN865203 | JN865191 | KF301559 | – |
| *Helicoma linderi* | NBRC 9207 | AY916454 | AY856895 | – | – |
| ***Helicoma liyui*** | **GZCC 22-2033** | **OP806858** | **OP806855** | **OP821895** | – |
| *Helicoma longisporum* | GZCC 22-2005 | OP508740 | OP508780 | OP698091 | OP698080 |
| *Helicoma longisporum* | GZCC 22-2026 | OP508738 | OP508778 | OP698089 | OP698078 |
| *Helicoma longisporum* | MFLUCC 16-0002 | MH558717 | MH558844 | MH550908 | MH551034 |
| *Helicoma longisporum* | MFLUCC 16-0005 | MH558718 | – | MH550909 | MH551035 |
| *Helicoma longisporum* | MFLUCC 16-0211 | MH558719 | MH558845 | MH550910 | MH551036 |
| *Helicoma longisporum* | MFLUCC 17-1997 | MH558720 | MH558846 | MH550911 | MH551037 |
| *Helicoma miscanthi* | MFLUCC 11-0375 | KF301525 | KF301533 | KF301554 | – |
| *Helicoma muelleri* | CBS 964.69 | AY916453 | AY856877 | – | – |
| *Helicoma muelleri* | UBC F13877 | AY916452 | AY856917 | – | – |
| *Helicoma multiseptatum* | GZCC 16-0080 | MH558721 | MH558847 | MH550912 | MH551038 |
| *Helicoma nematosporum* | MFLUCC 16-0011 | MH558722 | MH558848 | MH550913 | MH551039 |
| *Helicoma rubriappendiculatum* | MFLUCC 18-0491 | MH558723 | MH558849 | MH550914 | MH551040 |
| *Helicoma rufum* | MFLUCC 17-1806 | MH558724 | MH558850 | MH550915 | – |
| *Helicoma rugosum* | ANM 1169 | – | GQ850484 | – | – |
| *Helicoma rugosum* | ANM 196 | GQ856138 | GQ850482 | – | – |
| *Helicoma rugosum* | ANM 953 | GQ856139 | GQ850483 | – | – |
| ***Helicoma rugosum*** | **GZCC 22-2034** | **OP806859** | **OP806856** | **OP821896** | – |
| *Helicoma rugosum* | JCM 2739 | – | AY856888 | – | – |
| *Helicoma septoconstrictum* | MFLUCC 17-1991 | MH558725 | MH558851 | MH550916 | MH551041 |
| *Helicoma septoconstrictum* | MFLUCC 17-2001 | MH558726 | MH558852 | MH550917 | MH551042 |
| *Helicoma siamense* | MFLUCC 10-0120 | JN865204 | JN865192 | KF301558 | – |
| *Helicoma* sp. | HKUCC 9118 | – | AY849966 | – | – |
| *Helicoma tectonae* | MFLUCC 12-0563 | KU144928 | KU764713 | KU872751 | – |

新序列数据加粗显示. T：模式标本. –：GenBank 中无数据

New sequences are in bold. T represents the type specimen. – Means no data in GenBank.

最佳模型，并利用 MrBayes v.3.2.7a 构建贝叶斯树。系统发育树通过 FigTree v1.4.4 软件进行编辑。使用 Adobe PhotoShop 和 Adobe Illustrator 编辑系统发育树和物种的图版布局。

## 2 结果与分析

### 2.1 系统发育分析结果

构建系统发育树的序列矩阵由45个菌株序列组成，共包括3 437 bp，其中ITS长度为593 bp，LSU 长度为 887 bp，RPB2 长度为 1 045 bp，TEF1α 长度为 912 bp。外群为 *Acanthohelicospora aurea* (GZCC 16-0060)和 *A. pinicola* (MFLUCC10-0116)。通过 IQ-Tree v. 2 构建的最大似然树(图 2)显示，本研究报道的 GZCC 22-2034 菌株与 *H. rugosum* 分布在同一个分支，GZCC 22-2033 菌株与 *H. rugosum* 物种的亲缘关系最接近，而 GZCC 22-2035 菌株与海德蜗孢菌 *H. hydei* 形成姊妹分支。

### 2.2 形态学描述

**顶侧生蜗孢菌 新种 图 3**

***Helicoma acropleurogenum*** J. Ma, Y.Z. Lu & J.C. Kang, **sp. nov.** Fig. 3

**Index Fungorum: IF 900182**

Etymology: “acropleurogenum” refers to acropleurogenous helicoid conidia of this fungus.

Holotype: GZAAS 22–2035

Descriptions: Saprobic on decaying wood in a forest. Sexual morph: Undetermined. Asexual morph: Hyphomycetous, helicosporous. Colonies on natural substrate superficial, effuse, gregarious, brown. Mycelium partly immersed, partly superficial, composed of pale brown to brown, septate, branched hyphae, with a small number of glistening conidia. Conidiophores macronematous, mononematous, erect, straight or flexous, unbranched or branched, septate, cylindrical, 118–389 μm long, 5.5–8.5 μm wide ($\bar{x}$=219×6.5 μm, n=20), brown or dark brown at base, paler towards apex, smooth-walled. Conidiogenous cells mostly monoblastic, rarely polyblastic, integrated, mostly terminal, rarely intercalary, sympodial, cylindrical, 20–32 μm long, 5–8 μm wide ($\bar{x}$=25×6 μm, n=20), with denticles, pale brown, smooth-walled. Conidia solitary, acropleurogenous, helicoid, tapering towards flat end, rounded at tip, conicotruncate at base, septate, 21–24 μm diam. and conidial filament 8.5–10.5 μm wide ($\bar{x}$=22.0×9.5 μm, n=20), 48–58 μm long, tightly coiled 1½–1¾ times, 6–7-septate, guttulate, pale brown, smooth-walled.

Culture characteristics: Conidia germinating on water agar and germ tubes produced from conidia within 8 h. Colonies growing on PDA irregular, with rough surface, edge undulate, reaching 24 mm in 6 weeks at 25 °C, brown in PDA medium.

Material examined: CHINA, Hainan Province, Wuzhishan City, Shui Man Town, Wuzhishan National Nature Reserve, on decaying wood in a forest, 15 August 2021, Jian Ma, WZS32.1 (GZAAS 22-2035, holotype; HKAS 125909, isotype), ex-type living culture GZCC 22-2035.

Notes: The proposed new species, *viz*. *H. acropleurogenum*, is morphologically similar to *H. hydei* in conidia (Liu *et al*. 2019). However, its conidia are acropleurogenous while the latter are acrogenous (Liu *et al*. 2019). Some conidiophores of *H. acropleurogenum* are branched while *H. hydei* do not have this feature. Phylogenetically, *H. acropleurogenum* shares a sister relationship to *H. hydei* with high bootstrap support (Fig. 2). The phylogenetic analysis result showed that they are distinct species.

词源学：“*acropleurogenum*”特指该真菌的分生孢子着生方式为顶侧生。

主模式标本号：GZAAS 22-2035

描述：腐生于森林中的腐木上。有性型：未知。无性型：卷旋型丝孢菌。菌落疏展在自然基质表面上，由簇生的分生孢子梗，浅棕色的分生孢子组成。菌丝体部分埋生，部分表生，由分支、有隔、棕色的菌丝构成，有少量闪闪发光的分生孢子。分生孢子梗与营养菌丝异形，单独生长，直立，笔直或弯曲，分支或不分支，有隔，圆柱形，长 118–389 μm，宽 5.5–8.5 μm（$\bar{x}$=219×6.5 μm,

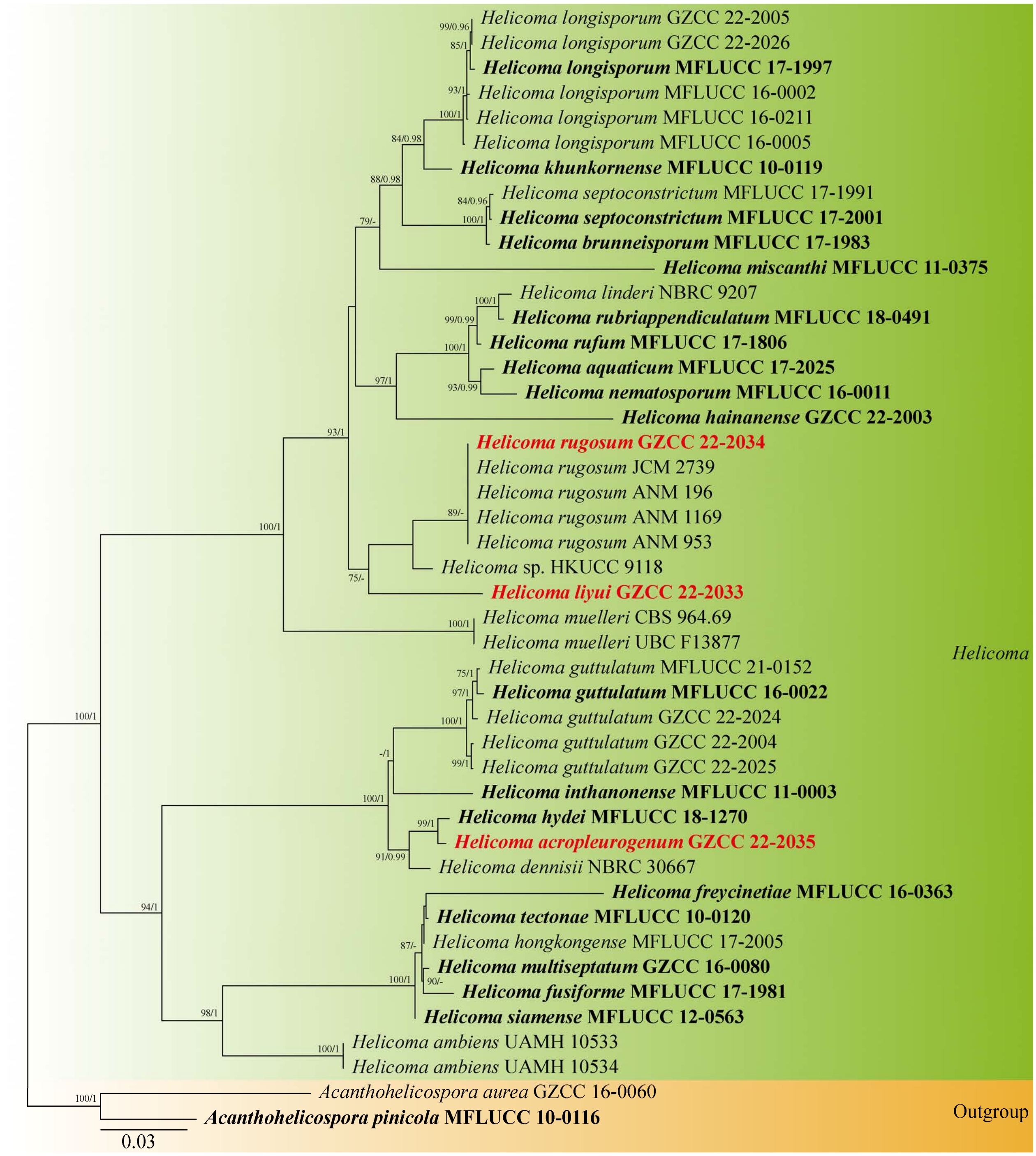

图 2 基于 ITS、LSU、RPB2 和 TEF1α 多基因片段构建的最大似然法系统发育树 ML 树的拓扑结构与贝叶斯分析结果相似，本图以 ML 拓扑结构展示. ML 自举值≥75%及贝叶斯后验概率≥0.95 (MLBP/BYPP)标注在节点位置. 模式菌株以粗体表示；本研究分离的菌株以红色加粗标注

Fig. 2 Phylogram generated from maximum likelihood analysis based on combined ITS, LSU, RPB2 and TEF1α sequence data. The tree topology of the maximum likelihood was similar to that of Bayesian and maximum parsimony analyses. ML bootstrap values ≥75% and Bayesian posterior probabilities ≥0.95 (MLBP/BYPP) are given above the nodes. Ex-type strains are indicated in bold; The strain isolated in this study is in red and bold.

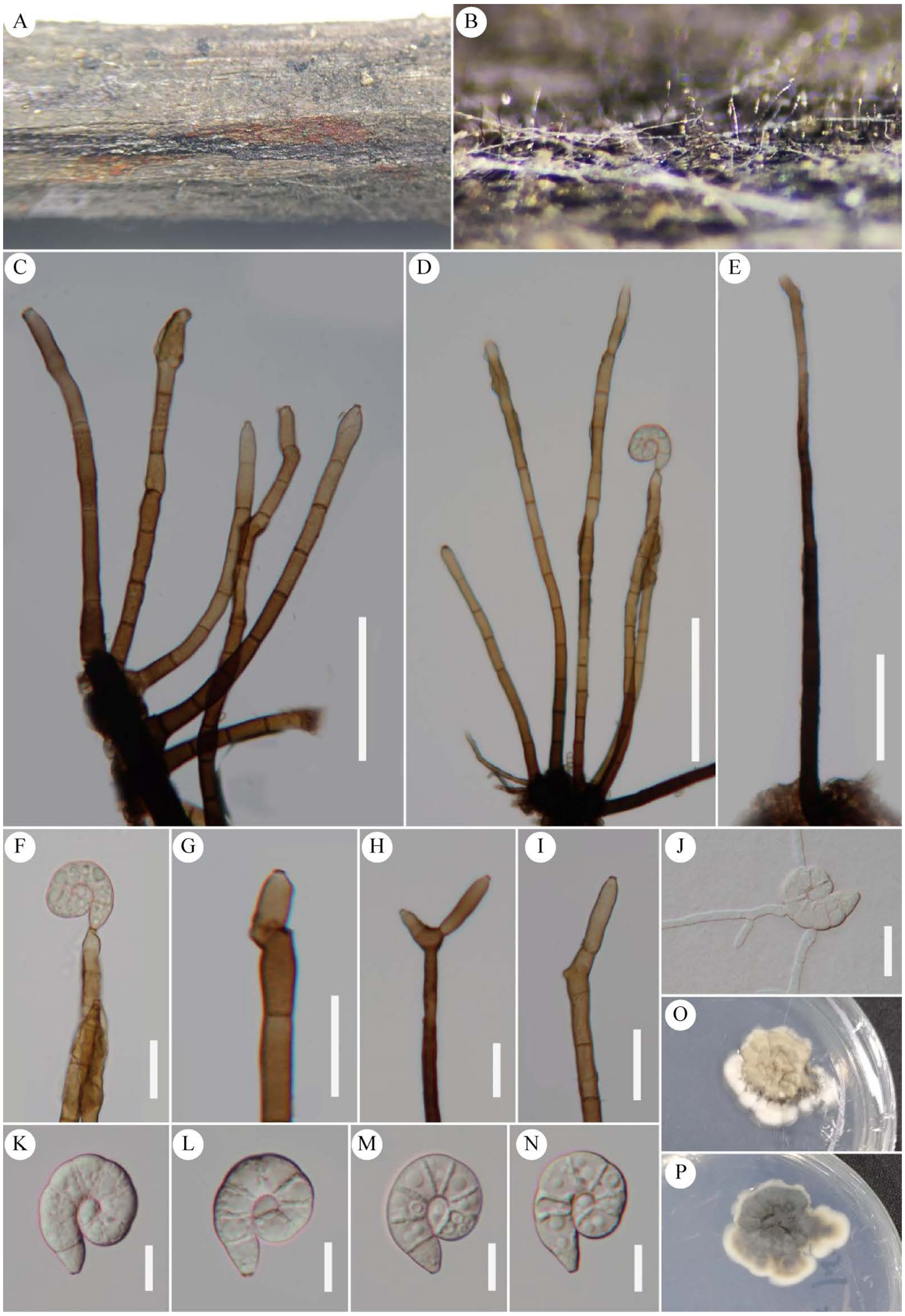

**图 3　顶侧生蜗孢菌(GZAAS 22-2035, holotype)**　A, B：自然基质上的菌落. C–E：分生孢子梗. F–I：产孢细胞. J：萌发的分生孢子. K–N：分生孢子. O, P：纯培养物正面和反面. 标尺：C–E=50 μm；F–J=20 μm；K–N=10 μm

Fig. 3　*Helicoma acropleurogenum* (GZAAS 22-2035, holotype). A, B: Colonies on natural substrate. C–E: Conidiophores. F–I: Conidiogenous cells. J: Germinated conidium. K–N: Conidium. O: Colonies on PDA from obverse. P: Colonies on PDA from reverse. Scale bars: C–E=50 μm; F–J=20 μm; K–N=10 μm.

n=20)，下部浅棕色至深棕色，顶端颜色逐渐变浅，表面光滑。产孢细胞大多数为单芽殖型，少许为多芽殖型，与分生孢子梗整合，多数顶生，少许间生，合轴，圆柱形，长 20–32 μm，宽 5–8 μm ($\bar{x}$=25×6 μm, n=20)，有齿状突起物，浅棕色，表面光滑。分生孢子顶侧生，单生，螺旋状，两端渐缩，顶端圆形，基部圆锥形，直径 21–24 μm，宽 8.5–10.5 μm ($\bar{x}$=22.0×9.5 μm, n=20)，长 48–58 μm，紧密卷旋 1½–1¾圈，具 6–7 个分隔，有液滴状内含物，浅棕色，表面光滑。

培养物特征：分生孢子在 WA 培养基上 8 h 后萌发，无色透明的芽管从孢子纤维丝四周萌发，无菌操作转接到新配置的 PDA 培养基中，25 ℃暗培养 6 周后直径达到 24 mm，菌落不规则，表面粗糙，边缘波浪形，浅棕色。

标本信息：采集地点：中国海南省五指山市水满乡，五指山国家自然保护区，标本生于森林中掉落在地表的腐木。采集时间：2021 年 8 月 15 日。采集人：马建。标本原始编号 WZS32.1 (主模式：GZAAS 22-2035；等模式：HKAS 125909；菌株号：GZCC 22-2035)。

讨论：新种顶侧生蜗孢菌 *H. acropleurogenum* 在分生孢子形态上与海德蜗孢菌 *H. hydei* 相似 (Liu *et al.* 2019)，但两者分生孢子梗及分生孢子着生方式不同。顶侧生蜗孢菌的分生孢子梗部分具分支、分生孢子顶侧生，海德蜗孢菌的分生孢子梗不分支、分生孢子顶生(Liu *et al.* 2019)。在系统发育树上，顶侧生蜗孢菌与海德蜗孢菌呈姊妹分支，且具有明显的支长区别及极高的支持率(图 2)，系统发育分析结果支持它们是不同的物种。

### 李玉蜗孢菌　新种　图 4

***Helicoma liyui*** J. Ma, Y.Z. Lu & J.C. Kang, **sp. nov.**　Fig. 4

**Index Fungorum: IF 900065**

Etymology: “*liyui*”, named in honour of academician LI Yu for his contributions to mycology.

Holotype: GZAAS 22–2033

Descriptions: Saprobic on moist decaying wood. Sexual morph: undetermined. Asexual morph: Hyphomycetous, helicosporous. Colonies on the substratum superficial, gregarious, pale brown. Mycelium partly immersed, partly superficial, composed of branched, septate, branched hyphae, pale brown to brown, with masses of crowded, glistening conidia. Conidiophores macronematous, mononematous, erect, flexuous or straight, branched or unbranched, septate, cylindrical, 103–200×7–11 μm ($\bar{x}$=144×9 μm, n=25), pale brown to brown, smooth-walled. Conidiogenous cells holoblastic, mono- to polyblastic, integrated, intercalary, sympodial, cylindrical, 9–17×7–11 μm ($\bar{x}$=13×9 μm, n=30), with denticles, arising laterally from conidiophores as tooth-like protrusions (3–7 μm long, 2–3 μm wide), hyaline to pale brown, smooth-walled. Conidia pleurogenous, solitary, helicoid, rounded at tip, 60–94 μm diam., and conidial filament 5–9 μm wide ($\bar{x}$=75×7 μm, n=30), 276–395 μm long, coiled $2^{1}/_{3}$–$3^{1}/_{3}$ times, becoming loosely coiled or uncoiled in water, indistinctly multi-septate, guttulate, pale brown, smooth-walled.

Culture characteristics: Conidia germinating on water agar and germ tubes produced from conidia within 8 h. Colonies growing on PDA circular, with flat surface, edge entire, reaching 34 mm in 4 weeks at 25 °C, pale brown in the center and brown at the edge in PDA medium.

Material examined: CHINA, Hainan Province, Qiongzhong Li and Miao Autonomous County, Baihualing Tropical Rainforest Cultural Tourism Zone, on moist decaying wood, 29 December 2021, Jian Ma, BH34.2 (GZAAS 22-2033, holotype; HKAS 125877, isotype), ex-type living culture, GZCC 22-2033.

Notes: The proposed new species, *Helicoma liyui*, is morphologically similar to *H. longisporum* and *H. septoconstrictum* in having branched conidiophores with helicoid conidia. However, it can be distinguished from *H. longisporum* by its narrower and shorter conidial filaments (5–9 μm wide, 276–395 μm long vs. 8–11 μm wide, 620–770 μm long), and from *H. septoconstrictum*

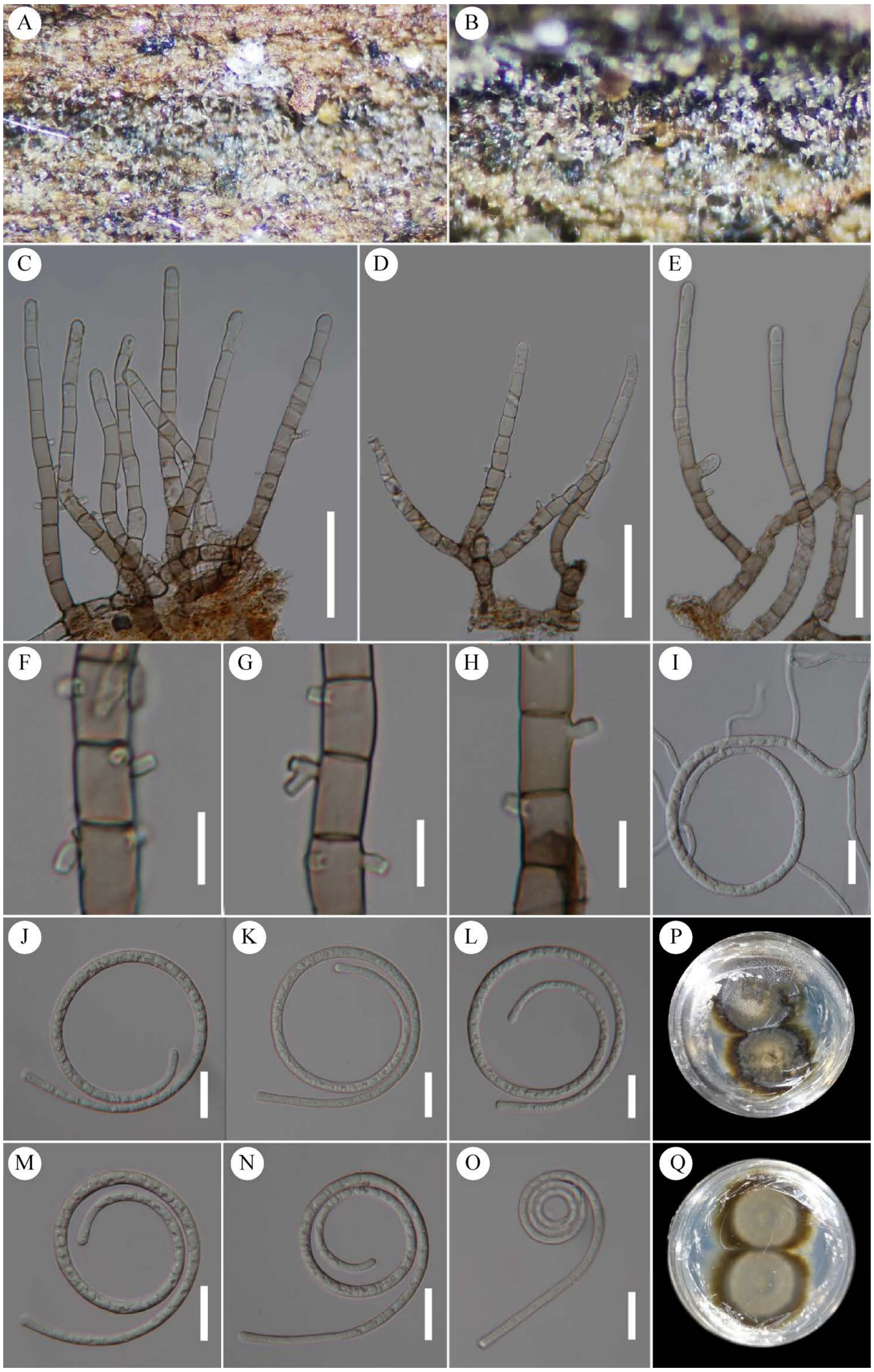

**图 4 李玉蜗孢菌 (GZAAS 22-2033, holotype)** A, B：自然基质上的菌落. C–E：分生孢子梗. F–H：产孢细胞. I：萌发的分生孢子. J–O：分生孢子. P, Q：纯培养物正面和反面. 标尺：C–E=50 μm；F–H=10 μm；I–O=20 μm

Fig. 4 *Helicoma liyui* (GZAAS 22-2033, holotype). A, B: Colonies on natural substrate. C–E: Conidiophores. F–H: Conidiogenous cells. I: Germinated conidium. J–O: Conidium. P: Colonies on PDA from obverse. Q: Colonies on PDA from reverse. Scale bars: C–E=50 μm; F–H=10 μm; I–O=20 μm.

by its smaller conidia (60–94 μm diam., 5–9 μm wide, 276–395 μm long vs. 85–140 μm diam., 8–12 μm wide, 730–840 μm long) (Lu *et al*. 2018b). Phylogenetically, *Helicoma liyui* is distinct from *H. longisporum* and *H. septoconstrictum*, while sharing a sister relationship to *H. rugosum* (Fig. 2). The multigene phylogenetic tree conclusively demonstrates that they are separate species.

词源学：“*liyui*”是为纪念李玉院士对真菌学做出的突出贡献而命名。

主模式标本号: GZAAS 22-2033

描述：腐生于潮湿的腐木上。有性型：未知。无性型：卷旋型丝孢菌。菌落疏展在自然基质表面上，由簇生的分生孢子梗，浅棕色的分生孢子组成。菌丝体部分埋生，部分表生，由分枝、有隔、浅棕色的菌丝构成，有大量拥挤，闪闪发光的分生孢子。分生孢子梗与营养菌丝异形，单独生长，直立，笔直或弯曲，分枝或不分枝，有隔，圆柱形，长 103–200 μm，宽 7–11 μm ($\overline{x}$=144×9 μm, n=25)，浅棕色到棕色，表面光滑。产胞细胞单芽殖型或多芽殖型，与分生孢子梗整合，间生，合轴，圆柱形，长 9–17 μm，宽 7–11 μm ($\overline{x}$=13×9 μm, n=30)，有齿状突起物，长 3–7 μm，宽 2–3 μm，近透明至浅棕色，表面光滑。分生孢子侧生，单生，螺旋状，尖端圆形，直径 60–94 μm，宽 5–9 μm ($\overline{x}$=75×7 μm, n=30)，长 276–395 μm，卷旋 $2^1/_3$–$3^1/_3$ 圈，在水中容易松散开，变成松散的卷旋状，具不明显的隔膜，有液滴状内含物，浅棕色，表面光滑。

培养物特征：分生孢子在 WA 培养基上 8 h 后萌发，无色透明的芽管从孢子纤维丝四周萌发，无菌操作转接到新配置的 PDA 培养基中，25 ℃暗培养 4 周后直径达到 34 mm，圆形，表面平整，边缘整齐，菌落中心呈浅棕色，边缘棕色。

标本信息：采集地点：中国海南省琼中黎族苗族自治县百花岭热带雨林文化旅游区，标本生于林中掉落在地表的腐木。采集时间：2021 年 12 月 29 日。采集人：马建。标本原始编号 BH34.2 (主模式：GZAAS 22-2033；等模式：HKAS 125877；菌株号：GZCC 22-2033)。

讨论：李玉蜗孢菌与 *H. longisporum* 和 *H. septoconstrictum* 在形态上相似，三者都具备直立或弯曲，有分支或不分支的分生孢子梗和卷旋型分生孢子，但分生孢子的大小不同。李玉蜗孢菌的分生孢子丝比 *H. longisporum* 的狭窄和短小(60–94 μm diam., 5–9 μm wide, 276–395 μm long vs. 8–11 μm wide, 620–770 μm long)，也明显小于 *H. septoconstrictum* (85–140 μm diam., 8–12 μm wide, 730–840 μm long) (Lu *et al*. 2018b)。在系统发育分析方面，李玉蜗孢菌与 *H. longisporum* 和 *H. septoconstrictum* 的进化关系较远，而与 *H. rugosum* 的亲缘关系较近(图 2)，但李玉蜗孢菌的分生孢子明显大于 *H. rugosum* (17–28 μm diam., 4–5 μm wide) (Boonmee *et al*. 2014)。多基因系统发育分析树支持它们是蜗孢属真菌类群中的不同物种。

### 皱壁蜗孢菌 新记录 图 5

***Helicoma rugosum*** (C. Booth) Boonmee & K.D. Hyde [as ‘rugosa’], Fungal Diversity 68: 266 (2014) Fig. 5

**Index Fungorum: IF 821048**

Descriptions: Saprobic on decaying wood in a freshwater stream. Sexual morph: See Boonmee *et al*. (2014). Asexual morph: Hyphomycetous, helicosporous. Colonies on the substratum superficial, gregarious, subhyaline to pale brown. Mycelium partly immersed, partly superficial, composed of branched, septate, branched hyphae, pale brown to brown, with masses of crowded, glistening conidia. Conidiophores macronematous, mononematous, flexuous or straight, unbranched, septate, cylindrical, 145–252×6–10 μm ($\overline{x}$=192×8 μm, n=25), pale brown to brown, smooth-walled. Conidiogenous cells holoblastic, mono- to polyblastic, integrated, intercalary, sympodial, cylindrical, 11–16×5–7 μm ($\overline{x}$=14×6 μm, n=30), with denticles, arising laterally from conidiophores as tooth-like protrusions (3–5 μm long, 2–3 μm

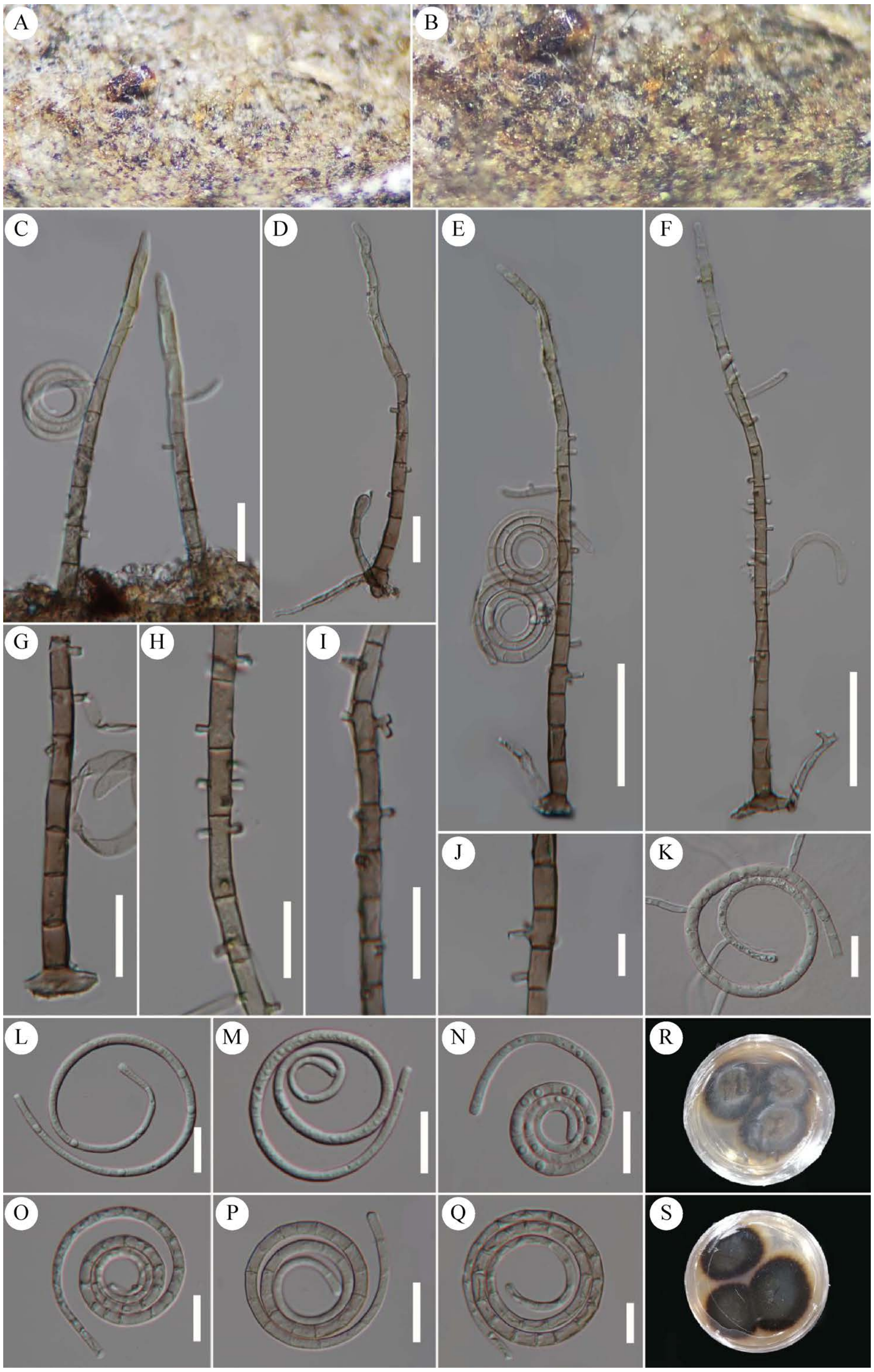

**图 5 *Helicoma rugosum* (GZAAS 22–2034)** A, B：自然基质上的菌落. C–F：分生孢子梗. G–J：产胞细胞. K：萌发的分生孢子. L–Q：分生孢子. R, S：纯培养物正面和反面. 标尺：C, D, G–Q=20 μm；E, F=50 μm

Fig. 5 *Helicoma rugosum* (GZAAS 22–2034). A, B: Colonies on natural substrate. C–F: Conidiophores. G–J: Conidiogenous cells. K: Germinated conidium. L–Q: Conidium. R, S: Colonies on PDA from obverse and reverse. Scale bars: C, D, G–Q=20 μm; E–F=50 μm.

wide), hyaline to pale brown, smooth-walled. Conidia pleurogenous, solitary, helicoid, rounded at tip, 41–50 μm diam., and conidial filament 4–6 μm wide ($\bar{x}$=46×5 μm, n=30), 258–393 μm long, coiled 3–$3^{1}/_{3}$ times, becoming loosely coiled in water, indistinctly multi-septate, pale brown, smooth-walled.

Culture characteristics: Conidia germinating on water agar and germ tubes produced from conidia within 8 h. Colonies growing on PDA circular, with flat surface, edge entire, reaching 48 mm in 5 weeks at 25 °C, brown in PDA medium. Mycelium superficial and partially immersed, branched, septate, hyaline to pale brown, smooth.

Material examined: CHINA, Hainan Province, Lingshui Lizu Autonomous County, Diaoluoshan National Nature Reserve, 18°43′ N, 109°43′ E, on decaying wood in a freshwater stream, 24 August 2021, Jian Ma, DL26.2 (GZAAS 22-2034), living culture GZCC 22-2034.

Notes: *H. rugosum* was introduced by Boonmee *et al*. (2014) based on phylogenetic and morphological evidence. In this study, a new colletion is identified as *H. rugosum* based on phylogenetic analysis. It is the first record of *H. rugosum* from China and its asexual morph found from natural woody substrate.

描述：腐生于淡水溪流中的腐木上。有性型：见 Boonmee *et al*. (2014)。无性型：卷旋型丝孢菌。菌落疏展在自然基质表面上，由簇生的分生孢子梗，浅棕色的分生孢子组成。菌丝体部分埋生，部分表生，由分支、有隔、浅棕色的菌丝构成，有大量拥挤，闪闪发光的分生孢子。分生孢子梗与营养菌丝异形，单独生长，直立，笔直或弯曲，不分支，有隔，圆柱形，长 145–252 μm，宽 6–10 μm ($\bar{x}$=192×8 μm, n=25)，浅棕色到棕色，表面光滑。产胞细胞单芽殖型或多芽殖型，与分生孢子梗整合，间生，合轴，圆柱形，长 11–16 μm，宽 5–7 μm ($\bar{x}$=14×6 μm, n=30)，有齿状突起物，长 3–5 μm，宽 2–3 μm，近透明至浅棕色，表面光滑。分生孢子侧生，单生，螺旋状，尖端圆形，直径 41–50 μm，宽 4–6 μm ($\bar{x}$=46×5 μm, n=30)，长 258–393 μm，卷旋 3–$3^{1}/_{3}$ 圈，在水中容易松散开，变成松散的卷旋状，具不明显的隔膜，部分有液滴状内含物，浅棕色，表面光滑。

培养物特征：分生孢子在 WA 培养基上 8 h 后萌发，无色透明的芽管从孢子纤维丝四周萌发，无菌操作转接到新配置的 PDA 培养基中，25 ℃暗培养 5 周后直径达到 48 mm，圆形，表面平整，边缘整齐，菌落中心呈棕色，边缘浅棕色。

标本信息：采集地点：中国海南省陵水黎族自治县吊罗山国家级自然保护区，标本生于小溪流中浸没的腐木。采集时间：2021 年 8 月 24 日。采集人：马建。标本原始编号 DL26.2 (GZAAS 22-2034；菌株号：GZCC 22-2034)。

讨论：皱壁蜗孢菌是由 Boonmee *et al*. (2014)根据形态特征和系统发育分析证据建立的物种，并报道了它的有性型及其纯培养物产生的无性型形态特征。基于系统发育结果，本研究将新采集的标本 GZAAS 22-2034 鉴定为皱壁蜗孢菌。该物种为中国新记录种，其无性型形态为首次从天然木质基质中被发现。

## 3 讨论

本研究通过形态学结合多基因系统发育分析，确定了 3 株分离自中国海南省的卷旋型丝孢菌的分类地位为蜗孢属真菌，包括 2 个新物种和 1 个中国新记录，为纪念李玉院士对菌物事业发展做出的突出贡献，特将其中一个新物种命名为李玉蜗孢菌。

蜗孢属、卷丝孢属 *Helicomyces* 和旋卷孢属 *Helicosporium* 是最典型的卷旋型丝孢真菌。这类真菌最独特的形态特征是其分生孢子丝在一个二维平面或三维空间卷旋至少 180°以上(Goos 1986；Zhao *et al*. 2007；Lu *et al*. 2018b)。由于形态相似，容易混淆，很多物种缺少 DNA 分子数据，加之缺乏统一且普遍认可的分类鉴定标

准，导致该类群的分类系统一直比较混乱，存在很多不准确鉴定及隐存物种(Lu *et al*. 2018b)。本课题组近年来一直在开展卷旋型丝孢真菌的分类研究，大量数据表明，该类群物种分生孢子的形态特征虽然具有一定的相似性，但是各属之间存在明显的个性特征。蜗孢属和旋卷孢属真菌的分生孢子梗较发达，但蜗孢属真菌在天然腐木基质上的菌落为浅棕色，分生孢子梗较粗壮，而旋卷孢属真菌在天然腐木基质上的菌落为黄绿色，其分生孢子梗呈刚毛状，较细长。此外，它们的分生孢子形态差异明显，蜗孢属真菌的分生孢子呈蜗牛状或孢子丝为 4–14 μm 的卷旋状，而后者的分生孢子丝小于 3 μm，通常为 1–2 μm。卷丝孢属真菌在天然腐木基质上菌落为白色近透明，分生孢子梗不发达，长度较短，且产孢细胞顶端呈截面状，无齿状突起物(Lu *et al*. 2018b)。在属内种间，存在形态特征极其相似但 DNA 分子数据差距较大的情况，如本文新种李玉蜗孢菌与 *H. longisporum* 和 *H. septoconstrictum* 在形态上非常相似，仅分生孢子大小存在差异，但系统发育树中新种与已知种亲缘关系较远，可以证明是两个不同的物种。同样在 *Neohelicosporium* 属中，*N. hyalosporum* 与 *N. parvisporum* 在分生孢子和分生孢子梗的形态上也具有较高的相似度，仅能根据分生孢子的大小进行区分，但系统发育分析表明它们是不同物种(Lu *et al*. 2018a, 2018b)。显然，卷旋型丝孢真菌各物种的准确鉴定需要依赖系统发育分析证据。近年来我国对包括海南省在内的热带地区腐生木生真菌进行了比较深入的研究，发现了大量的新分类单元(李玉等 2016；吴芳等 2020；戴玉成等 2021；马海霞等 2022)，但是上述研究基本都是大型腐生木生菌，而目前对小型腐生木生菌的研究还很薄弱。本研究所报道的海南省蜗孢属 2 个新种和 1 个中国新记录，是对我国热带地区小型腐生木生菌的补充，也说明我国热带地区小型腐生木生菌的多样性还有待提高。

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