Multi-gene phylogenetic evidence indicates that *Pleurodesmospora* belongs in Cordycipitaceae (Hypocreales, Hypocreomycetidae) and *Pleurodesmospora lepidopterorum* sp. nov. on pupa from China

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Abstract

A new species, *Pleurodesmospora lepidopterorum*, isolated from a pupa, is introduced. Morphological comparisons and phylogenetic analyses based on multigene datasets (ITS+RPB1+RPB2+TEF) support the establishment of the new species. *Pleurodesmospora lepidopterorum* is distinguished from *P. coccorum* by its longer conidiogenous pegs located in the terminal or lateral conidiophores, and smaller subglobose or ellipsoidal conidia. A combined dataset of RPB1, RPB2, and TEF confirmed the taxonomic placement of *Pleurodesmospora* in Cordycipitaceae for the first time.

Keywords

Insect, morphological characteristic, new species, phylogenetic analysis, taxonomic placement

Introduction

The genus *Pleurodesmospora* was established for the type species *P. coccorum* (Petch) Samson, W. Gams & H.C. Evans (Samson et al. 1980). The typical characteristic of *Pleurodesmospora* is its erect or procumbent conidiophores, which bear numerous min-
ute phialidic conidiogenous pegs in the terminal or mostly intercalary position, often in whorls below the septa. Conidiogenous pegs are short-cylindrical and give rise to short chains of conidia. Conidia are ellipsoid to dacyroid with a slightly truncate base (Samson et al. 1980).

*Pleurodesmospora* species have diverse ecological characteristics, and have been found on scale insects, whitefly, aphids, leaf-hoppers, spider and scavenger mites (Petch 1931; Samson and McCoy 1982; Samson et al. 1980). Li et al. (1991) reported *Pleurodesmospora* as a newly recorded genus in China and confirmed for the first time that *P. coccorum* has strong pathogenicity to black whitefly. According to Index Fungorum, the taxonomic status of *Pleurodesmospora* is incertae sedis.

During a survey of entomopathogenic fungi from Southwest China, a new insect-associated species was found. The morphological characteristics of the new species resembled *Pleurodesmospora*. In our phylogenetic analyses of combined RPB1, RPB2 and TEF sequences, *Pleurodesmospora* clustered in Cordycipitaceae (Hypocreales, Hypocreomycetidae) with strong statistical support and was closely related to *Beauveria* Vuill. and *Akanthomyces* Lebert. Thus, we propose that *Pleurodesmospora* belongs to family Cordycipitaceae and introduce *Pleurodesmospora lepidopterorum* sp. nov. as a new insect-associated species on the basis of morphological comparison and molecular phylogenetic analyses.

**Materials and methods**

**Specimen collection and identification**

An infected pupa of Lepidoptera specimen (DY1050) was collected from Duyun City (26°21’24.71”N, 107°22’48.22”E), Qiannan Buyi and Miao Autonomous Prefecture, Guizhou Province, on 1 October 2019. Isolation of strains was conducted as described by Chen et al. (2019). Fungal colonies emerging from specimens were isolated and cultured at 25 °C for 14 days under 12 h light/12 h dark conditions following protocols described by Zou et al. (2010). Specimens and the isolated strains were deposited in the Institute of Fungus Resources, Guizhou University (formally Herbarium of Guizhou Agricultural College; code, GZAC), Guiyang City, Guizhou, China.

Macroscopic and microscopic morphological characteristics of the fungi were examined and the growth rates were determined from potato dextrose agar (PDA) and oatmeal agar (OA) cultures incubated at 25 °C for 14 days. Hyphae and conidiogenous structures were mounted in lactophenol cotton blue or 20% lactate solution and observed with an optical microscope (OM, DM4 B, Leica, Germany).

**DNA extraction, polymerase chain reaction amplification and nucleotide sequencing**

DNA extraction was carried out by Fungal genomic DNA Extraction Kit (DP2033, BioTekte Corporation) in accordance with Liang et al. (2011). The extracted DNA was stored at −20 °C. The internal transcribed spacer (ITS) region, RNA polymerase II
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largest subunit 1 (RPB1), RNA polymerase II largest subunit 2 (RPB2) and translation elongation factor 1 alpha (TEF) were amplified by PCR as described by White et al. (1990), Castlebury et al. (2004) and van den Brink et al. (2004), respectively. PCR products were purified and sequenced at Sangon Biotech (Shanghai) Co. The resulting sequences were submitted to GenBank.

Sequence alignment and phylogenetic analyses

Lasergene software (version 6.0, DNASTAR) was applied for the assembling and editing of DNA sequence. The ITS, RPB1, RPB2 and TEF sequences were downloaded from GenBank, based on Mongkolsamrit et al. (2018, 2020) and others selected on the basis of BLAST algorithm-based searches in GenBank (Table 1). The multiple datasets of ITS, RPB1, RPB2 and TEF were aligned and edited by MAFFT v7.037b (Katoh and Standley 2013) and MEGA6 (Tamura et al. 2013). Assembling of the combined datasets (RPB1+RPB2+TEF and ITS+RPB1+RPB2+TEF) was performed by SequenceMatrix v.1.7.8 (Vaidya et al. 2011). The model was selected for Bayesian analysis by ModelFinder (Kalyaanamoorthy et al. 2017) in the software PhyloSuite (Zhang et al. 2020).

The datasets (RPB1+RPB2+TEF and ITS+RPB1+RPB2+TEF) were analyzed by Bayesian inference (BI) and maximum likelihood (ML) methods to determine the relationship among Pleurodesmospora and related genera in the order Hypocreales (analysis 1) and the relationship among Pleurodesmospora and related genera in the family Cordycipitaceae (analysis 2), respectively. For BI, a Markov chain Monte Carlo (MCMC) algorithm was used to generate phylogenetic trees with Bayesian probabilities using MrBayes v.3.2 (Ronquist et al. 2012) for the combined sequence datasets. The Bayesian analysis resulted in 20,001 trees after 10,000,000 generations. The first 4,000 trees, representing the burn-in phase of the analyses, were discarded, while the remaining 16,001 trees were used for calculating posterior probabilities in the majority rule consensus tree. After the analysis was finished, each run was examined using the program Tracer v1.5 (Drummond and Rambaut 2007) to determine burn-in and confirm that both runs had converged. ML analyses were constructed with RAxMLGUI (Silvestro et al. 2012). The GTRGAMMA model was used for all partitions, in accordance with recommendations in the RAxML manual against the use of invariant sites.

Results

Phylogenetic analyses

Clonostachys rosea (Link) Schroers, Samuels, Seifert & W. Gams isolates (AFTOL ID.187 and GJS 90227) were used as the outgroup in analysis 1 (Fig. 1), and Purpureocillium lilacinum (Thom) Luangs-a-ard, Houbraken, Hywel-Jones & Samson isolates (CBS 284.36 and CBS 431.87) were used as the outgroup in analysis 2 (Fig. 2).
Table 1. Taxa included in the phylogenetic analyses.

| Species                        | Strain No. | GenBank accession No. |
|--------------------------------|------------|-----------------------|
|                                |            | ITS   | RPB1          | RPB2 | TEF          |
| Akanthomyces aculeatus         | HUA 186145 | –     | –             | –    | MF416465     |
| Akanthomyces attenuates        | CBS 402.78 | –     | EF468888      | EF468935 | EF468782 |
| Akanthomyces tecanii           | CBS 101247 | –     | DQ522407      | DQ522466 | DQ522359 |
| Akanthomyces wuldergamsii      | TBRC 7251  | –     | MF140781      | MF140805 | MF140833 |
|                                | TBRC 7252  | –     | MF140782      | MF140806 | MF140834 |
| Ascopolyporus polychrous       | ARSEF 6355 | –     | DQ127236      | –    | DQ118745     |
| Ascopolyporus villorosus       | ARSEF 546  | –     | DQ127241      | –    | DQ118750     |
| Beauveria bassiana             | ARSEF 1564 | HQ880761 | HQ880833 | HQ880905 | HQ880974     |
|                                | ARSEF 7518 | HQ880762 | HQ880834 | HQ880906 | HQ880975     |
| Beauveria brongniarti          | ARSEF 617  | –     | HQ880854      | HQ880926 | HQ880991     |
| Beauveria caleldonica          | ARSEF 2567 | –     | HQ880889      | HQ880961 | EF469057     |
| Blackwellomyces cardinalis     | OSC 93609  | –     | DQ522370      | DQ522370 | DQ522325     |
|                                | OSC 93610  | JN049843 | EF469088     | EF469106 | EF469059     |
| Claviceps purpurea             | P.C. 546   | –     | DQ127240      | –    | DQ862029     |
| Claviceps villosus             | ARSEF 6355 | –     | DQ127241      | –    | DQ118750     |
| Claviceps purpurea             | AFTOL ID.187 | –     | –             | –    | –             |
| Clonostachys rosea             | AFTOL ID.187 | –     | –             | –    | DQ127240     |
| Conidiocerella luteorostrata   | NHJ 11343  | –     | EF468906      | –    | EF468801     |
|                                | NHJ 12516  | –     | EF468905      | EF468946 | EF468800     |
| Cordyceps kyurogusensis        | EFCC 5886  | –     | EF468863      | –    | EF468754     |
| Cordyceps militaris            | OSC 93623  | JN049825 | DQ522377     | –    | DQ522332     |
| Cordyceps ninchukipora         | E.G.S.38.165 | –     | EF468900      | –    | EF468795     |
|                                | E.G.S.38.166 | –     | EF468901      | –    | EF468794     |
| Cordyceps piperis              | CBS 116719 | –     | DQ127240      | EU369083 | DQ118749     |
| Gibellula gamsii               | BCC 25798  | MH152532 | EU369056     | EU369076 | EU369018     |
|                                | BCC 27968  | MH152529 | MH152547      | –    | MH152560     |
| Hevansia novoguineensis        | CBS 610.80 | MH352831 | –             | MH521844 | MH521885     |
|                                | NHJ 11923  | –     | EU369052      | EU369072 | EU369013     |
| Hyperdermium pulvinatum         | P.C. 602   | –     | DQ127237      | –    | DQ118746     |
| Lecaniciellum antillanum       | CBS 350.85 | MH861888 | DQ522396     | DQ522450 | DQ522350     |
| Lecaniciellum paliotae         | CBS 101270 | –     | EF469096      | EF469112 | EF469067     |
|                                | CBS 532.81 | –     | EF469095      | EF469113 | EF469066     |
| Lecaniciellum tensipes          | CBS 309.85 | –     | DQ522387      | DQ522439 | DQ522341     |
| Metarhizium anisopliae         | ARSEF 7487 | –     | DQ468355      | DQ468370 | DQ463996     |
|                                | CBS 130.71 | –     | MT078861      | MT078918 | MT078845     |
|                                | CBS 700.74 | –     | MT078863      | MT078919 | MT078846     |
|                                | CBS 700.74 | –     | MT078863      | MT078920 | MT078847     |
| Neoturrabilla chinghricoida    | BCC 39684  | –     | MK632071      | MK632181 | MK632148     |
|                                | BCC 80733  | –     | MK632072      | MK632176 | MK632149     |
| Ophiocordyceps gracilis        | EFCC 8572  | –     | EF468859      | EF468912 | EF468751     |
|                                | EFCC 7287  | –     | EF468874      | EF468924 | EF468767     |
| Ophiocordyceps sinensis        | EFCC 8572  | –     | EF468874      | EF468924 | EF468767     |
| Orbiocrella petchii            | NHJ 6209   | –     | EU369061      | EU369081 | EU369023     |
| Pleurodesmospora cocorum       | CBS 458.73 | MH860741 | –             | –    | –             |
|                                | CBS 459.73 | MH860742 | –             | –    | –             |
|                                | CBS 460.73 | MH860743 | –             | –    | –             |
| Pleurodesmospora lepidopterorum| ARSEF 1424 | –     | DQ127245      | KF049671 | DQ118754     |
| Polycephalomyces formosus      | ARSEF 10742 | –   | KF049647      | KF049669 | KF049685     |
| Polycephalomyces paracuboideus | ARSEF 2181 | –     | EF468906      | EF468940 | EF468790     |
| Purpureocillium lilacinum      | CBS 431.87 | –     | EF468907      | EF468940 | EF468791     |
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| Species                        | Strain No. | GenBank accession No. |
|-------------------------------|------------|-----------------------|
|                               |            | ITS    | RPB1  | RPB2  | TEF   |
| Purpureocillium lilacinum     | CBS 284.36 | MH855800 | EF468898 | EF468941 | EF468792 |
| Samsoniella auranti            | TBRC 7271  | –      | MF140791 | –      | MF140846 |
|                               | TBRC 7272  | MF140763 | –      | MF140817 | MF140845 |
| Simplicillium lanosoniveum    | CBS 101267 | –      | DQ522405 | DQ522463 | DQ522357 |
|                               | CBS 704.86 | AJ292396 | DQ522406 | DQ522464 | DQ522358 |
| Yosiokobayasia kusanagiensis  | TNS–F18494 | –      | –      | JN049890 | –      |

Figure 1. Phylogenetic relationships among Pleurodesmospora and related genera in the order Hypocreales based on a multigene dataset (RPB1, RPB2, and TEF). Statistical support values (≥ 50%/0.5) are shown at the nodes for maximum likelihood bootstrap support/ Bayesian inference posterior probabilities.
Figure 2. Phylogenetic relationships among Pleurodesmospora and related genera in the family Cordycipitaceae based on a multigene dataset (ITS, RPB1, RPB2 and TEF). Statistical support values (≥ 50%/0.5) are shown at the nodes for maximum likelihood bootstrap support/Bayesian inference posterior probabilities.

The concatenated sequences of analysis 1 and 2 included 23 and 21 taxa, respectively, and consisted of 2,262 (RPB1, 561; RPB2, 821; and TEF, 880) and 2,711 (ITS, 597; RPB1, 508; RPB2, 852; and TEF, 754) characters with gaps, respectively.

Analysis 1: The final value of the highest scoring tree was −18,860.236896, which was obtained from the ML analysis of the dataset (RPB1+RPB2+TEF). The parameters of GTR model to analysis of the dataset were estimated base frequencies; A = 0.240138,
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C = 0.290732, G = 0.262224, T = 0.206905; substitution rates AC = 1.004710, AG = 3.103423, AT = 0.837508, CG = 0.886482, CT = 5.821155, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.309925$. The selected model for BI analysis were K2P+G4 (RPB2) and GTR+F+I+G4 (RPB1+TEF). In the order-level phylogenetic tree (Fig. 1), the maximum likelihood and Bayesian inference trees were generally congruent, and most branches were strongly supported. The new strains clustered with the genera Cordyceps, Akanthomyces, and Beauveria, and belonged to family Cordycipitaceae.

Analysis 2: The final value of the highest scoring tree was $-19,321.404482$, which was obtained from the ML analysis of the dataset (ITS+RPB1+RPB2+TEF). The parameters of GTR model to analysis of the dataset were estimated base frequencies; A = 0.238334, C = 0.298168, G = 0.261443, T = 0.202055; substitution rates AC = 0.963749, AG = 2.807654, AT = 0.822463, CG = 0.766574, CT = 5.738062, GT = 1.000000; gamma distribution shape parameter $\alpha = 0.339059$. The selected model for BI analysis were HKY+F+G4 (ITS) and GTR+F+I+G4 (RPB1+RPB2+TEF). In the family-level phylogenetic tree (Fig. 2), the maximum likelihood and Bayesian inference trees were generally congruent, and most branches were strongly supported. The new strains formed an independent branch but clustered with Pleurodesmospora coccorum; therefore, these strains represent a new species described as P. lepidopterorum.

**Taxonomy**

*Pleurodesmospora lepidopterorum* W.H. Chen, Y.F. Han & Z.Q. Liang, sp. nov.

MycoBank No: 839148

Figure 3

**Diagnosis.** Differs from *P. coccorum* by having longer conidiogenous pegs located in the terminal or lateral conidiophores, and smaller subglobose or ellipsoidal conidia.

**Type.** China, Guizhou Province, Qiannan Buyi and Miao Autonomous Prefecture, Duyun City (26°21’24.71”N, 107°22’48.22”E), 1 October 2019, Wanhao Chen, holotype GZAC DY1050, ex-type culture GZAC DY10501. Sequences from isolated strain DY10501 have been deposited in GenBank with accession numbers: ITS = MW826576, RPB1 = MW834315, RPB2 = MW834316 and TEF = MW834317.

**Description.** Colonies on PDA, 3.9–4.1 cm diam. in 14 d at 25 °C, white, consisting of a basal felt and cottony, floccose hyphal overgrowth, reverse pale yellowish. Prostrate hyphae smooth, septate, hyaline, 1.3–1.9 μm diam. Erect or procumbent conidiophores usually arising from aerial hyphae, barely differentiated from vegetative hyphae, usually branched. Conidiogenous cells polyphialidic, terminal and intercalary, bearing numerous short-cylindrical, 1.8–3.5 μm long and 0.7–1.3 μm wide conidiogenous pegs, in whors often below the septa. The terminal or lateral conidiogenous cells cylindrical, 5.9–12.0 × 1.8–2.2 μm. Conidia in chains, hyaline, smooth-walled, subglobose or ellipsoidal, one-celled, 2.3–3.6 × 1.7–3.3 μm. Chlamydospores and synnemata not observed. Size and shape of phialides and conidia similar in culture on PDA, OA agar and on natural substrate. Sexual state not observed.

**Host.** Pupa, order Lepidoptera.
Figure 3. Pleurodesmospora lepidopterorum A infected pupa (Lepidoptera) B, C top (B) and underside (C) of a colony cultured on PDA medium at 14 d D–J conidiogenous pegs and conidia K conidia in chains. Scale bars: 10 mm (B, C) 10 μm (D–K).

**Distribution.** Duyun City, Qiannan Buyi and Miao Autonomous Prefecture, Guizhou Province, China.

**Etymology.** Referring to its insect host, which belongs to order Lepidoptera.

**Remarks.** Pleurodesmospora lepidopterorum was readily identified as belonging to Pleurodesmospora in the family-level phylogenetic tree (Fig. 2). When compared with the typical characteristics of P. coccorum, P. lepidopterorum was easily distinguished by its longer conidiogenous pegs located in the terminal or lateral conidiophores, and smaller subglobose or ellipsoidal conidia.

**Discussion**

BLAST results of ITS, RPB1, RPB2, and TEF sequence data revealed that the strain DY10501 was similar to several taxa in GenBank: ITS, 98.62% similar to Lecanicillium sp. (isolate ICMP:20146); RPB1, 88.55% similar to Beauveria caledonica Bissett & Widden (isolate ARSEF 7117); RPB2, 86.53% similar to Cordyceps sp. (isolate
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A12116); TEF, 95.33% similar to Beauveria bassiana (Bals.-Criv.) Vuill. (isolate CHE-CNRCB 82). In the family-level phylogenetic tree, strains DY10501 and DY10502 formed an independent branch and clustered with P. coccorum in a subclade.

Samson et al. (1980) introduced the genus Pleurodesmospora with P. coccorum, but the taxonomic status of the genus was unclear. Unfortunately, P. coccorum lacked RPB1, RPB2, and TEF sequences in GenBank. Therefore, P. lepidopterorum was used for multigene analysis of Pleurodesmospora and related genera in the order Hypocreales. In the order-level phylogenetic tree, P. lepidopterorum clustered into Cordycipitaceae (Hypocreales, Hypocreomycetidae, Sordariomycetes). Thus, the combined dataset of RPB1, RPB2, and TEF confirmed the taxonomic placement of Pleurodesmospora in Cordycipitaceae for the first time.

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Supplementary material 1

Dataset for Figure 1
Authors: Wan-Hao Chen, Yan-Feng Han, Jian-Dong Liang, Wei-Yi Tian, Zong-Qi Liang
Data type: molecular data
Explanation note: A dataset of RPB1, RPB2 and TEF for Figure 1.
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Link: https://doi.org/10.3897/mycokeys.80.66794.suppl1

Supplementary material 2

Dataset for Figure 2
Authors: Wan-Hao Chen, Yan-Feng Han, Jian-Dong Liang, Wei-Yi Tian, Zong-Qi Liang
Data type: molecular data
Explanation note: A dataset of ITS, RPB1, RPB2 and TEF for Figure 2
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Supplementary material 3

Table S1. Taxa included in the phylogenetic analyses
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Data type: molecular data
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Link: https://doi.org/10.3897/mycokeys.80.66794.suppl3