

Liu, Guo, Yu & Zang, and *Hirsutella* ant pathogen clades.

A series of surveys were conducted to reveal the species diversity of entomopathogenic fungi in Kunming, Yunnan Province, China [16–20]. To be specific, the richness of cordycipitoid fungi was found to be relatively higher in Kunming Wild Duck Lake Forest Park. On the whole, 41 species were found here (with 20 species proposed as new species), belonging to eight genera of three families (i.e., Clavicipitaceae, Cordycipitaceae and Ophiocordycipitaceae), which are *Flavocillium*, *Cordyceps*, *Beauveria*, *Samsoniella*, *Simplicillium*, *Ophiocordyceps*, *Polycephalomyces*, and *Metarhizium*. Among these species, a fungus attacking caterpillar was determined as a novel taxon of *Ophiocordyceps* by conducting the analyses of both morphology and molecular phylogeny. This study attempts to introduce the new species and investigate its biological and phylogenetic status.

2. Materials and methods

2.1. Specimen collection and strain isolation

In the present study, a specimen of the novel species was collected from the Kunming Wild Duck Lake Forest Park, Yunnan Province, China, in August 2018. The isolate was obtained with the methods presented by Wang et al. [18]. The specimen was deposited in Yunnan Herbal Herbarium (YHH), Yunnan University. The cultures were deposited at Yunnan Fungal Culture Collection (YFCC), Yunnan University. To describe the new species, the macro- and micromorphological characteristics were observed by complying with Wang et al. [20].

2.2. Morphological observations

The sample was photographed with a digital camera and Olympus SZ61 (Tokyo, Japan) stereomicroscope. Subsequently, the macromorphological characteristics were recorded (e.g., texture, shape, color, length, diameter of the stroma and color, shape, length, diameter of the fertile head, and host type). Furthermore, Olympus CX40 (Tokyo, Japan) and BX53 (Tokyo, Japan) microscopes were employed to observe the micromorphological characteristics of perithecia, asci, ascospores and ascospores. Next, the morphology of cultures was characterized by using the method presented by Wang et al. [16].

2.3. DNA extraction, PCR, and sequencing

The total genomic DNAs were extracted by employing the CTAB method of Liu et al. [21]. Five nuclear gene regions were amplified and sequenced,

i.e., the small subunit of ribosomal DNA (nrSSU), the large subunit of ribosomal DNA (nrLSU), translation extension factor 1-gene (tef-1 α), the largest subunit of RNA polymerase II (rpb1), as well as the second largest subunit of RNA polymerase II (rpb2) [5,22,23]. Polymerase chain reaction (PCR) was performed by adopting the method presented by Wang et al. [20]. Moreover, amplifications were conducted in 25 μ L, and PCR conditions were referenced from Sung et al. [5]. Furthermore, PCR products were sequenced by the Beijing Genomics Institute (Shenzhen, China).

2.4. Phylogenetic analyses

Five-gene sequences (i.e., nrSSU, nrLSU, tef-1 α , rpb1, and rpb2) of taxa pertaining to *Hirsutella*, *Ophiocordyceps*, and *Polycephalomyces* were downloaded from GenBank, and combined with those generated in here. Table 1 lists the specimen accession information and GenBank numbers of the five loci. Sequences were aligned by employing the programs Clustal X2.0 and MEGA5 [24]. Phylogenetic analyses were conducted with Bayesian inference (BI) and maximum-likelihood (ML) methods with the use of the programs MrBayes v.3.1.2 and RaxML7.0.3 [25,26], respectively. In addition, the BI analysis was conducted on MrBayes v.3.1.2 for five million generations with the GTR + G + I model, as determined by jModelTest version 2.1.4 [27]. Specific to the ML analysis based on RaxML7.0.3, GTR + I acted as the optimal model, and 500 fast bootstrap replications were conducted on the five-locus dataset. Trees were sampled every 100 generations. The first 25% trees were discarded as burn-in and the remaining trees were used to create a consensus tree using the sumt demand.

3. Results

3.1. Phylogenetic analyses

In ML and BI phylogenetic analyses, five-gene sequences of eighty taxa from *Hirsutella*, *Ophiocordyceps*, and the outgroup taxa *Cordyceps tenuipes* (Peck) Kepler, B. Shrestha & Spatafora and *C. militaris* (L.) Fr. were retrieved from GenBank, which were combined with those generated in the present study. The combined dataset consisted of 4082 bp (i.e., 794 bp for tef-1 α , 859 bp for nrLSU, 999 bp for nrSSU, 543 bp for rpb1, as well as 887 bp for rpb2). Phylogenetic trees analyzed by ML and BI exhibited the nearly identical overall topologies (Figure 1). The mentioned results shared similar phylogenetic structures with existing analyses [14,15,18,19]. The phylogenetic trees recognized four statistically well-supported clades in

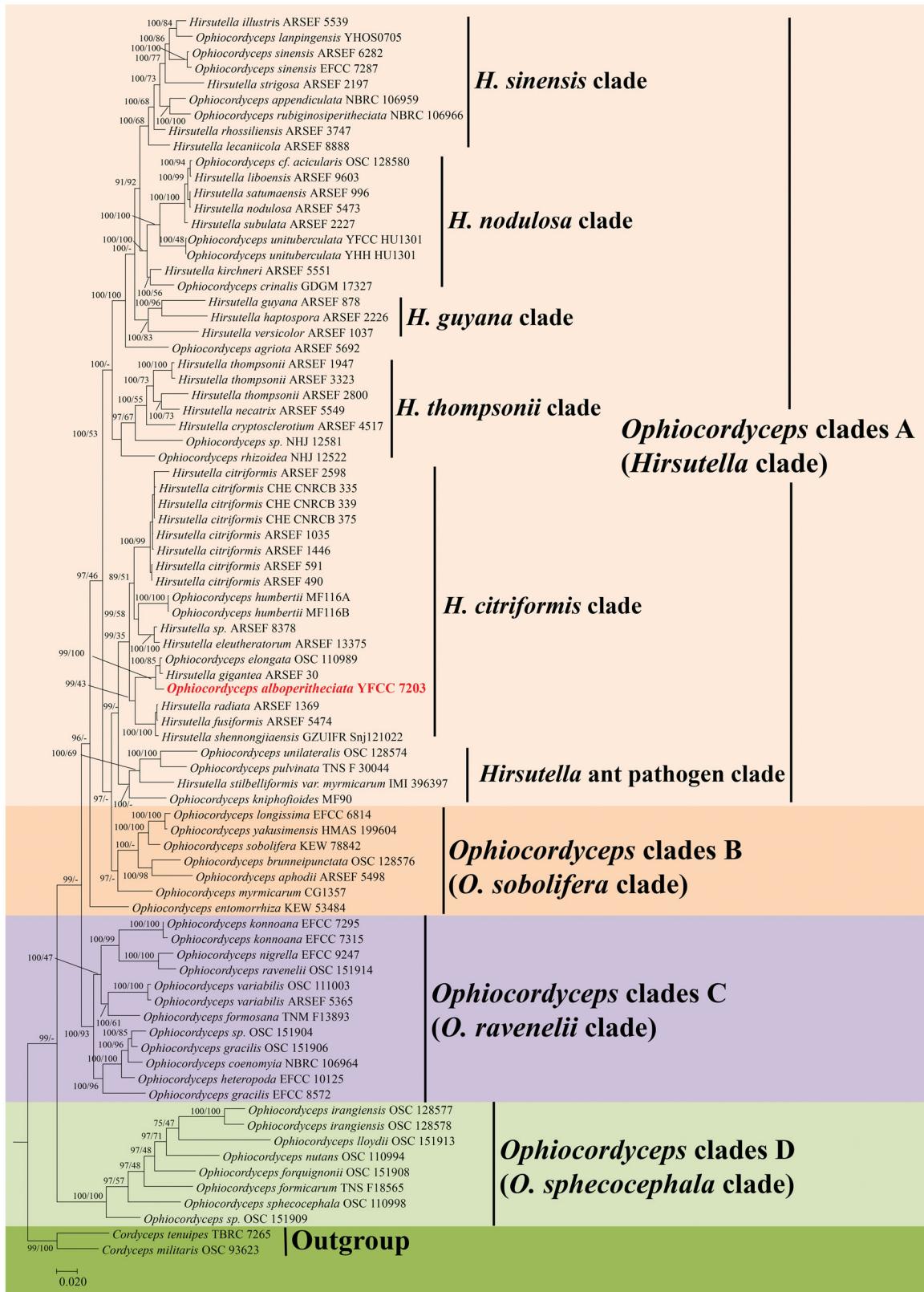


Figure 1. Phylogenetic placement of *Ophiocordyceps alboperithecata* inferred from BI and ML analyses based on five-gene (nrSSU, nrLSU, tef-1 α , rpb1, and rpb2) sequence dataset. Values at the nodes before and after the backslash are BI posterior probabilities and ML bootstrap proportions, respectively. Support values of ML bootstrap proportions greater than 40% are indicated at the nodes.

clustered together and linked to Lepidoptera, other six species displayed the respective association with Hymenoptera, Hemiptera, Diptera, Orthoptera, Dermaptera, and Anoplura.

The family Ophiocordycitaceae was proposed according to the type genus *Ophiocordyceps* with the sexual morph characterized by the production of whole septate ascospores, which usually did not

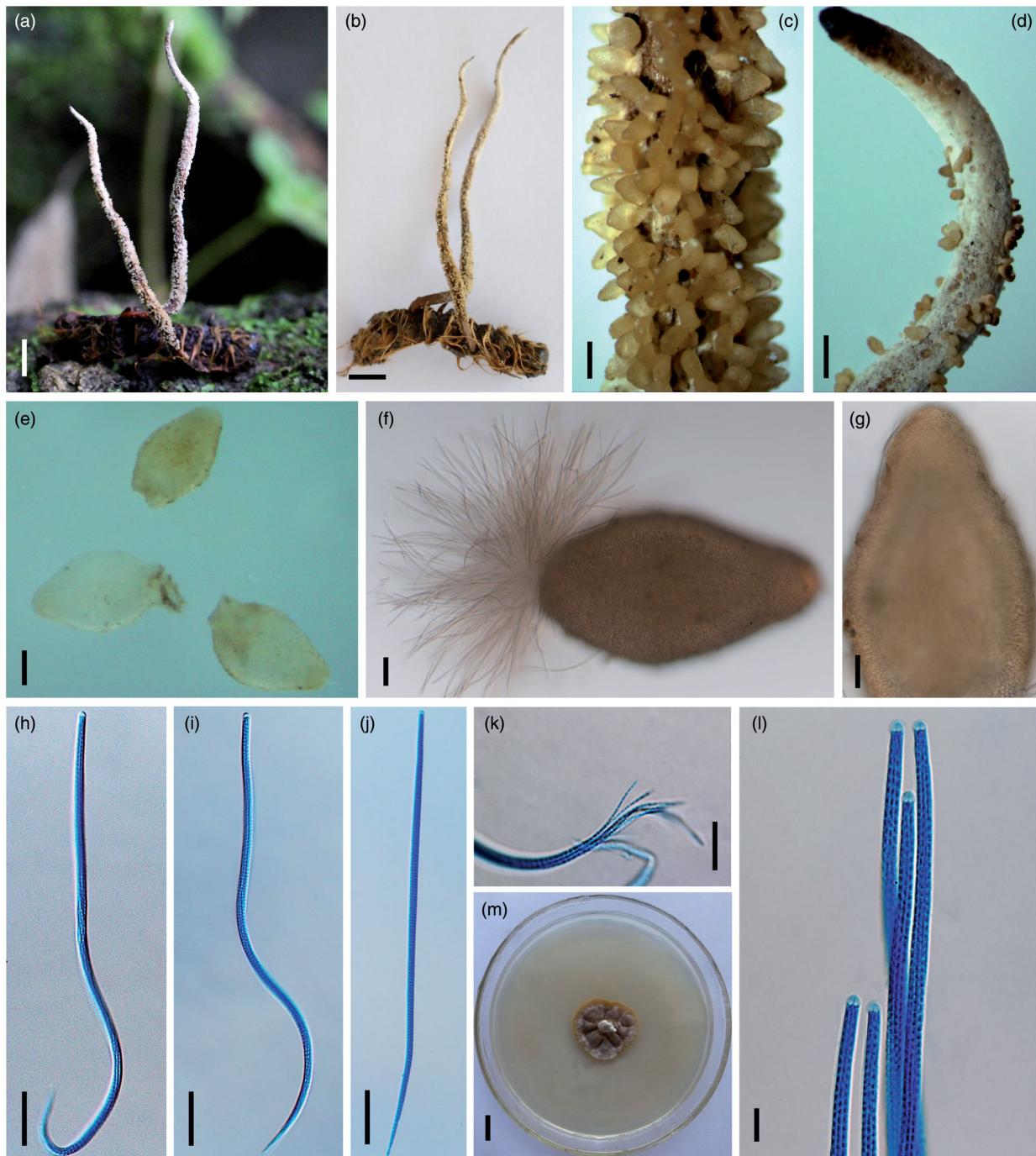


Figure 2. Morphological characteristics of *Ophiocordyceps alboperitheciata*. (a, b) Stromata on a larva of Noctuidae; (c) Fertile part; (d) Sterile tip; (e-g) Perithecia; (h-j, l) Ascospores; (k) Ascospores; (m) Colony on PDA. Scale bars: a, b = 1 cm; c = 600 µm; d = 1 mm; e-f = 100 µm; g-j = 50 µm; k, l = 20 µm; m = 1 cm.

disarticulate into part-spores at maturity, and ascospores had an apical hemispheric cap. The *Hirsutella*, as the old asexual generic name associated with the *Ophiocordyceps*, is synonymized under *Ophiocordyceps*, most species occurring from adult insects are formerly employed in the *Ophiocordyceps* clade A [1,3,5]. Phylogenetic studies of *Hirsutella* species from the USA were conducted by three loci providing evidence for taxonomic revisions under novel rules [14,15]. The available molecular data have facilitated the use of the mentioned fungi and associated data to conduct in-depth phylogenetic classification studies on *Hirsutella*

and *Ophiocordyceps*. The phylogenetic tree of *Hirsutella* and *Ophiocordyceps* of this study complies with the existing studies of Ophiocordycipitaceae [5,10,14,15]. The genus *Ophiocordyceps* with *Hirsutella* morph comprises six distinct groups, i.e., *H. citriforis*, *H. thompsoni*, *H. nodulosa*, *H. guyana*, *H. sinensis*, and *Hirsutella* ant pathogen clades. The insect pathogen *O. alboperitheciata* pertains to the *H. citriforis* clade, which is obviously separated from other allied species.

The present phylogenetic tree covers nine species cluster in the *H. citriforis* clade. Our result is

Table 2. A morphological comparison of *Ophiocordyceps alboperithecata* and its related species.

Species	Host	Habitat	Synnemata/stromata	Perithecia	Asci	Ascospores	Conidiogenous cells	Conidia	References
<i>O. alboperithecata</i>	Larva of Noctuidae (Lepidoptera)	Buried in fallen leaves	Stromata in pairs, rigid, the stalk is smooth, unbranched, long 54–65 mm, light brown to dark brown, with a clavate fertile part, white to light brown, 4.1–4.5 × 0.8–1.4 mm, and a sterile tip.	Perithecia superficial, scattered or crowded, size 0.41–0.55 × 0.23–0.32 mm, nearly ovoid, white nearly light brown.	Asci hyaline, cylindrical, 8-spores, 144–246 × 3.5–4.7 µm, with a hemispherical apical cap, 3.2–4.2 × 2.3–2.5 µm.	Ascospores hyaline, cylindric, multiseptate, 0.5–0.6 µm diameter, with septa 1.1–1.3 µm apart. Part-spores were not seen.	Undetermined	Undetermined	This study
<i>O. elongata</i>	Pupae and larvae of <i>Apateia americana</i> (Lepidoptera).	Unknown	The stalk is flexuose, longitudinally sulcate and twisted, 110 mm long, pale brown.	The perithecia are immersed, scattered or crowded, ovato-conoid, size 0.5 × 0.3 mm, apex subacute, wall yellow by transmitted light.	The asci are 220 µm long, 8 µm diameter.	Ascospores cylindric, 2 µm diameter, with septa 4–12 µm apart. Part-spores were not seen.	Unknown	Unknown	[28]
<i>O. humbertii</i>	Hymenoptera	Unknown	Several, 7 mm long, dark brown, with an oval swelling, 1 × 0.4 mm.	Perithecia, scattered, dark amber, subtranslucent, flask-shaped with a truncate apex, 275 × 120 µm.	The asci are 130 µm long, 10 µm diameter, capitate, fusoid or narrow-fusoid, septate at intervals of 6–16 µm, not dividing into part-spores.	Ascospores are 75 µm long, 25 µm diameter, narrow-fusoid, septate at intervals of 6–16 µm, not dividing into part-spores.	None	Unknown	[29]
<i>H. gigantea</i>	Pupae and larvae of <i>Apateia Americana</i> (Lepidoptera)	On wood	Branched, longitudinally sulcate, glabrous, ashy and minutely setose above, size 40 × 0.6 mm, brown below.	Branched, longitudinally sulcate, glabrous, ashy and minutely setose above, size 40 × 0.6 mm, brown below.	None	None	Phialides up to 40 µm high, with a flask-shaped base, 16–20 × 8–9 µm, and a long, stout sterigma, 1 µm diameter.	The spore cluster is lemon-shaped, 10 × 6 µm, becoming globose, 10 µm diameter, and the separate conidia are broadly cymbiform with obtuse tips,	[28]
<i>H. citriniformis</i>	Adult of Fulgoridae (Hemiptera)	Unknown	Synnemata usually long, flexible, simple or branched, branches often short and easily detached, brown in color	Synnemata usually long, flexible, simple or branched, branches often short and easily detached, brown in color	None	None	Sporophores simple, sessile or subsessile, with rather short, delicate sterigmate 20–30 µm	9–10 × 3–4 µm Spores fusoid, hyaline, 5.5–8.5 × 1.5–18 µm	[13]
<i>H. radiata</i>	Fly (Diptera)	Unknown	Rigid, branched, size 18–19 mm, dark brown or rufous brown, cinereous toward the tips, with a matt surface	Rigid, branched, size 18–19 mm, dark brown or rufous brown, cinereous toward the tips, with a matt surface	None	None	The phialides have a conical base, 5–8 × 3–4 µm, merging into a stout sterigma, 9–14 µm long, or a cylindrical base, 6–18 × 2 µm, with a sterigma 6 µm long	The spore cluster is oval, 9–11 × 6–7 µm, and the individual conidia are cymbiform, 6–9 × 2–2.5 µm, or oval, 7–8 × 3–4 µm	[28]

(continued)

Table 2. Continued.

Species	Host	Habitat	Synnemata/stromata	Perithecia	Asci	Ascospores	Conidiogenous cells	Conidia	References
<i>H. fusiformis</i>	Cricket adult (Orthoptera)	Unknown	Synnemata erect, straight, unbranched, uniform in height, measuring 4–5 mm, nearly black in color	None	None	None	Sporophores simple, sessile, the inflated basal portion tapering gradually to rather short 25–35 µm	Spores fusoid cylindrical, hyaline, size 9–10 × 2 µm	[28]
<i>H. shennongjiaensis</i>	Earwigs (Dermaptera)	Unknown	Synnemata cylindrical, size 60.0 × 1.0–2.0 mm, brown	None	None	None	Conidiogenous cells solitary, phialides cylindrical or awl-like, 14.4–26.1 or 6.3–14.4 µm	Conidia hyaline, aseptate, smooth, sausage-shaped, single or double from the apex of the neck, 6.3–10.8 × 3.6–6.3 µm	[30]
<i>H. eleutherotorum</i>	Coleoptera (Anoplura)	Unknown	Synnemata simple or branching, 3–5 mm, cinereous to violaceous gray to dull brown, often paler at the apex	None	None	None	Conidiogenous cells ellipsoid, base 8–10 × 5–6 µm, tapering rather abruptly into a long neck, 30–35 µm long	Conidia cymbiform to narrow ellipsoid, 4–7 × 1–2 µm, forming citriform clusters 8 × 6 µm	[31]

consistent with existing findings, i.e., *H. radiata*, *H. fusiformis*, and *O. shennongjiaensis*, and *H. gigantean* and *O. elongate* group cluster closely, respectively [14,15,32]. Three species, i.e., *O. alboperitheciata*, *O. elongate*, and *H. gigantea*, are closely clustered together, whereas they are noticeably inconsistent with each other in morphological and ecological characteristics. According to both molecular phylogeny and morphology, a consistent relationship between *O. alboperitheciata* and other relatives in the *H. citriformis* clade is evidenced. Thus, the novel species *O. alboperitheciata* is proposed in genus *Ophiocordyceps*.

Disclosure statement

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