Resolution of phylogenetic position of Nigrofomitaceae within Hymenochaetales (Basidiomycota) and Nigrofomes sinomelianoporus sp. nov. (Nigrofomitaceae) from China
Li-Wen Zhou, Xue-Wei Yang, Josef Vlasák, Guo-Juan Ren
Research Article
doi: 10.3997/mycokeys.29.21250
12-01-2018  Unique: 387  Total: 804  1-13  Reprint: € 4.80

An overview of the genus Coprotus (Pezizales, Ascomycota) with notes on the type species and description of C. epithectoides sp. nov.
Ivana Kusan, Noven Marode, Margita Jadan, Zdenko Tkalčec, Amín Moshá
Research Article
doi: 10.3997/mycokeys.29.225978
12-01-2018  Unique: 555  Total: 1060  15-47  Reprint: € 10.50

Curvularia microspora sp. nov. associated with leaf diseases of Hippeastrum striatum in China
Yin Liang, Shuang-Fei Ren, Jayarama Bhao, Kevin D. Hyde, Yong Wang, De-Gang Zhao
Research Article
doi: 10.3997/mycokeys.29.21122
18-01-2018  Unique: 465  Total: 804  49-61  Reprint: € 4.80

Phylogenetic affinities of the sequestrate genus Rhodactina (Boletaceae), with a new species, R. rastrispora from Thailand
Santithid Vachhaneerat, Olivier Reppé, Saisemorn Lumyong
Research Article
doi: 10.3997/mycokeys.29.22572
25-01-2018  Unique: 650  Total: 1127  69-80  Reprint: € 5.90

Elaphroporia altaoshanensis gen. et sp. nov. in Polyporales (Basidiomycota)
Zi-Qiong Wu, Tai-Min Xu, Shan Shen, Xiang-Fu Liu, Kai-Yue Luo, Chang-Lin Zhao
Research Article
doi: 10.3997/mycokeys.29.22006
30-01-2018  Unique: 460  Total: 829  81-95  Reprint: € 4.80
Elaphroporia ailaoshanensis gen. et sp. nov. in Polyporales (Basidiomycota)

Zi-Qiang Wu¹, Tai-Min Xu², Shan Shen³, Xiang-Fu Liu³, Kai-Yue Luo³, Chang-Lin Zhao¹,³

¹ Key Laboratory of Forest Disaster Warning and Control of Yunnan Province, Southwest Forestry University, Kunming 650224, P.R. China ² College of Life Sciences, Southwest Forestry University, Kunming 650224, P.R. China ³ College of Biodiversity Conservation and Utilisation, Southwest Forestry University, Kunming 650224, P.R. China

Corresponding author: Chang-Lin Zhao (fungichanglinz@163.com)

Citation: Wu Z-Q, Xu T-M, Shen S, Liu X-F, Luo K-Y, Zhao C-L (2018) Elaphroporia ailaoshanensis gen. et sp. nov. in Polyporales (Basidiomycota). MycoKeys 29: 81–95. https://doi.org/10.3897/mycokeys.29.22086

Abstract
A new poroid wood-inhabiting fungal genus, Elaphroporia, typified by E. ailaoshanensis sp. nov., is proposed based on a combination of morphological features and molecular evidence. The genus is characterised by an annual growth habit, resupinate basidiocarps, becoming rigid and light-weight up on drying, a monomitic hyphal system with thick-walled generative hyphae bearing both clamp connections and simple septa, slightly amyloid, CB+ and ellipsoid, hyaline, thin-walled, smooth and IKI–, CB– basidiospores. Sequences of ITS and LSU nrRNA gene regions of the studied samples were generated, and phylogenetic analyses were performed with maximum likelihood, maximum parsimony and bayesian inference methods. The phylogenetic analysis based on molecular data of ITS+nLSU sequences showed that Elaphroporia belonged to the residual polyporoid clade and was closely related to Junghuhnia crustacea. Further investigation was obtained for more representative taxa in the Meruliaceae based on ITS+nLSU sequences, in which the result demonstrated that the genus Elaphroporia formed a monophyletic lineage with a strong support (100 % BS, 100 % BR, 1.00 BPP) and then grouped with Flaviporus and Steccherinum.

Keywords
Meruliaceae, phylogeny, polypore, taxonomy, wood-inhabiting fungi
Introduction

The Polyporales is a large group of Agaricomycetes and includes more than 1800 taxa at species level belonging to 216 genera and 13 families (Kirk et al. 2008). Species in Polyporales are the key players amongst the wood-rotting fungi because of their importance in the carbon cycle (Floudas et al. 2012) and the pathogenic and potential application in biomedical engineering and biodegradation (Dai et al. 2009, Levin et al. 2016).

Molecular systematics has played a powerful role in inferring phylogenies within fungal groups since the early 1990s (White et al. 1990, Hibbett et al. 2007, Larsson 2007, Miettinen et al. 2011, Binder et al. 2013, Dai et al. 2015, Choi and Kim 2017). Recently, molecular studies involving Meruliaceae P. Karst. have been carried out (Binder et al. 2005, 2013, Miettinen and Larsson 2011, Miettinen and Rajchenberg 2012, Hibbett et al. 2016, Miettinen et al. 2016).

Larsson (2007) introduced a new division for part of the Polyporales, effectively renaming the phlebioid and residual polyporoid clades as the Meruliaceae, Phanerochaetaceae Jülich, and Byssomerulius Parmasto families. A phylogenetic study of Meruliaceae employing multi-genes suggested that 1) this family included species with both poroid and hydnoid hymenophore configurations, and 2) the genera of Flabellophora G. Cunn., Flaviporus Murrill, Junghuhnia Corda, Steccherinum Gray and Xanthoporus Audet belong to this family (Miettinen et al. 2011). Moreover, further study employing a six-gene (5.8S, nrLSU, nrSSU, rpb1, rpb2, tef1) dataset has constructed a phylogenetic and phylogenomic overview of the Polyporales, which showed that the species of Meruliaceae fall into the residual polyporoid clade (Binder et al. 2013).

Wood-rotting fungi is a cosmopolitan group and it has a rich diversity on the basis of growing on boreal, temperate, subtropical, and tropical vegetations (Gilbertson and Ryvarden 1987, Núñez and Ryvarden 2001, Dai 2012, Ryvarden and Melo 2014, Dai et al. 2015). During investigations on wood-inhabiting fungi in southern China, an additional taxon was found which could not be assigned to any described genus. It produces annual, resupinate basidiocarps, a monomitic hyphal system with generative hyphae bearing both simple septa and clamp connections, slightly amyloid, CB+ and ellipsoid, hyaline, thin-walled, smooth basidiospores. These characters make it distinguishable from all known poroid and hydnoid wood-inhabiting fungal genera (Gilbertson and Ryvarden 1987, Núñez and Ryvarden 2001, Bernicchia and Gorjón 2010, Ryvarden and Melo 2014). In this study, the authors expand samplings from previous studies to examine taxonomy and phylogeny of this new genus within the Polyporales, based on the internal transcribed spacer (ITS) regions and the large subunit nuclear ribosomal RNA gene (nLSU) sequences.

Materials and methods

Morphological studies. The specimens studied are deposited at the herbarium of Southwest Forestry University (SWFC). Macro-morphological descriptions are based on
Elaphroporia ailaoshanensis gen. et sp. nov. in Polyporales (Basidiomycota)

Field notes. Special colour terms follow Petersen (1996). Micro-morphological data were obtained from the dried specimens and observed under a light microscope following Dai (2010). The following abbreviations were used: KOH = 5% potassium hydroxide, CB = Cotton Blue, CB– = acyanophilous, IKI = Melzer’s reagent, IKI– = both inamyloid and indextrinoid, IKI+ = amyloid, L = mean spore length (arithmetic average of all spores), W = mean spore width (arithmetic average of all spores), Q = variation in the L/W ratios between the specimens studied, n (a/b) = number of spores (a) measured from given number (b) of specimens.

DNA extraction and sequencing. CTAB rapid plant genome extraction kit-DN14 (Aidlab Biotechnologies Co., Ltd, Beijing) was used to obtain genomic DNA from dried specimens, according to the manufacturer’s instructions with the modification that a small piece of dried fungal specimen (about 30 mg) was ground to powder with liquid nitrogen. The powder was transferred to a 1.5 ml centrifuge tube, suspended in 0.4 ml of lysis buffer and incubated in a 65 °C water bath for 60 min. After that, 0.4 ml phenol-chloroform (24:1) was added to each tube and the suspension was shaken vigorously. After centrifugation at 13 000 rpm for 5 min, 0.3 ml supernatant was transferred to a new tube and mixed with 0.45 ml binding buffer. The mixture was then transferred to an adsorbing column (AC) for centrifugation at 13 000 rpm for 0.5 min. Then, 0.5 ml inhibitor removal fluid was added in AC for a centrifugation at 12 000 rpm for 0.5 min. After washing twice with 0.5 ml washing buffer, the AC was transferred to a clean centrifuge tube, and 100 ml elution buffer was added to the middle of the adsorbed film to elute the genome DNA. The ITS region was amplified with primer pairs ITS5 and ITS4 (White et al. 1990). The nuclear LSU region was amplified with primer pairs LR0R and LR7 (https://sites.duke.edu/vilgalyslab/rdna_primers_for_fungi/). The PCR procedure for ITS was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 94 °C for 40 s, 58 °C for 45 s and 72 °C for 1 min, and a final extension of 72 °C for 10 min. The PCR procedure for nLSU was as follows: initial denaturation at 94 °C for 1 min, followed by 35 cycles at 94 °C for 30 s, 48 °C for 1 min and 72 °C for 1.5 min, and a final extension of 72 °C for 10 min. The PCR products were purified and directly sequenced at Kunming Tsingke Biological Technology Limited Company. All newly generated sequences were deposited at GenBank (Table 1).

Phylogenetic analysis. Sequencher 4.6 (GeneCodes, Ann Arbor, MI, USA) was used to edit the DNA sequence. Sequences were aligned in MAFFT 6 (Katoh and Toh 2008, http://mafft.cbrc.jp/alignment/server/) using the “G-INS-I” strategy and manually adjusted in BioEdit (Hall 1999). The sequence alignment was deposited in TreeBase (submission ID 21778). Sequences of Heterobasidion annosum (Fr.) Bref. and Stereum hirsutum (Willd.) Pers. obtained from GenBank were used as outgroups to root trees following Binder et al. (2013) in Figure 1 and Xanthoporus syringae (Parmasto) Audet. obtained from GenBank was used as an outgroup to root trees following Miettinen et al. (2011) in the ITS+nLSU analyses (Fig. 2).

Maximum parsimony analysis was applied to the ITS+nLSU dataset sequences. Approaches to phylogenetic analysis followed Li and Cui (2013) and the tree construc-
### Table 1. A list of species, specimens and GenBank accession number of sequences used in this study.

| Species name               | Sample no. | GenBank accession no. | References                  |
|----------------------------|------------|-----------------------|-----------------------------|
| **Abortiporus biennis**    | TFRI 274   | EU232187 EU232235     | Larsson (2007)              |
| **Antrodia albida**        | CBS 308.82 | DQ491414 AY515348     | Kim et al. (2007)           |
| **Antrodia heteromorpha**  | CBS 200.91 | DQ491415 AY515350     | Kim et al. (2007)           |
| **Antrodia americana**     | Gothenburg 3161 | JN710509 JN710509     | Miettinen et al. (2011)     |
| **Antrodia pallasi**       | Renvall 89a | AF126896 –            | Binder et al. (2013)        |
| **Antrodia semisupina**    | FCUG 960   | EU232182 EU232266     | Binder et al. (2005)        |
| **Antrodiella sp.**        | X 418      | JN710523 JN710523     | Miettinen et al. (2011)     |
| **Atraphiella neotropica** | Ryvarden 44447 | HQ659221 HQ659221     | Miettinen and Rajchenberg (2012) |
| **Ceriporia viridans**     | Dai 7759   | KC182777 –            | Jia et al. (2014)           |
| **Ceriporiopsis balaenae** | H7002389   | FJ496669 FJ496717     | Tomšovský et al. (2010)     |
| **Ceriporiopsis consobrina** | Rivoire 977 | FJ496667 FJ496716     | Tomšovský et al. (2010)     |
| **Ceriporiopsis gilvescens** | BRNM 667882 | FJ496685 FJ496719     | Tomšovský et al. (2010)     |
| **Ceriporiopsis gilvescens** | BRNM 710166 | FJ496684 FJ496720     | Tomšovský et al. (2010)     |
| **Ceriporiopsis gilvescens** | Yuan 2752   | KF845946 KF845953     | Zhao and Cui (2014)         |
| **Ceriporiopsis guidella** | HUBO 7659  | FJ496687 FJ496722     | Tomšovský et al. (2010)     |
| **Cineromyces lindbladii** | FBCC 177   | HQ659223 HQ659223     | Miettinen and Rajchenberg (2012) |
| **Climacocystis borealis** | KH 13318  | JQ031126 JQ031126    | Binder et al. (2013)        |
| **Coriolopsis aperta**     | LE(BIN)-0677 | AB158316 AB158316    | Tomšovský et al. (2010)     |
| **Dacryobolus karstenii**  | KHL 11162  | EU118624 EU118624     | Binder et al. (2005)        |
| **Daedalea quercina**      | DSM 4935   | DQ491425 DQ491425     | Kim et al. (2007)           |
| **Diplomitoporus flavescens** | X 84      | FN907908 –            | Miettinen et al. (2011)     |
| **Earliella scabrosa**     | PR1209     | JN165009 JN164793     | Justo and Hibbett (2011)    |
| **Etheirodon fimbriatum**  | Larsson 11905 | JN710530 JN710530    | Miettinen et al. (2011)     |
| **Flabelliporia sp.1**     | X 1357     | JN710533 JN710533     | Miettinen et al. (2011)     |
| **Flabelliporia sp.2**     | X 340      | JN710534 JN710534     | Miettinen et al. (2011)     |
| **Flabelliporia sp.3**     | X 1277     | JN710535 JN710535     | Miettinen et al. (2011)     |
| **Flabelliporia sp.4**     | X 439      | JN710536 JN710536     | Miettinen et al. (2011)     |
| **Flaviporus brownii**     | X 1216     | JN710537 JN710537     | Miettinen et al. (2011)     |
| **Flaviporus liebmannii**  | X 251      | JN710541 JN710541     | Miettinen et al. (2011)     |
| **Flaviporus liebmannii**  | X 249      | JN710539 JN710539     | Miettinen et al. (2011)     |
| **Flaviporus liebmannii**  | X 666      | JN710540 JN710540     | Miettinen et al. (2011)     |
| **Fomitopsis pinicola**    | CBS 221.39 | DQ491405 DQ491405     | Kim et al. (2007)           |
| **Fomitopsis rosea**       | ATCC 76767 | DQ491410 DQ491410     | Kim et al. (2007)           |
| **Fragiliporia fragilis**  | Dai 13559  | KJ734260 KJ734264     | Zhao et al. (2015)          |
| **Fragiliporia fragilis**  | Dai 13561  | KJ734261 KJ734265     | Zhao et al. (2015)          |
| **Frantisekia mentschulensis** | BRNM 710170 | FJ496728 –           | Tomšovský et al. (2010)     |
| **Ganoderma lingzhi**      | Wu 1006-38 | JQ781858 –           | Zhao et al. (2015)          |
| **Gelatoporia subvermispora** | BRNU 592909 | FJ496694 FJ496706    | Tomšovský et al. (2010)     |
| **Gloeoporus dichrous**    | KHL 11173  | EU118627 EU118627     | Binder et al. (2005)        |
| **Grammothelopsis subtropica** | Cui 9035  | JQ845094 JQ845097     | Zhao et al. (2015)          |
| **Heterobasidion annosum** | PFC 5252   | KC492906 KC492906    | Binder et al. (2013)        |
| **Horndonermoporus martius** | MUCCL 41677 | FJ411092 FJ398359    | Zhao et al. (2015)          |
| **Hypocniicum bombycinum** | MA 15305   | FN552537 –           | Binder et al. (2013)        |
| **Hypocniicum tyndoniae**  | NL 041031  | JX124704 JX124704     | Binder et al. (2005)        |
| Species name                              | Sample no. | GenBank accession no. | References               |
|-------------------------------------------|------------|-----------------------|--------------------------|
| Junghuhnia crustacea                      | X 1127     | JN710554 JN710554     | Miettinen et al. (2011)  |
| Junghuhnia crustacea                      | X 262      | JN710553 JN710553     | Miettinen et al. (2011)  |
| Junghuhnia micropora                      | Spirin 2652| JN710559 JN710559     | Miettinen et al. (2011)  |
| Junghuhnia nitida                         | KHL 11903  | EU118638 EU118638     | Binder et al. (2005)     |
| Loweomyces fractipes                       | X 1149     | JN710570 JN710570     | Miettinen et al. (2011)  |
| Loweomyces fractipes                       | X 1253     | JN710569 JN710569     | Miettinen et al. (2011)  |
| Loweomyces fractipes                       | X 1250     | JN710568 JN710568     | Miettinen et al. (2011)  |
| Mycoacia fuscoatra                         | KHL 13275  | JN649352 JN649352     | Tomšovský et al. (2010)  |
| Mycoacia notobifagi                        | KHL 13750  | GU480000 GU480000     | Tomšovský et al. (2010)  |
| Nigroporus vinosus                         | X 839      | N710576 N710576       | Miettinen et al. (2011)  |
| Nigroporus vinosus                         | 8182       | JN710728 JN710728     | Miettinen et al. (2011)  |
| Obba rivulosa                              | KCTC 6892  | FJ496693 FJ496710     | Miettinen and Rajchenberg (2012) |
| Obba valdiviana                            | FF 503     | HQ659235 HQ659235     | Miettinen and Rajchenberg (2012) |
| Panus conchatus                            | X 1234     | JN710579 JN710579     | Miettinen et al. (2011)  |
| Panus strigellas                           | INPA 243940| JQ955725 JQ955732     | Binder et al. (2013)     |
| Perenniporia medulla-panis                 | MUCL 49581 | FJ411088 FJ393876     | Robledo et al. (2009)    |
| Perenniporia neofulva                      | MUCL 45091 | FJ411080 FJ393852     | Robledo et al. (2009)    |
| Phlebia unica                              | KHL 11786  | EU118657 EU118657     | Binder et al. (2013)     |
| Phlebia radiata                            | UBCF 19726 | HQ604797 HQ604797     | Binder et al. (2013)     |
| Physiporinus sanguinolentus                | BRNM 699576| FJ496671 FJ496725     | Tomšovský et al. (2010)  |
| Physiporinus vitreus                       | 3163       | JN710580 JN710580     | Miettinen et al. (2011)  |
| Piloporia sajanensis                       | Mannine 2733a| HQ659239 HQ659239     | Miettinen and Rajchenberg (2012) |
| Podocypa venustula                         | CBS 65684  | JN649367 JN649367     | Binder et al. (2013)     |
| Polyporus tuberaster                       | CuITENN 8976| AF516598 AJ488116     | Binder et al. (2005)     |
| Postia guttulata                           | KHL 11739  | EU11865 Eu11865       | Kim et al. (2007)        |
| Pseudolagarobasidium acaciicola            | CBS 115543 | DQ517883 –            | Miettinen and Rajchenberg (2012) |
| Pseudolagarobasidium acaciicola            | CBS 115544 | DQ517882 –            | Miettinen and Rajchenberg (2012) |
| Pseudolagarobasidium belizensc             | CFMR 04-31 | JQ070173 –            | Miettinen and Rajchenberg (2012) |
| Skeletocutis amorpha                       | Miettinen 11038| FN907913 FN907913     | Tomšovský et al. (2010)  |
| Skeletocutis portorosensis                 | LY 3493    | FJ496689 FJ496689     | Tomšovský et al. (2010)  |
| Skeletocutis jelicii                       | H 6002113  | FJ496690 FJ496727     | Tomšovský et al. (2010)  |
| Skeletocutis novae-zelandiae               | Ryvarden 38641| JN710582 JN710582     | Miettinen et al. (2011)  |
| Spongipellis spumeus                       | PRM 891931 | HQ728287 HQ729021     | Tomšovský et al. (2010)  |
| Spongipellis spumeus                       | BRNM 712630| HQ728288 HQ728288     | Tomšovský et al. (2010)  |
| Spongipellis spumeus                       | BRNM 734877| HQ728283 HQ728283     | Tomšovský et al. (2010)  |
| Steccerinum fimbriatum                     | KHL 11905  | EU118668 EU118668     | Tomšovský et al. (2010)  |
| Steccerinum ochraceum                      | Ryberg s.n. | EU118669 EU118670     | Larson (2007)            |
| Steccerinum ochraceum                      | KHL 11902  | JQ031130 JQ031130     | Miettinen et al. (2011)  |
| Stereum hirsutum                           | NBRC 6520  | AB733150 AB733325     | Binder et al. (2013)     |
| Truncospora ochroleuca                     | MUCL 39726 | FJ411098 FJ393865     | Robledo et al. (2009)    |
| Tyromyces chionae                          | Cui 10225  | KF698745 KF698756     | Zhao et al. (2015)       |
| Xanthoporus syringae                       | X 339      | JN710606 JN710606     | Miettinen et al. (2011)  |
| Xanthoporus syringae                       | Cui 2177   | DQ789395 –            | Miettinen et al. (2011)  |
| Xanthoporus syringae                       | Gothenburg 1488 | JN710607 JN710607   | Miettinen et al. (2011)  |
| Elaphroporia ailaoshanensis                | CLZhao 595 | MG231568 MG748854     | Present study            |
tion procedure was performed in PAUP* version 4.0b10 (Swofford 2002). All characters were equally weighted and gaps were treated as missing data. Trees were inferred using the heuristic search option with TBR branch swapping and 1000 random sequence additions. Max-trees were set to 5000, branches of zero length were collapsed and all parsimonious trees were saved. Clade robustness was assessed using a bootstrap (BT) analysis with 1,000 replicates (Felsenstein 1985). Descriptive tree statistics

| Species name                  | Sample no. | GenBank accession no. | References      |
|-------------------------------|------------|-----------------------|-----------------|
| Elaphroporia ailaoshanensis   | CLZhao 596 | MG231572, MG748855    | Present study   |
| Elaphroporia ailaoshanensis   | CLZhao 597 | MG231847, MG748856    | Present study   |
| Elaphroporia ailaoshanensis   | CLZhao 598 | MG231823, MG748857    | Present study   |

Figure 1. Maximum parsimony strict consensus tree illustrating the phylogeny of *Elaphroporia ailaoshanensis* and related species in Polyporales based on ITS+nLSU sequences. Branches are labelled with parsimony bootstrap values (before slash) higher than 50 % and Bayesian posterior probabilities (after slash) equal to and more than 0.95. Clade names follow Binder et al. (2013).
Elaphroporia ailaoshanensis gen. et sp. nov. in Polyporales (Basidiomycota)

Figure 2. Maximum parsimony strict consensus tree illustrating the phylogeny of Elaphroporia ailaoshanensis and related species in the residual polyporoid clade based on ITS+nLSU sequences. Branches are labelled with parsimony bootstrap values (before slash) higher than 50% and Bayesian posterior probabilities (after slash) equal to and more than 0.95. Clade names follow Miettinen et al. (2011).

length (TL), consistency index (CI), retention index (RI), rescaled consistency index (RC) and homoplasy index (HI) were calculated for each Maximum Parsimonious Tree (MPT) generated. Sequences were also analysed using Maximum Likelihood (ML) with RAxML-HPC2 through the Cipres Science Gateway (www.phylo.org; Miller et al. 2009). Branch support for ML analysis was determined by 1000 bootstrap replicates.

MrModeltest 2.3 (Posada and Crandall 1998, Nylander 2004) was used to determine the best-fit evolution model for each data set for Bayesian Inference (BI). Bayesian Inference was calculated with MrBayes 3.1.2 with a general time reversible (GTR) model of DNA substitution and a gamma distribution rate variation across sites (Ronquist and Huelsenbeck 2003). Four Markov chains were run for 2 runs from random starting trees for 5 million generations (Fig. 1), for 3 million generations (Fig. 2) and trees were sampled every 100 generations. The first one-fourth generations were discarded as burn-in. A majority rule consensus tree of all remaining trees was calculated. Branches that received bootstrap support for maximum likelihood (BS), maximum parsimony (BP) and Bayesian posterior probabilities (BPP) greater than or equal to 75% (BP) and 0.95 (BPP) respectively, were considered as significantly supported.
Phylogeny results

The ITS+nLSU dataset (Fig. 1) included sequences from 60 fungal specimens representing 52 taxa. The dataset had an aligned length of 2143 characters, of which 1251 characters were constant, 206 parsimony-uninformative and 686 parsimony-informative. MP analysis yielded 6 equally parsimonious trees (TL = 4744, CI = 0.322, HI = 0.678, RI = 0.578, RC = 0.186). The best-fit model for ITS+nLSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI resulted in a similar topology with an average standard deviation of split frequencies = 0.001755.

The phylogenetic tree (Fig. 1), inferred from ITS+nLSU sequences, demonstrated seven major clades for 60 sampled species of the Polyporales. The new genus *Elaphroporia* fell into the Meruliaceae within the residual polyporoid clade. It was closely related to *Junghuhnia crustacea* (Jungh.) Ryvarden with a good support (95% BS, 89% BP, 0.97 BPP).

The ITS+nLSU (Fig. 2) dataset included sequences from 48 fungal specimens representing 31 taxa. The dataset had an aligned length of 2163 characters, of which 1429 characters were constant, 169 parsimony-uninformative and 565 parsimony-informative. MP analysis yielded 8 equally parsimonious trees (TL = 2806, CI = 0.423, HI = 0.576, RI = 0.673, RC = 0.285). The best-fit model for ITS+nLSU alignment estimated and applied in the BI was GTR+I+G, lset nst = 6, rates = invgamma; prset statefreqpr = dirichlet (1,1,1,1). BI resulted in a similar topology with an average standard deviation of split frequencies equal to 0.005758.

A further phylogeny (Fig. 2) inferred from the combined ITS+nLSU sequences was obtained for 48 fungal specimens representing 31 taxa within the residual polyporoid clade and demonstrated that the new genus formed a monophyletic entity with a high 100 % BS, 100 % BP and 1.00 BPP and sisters to *Junghuhnia crustacea* and then grouped with *Flaviporus* and *Steccherinum*.

Taxonomy

*Elaphroporia* Z.Q. Wu & C.L. Zhao, gen. nov.
MycoBank MB 823915

**Diagnosis.** Differs from other genera in Polyporales by resupinate basidiocarps becoming rigid and light-weight upon drying, a monomitic hyphal system, thick-walled generative hyphae bearing both clamp connections and simple septa and hyaline, thin-walled, smooth, IKI–, CB– basidiospores.

**Type species.** *Elaphroporia ailaoshanensis* Z.Q. Wu & C.L. Zhao.

**Etymology.** *Elaphroporia* (Lat.): referring to the basidiocarps light-weight upon drying.
Basidiocarps annual, resupinate, becoming rigid and light-weight up on drying. Pore surface cream to pale yellow when fresh, turning to yellow upon drying. Hyphal system monomitic; generative hyphae thick-walled bearing both clamp connections and simple septa, slightly amyloid, CB+. Basidiospores ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–.

*Elaphroporia ailaoshanensis* Z.Q. Wu & C.L. Zhao, sp. nov.
MycoBank MB 823916
Figs 3, 4

**Diagnosis.** This species is distinguished by the cream to yellow pore surface upon drying; pores angular, 7–9 per mm. Hyphal system monomitic; generative hyphae thick-walled bearing both clamp connections and simple septa, slightly amyloid, CB+. Basidiospores ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, 1.9–2.5 × 1.5–2 μm.

**Holotype.** CHINA. Yunnan Province: Jingdong county, Ailaoshan Nature Reserve, 2 October 2016, on the angiosperm trunk, CLZhao 595 (Holotype in SWFC).

**Etymology.** *Ailaoshanensis* (Lat.): referring to the locality (Ailaoshan) of the type specimens.

**Basidiocarps.** Annual, resupinate, easy to separate from substrate, soft corky when fresh, without odour or taste when fresh, becoming rigid and light-weight up on drying, up to 5 cm long, 3.5 cm wide, 4 mm thick at centre. Pore surface cream to pale yellow when fresh, turning to yellow upon drying; pores angular, 7–9 per mm; dissepiments thin, entire. Sterile margin narrow, cream, up to 1 mm wide. Subiculum thin, cream, corky, up to 0.2 mm thick. Tubes concolorous with pore surface, hard corky, up to 3.8 mm long.

**Hyphal structure.** Hyphal system monomitic; generative hyphae thick-walled, slightly amyloid, CB+; tissues unchanged in KOH.

**Subiculum.** Generative hyphae hyaline, thick-walled bearing both clamp connections and simple septa, simple septa more frequent than clamps, occasionally branched, interwoven, 3.5–5.5 μm in diam.

**Tubes.** Generative hyphae hyaline, thick-walled bearing simple septa only, occasionally branched, 3–5 μm in diameter. Cystidia and cystidioles absent; basidia clavate, with four sterigmata and a basal clamp connection, 10.5–14.5 × 3.5–4.5 μm; basidioles dominant, in shape similar to basidia, but slightly smaller.

**Spores.** Basidiospores ellipsoid, hyaline, thin-walled, smooth, IKI–, CB–, (1.7–)1.9–2.5(–2.9) × (1.3–)1.5–2(–2.2) μm, L = 2.29 μm, W = 1.74 μm, Q = 1.33–1.81 (n = 120/4).

**Additional specimens examined** (paratypes). CHINA. Yunnan Province: Jingdong county, Ailaoshan Nature Reserve, 2 October 2016, on the angiosperm trunk, CLZhao 596, CLZhao 597, CLZhao 598 (SWFC).
Figure 3. Basidiomata of *Elaphroporia ailaoshanensis* (holotype). Scale bars: 1 cm (A); 1 mm (B).
Elaphroporia ailaoshanensis gen. et sp. nov. in Polyporales (Basidiomycota)
(Núñez and Ryvarden 2001, Ryvarden and Melo 2014). *Flaviporus* is separated from *Elaphroporia* by the dark brown to bay pileus, a dimitic hyphal system and presence of the metuloid cystidia (Murrill 1905). *Steccherinum* differs in its odontoid to hydnoid hymenophore and cyanophilous basidiospores (Bernicchia and Gorjón 2010).

Morphologically, *Elaphroporia* resembles *Ceriporia* Donk and *Phlebiporia* Jia J. Chen, B.K. Cui & Y.C. Dai. *Ceriporia* is similar to *Elaphroporia* in an annual growth habit with poroid hymenophore, a monomitic hyphal structure and hyaline, thin-walled and smooth basidiospores. In addition, both genera cause a white rot. However, *Ceriporia* differs from *Elaphroporia* by the generative hyphae IKI–, CB– (Jia et al. 2014). Additionally, in molecular studies, *Ceriporia* fell into the phlebia clade (Miettinen and Larsson 2011, Miettinen and Rajchenberg 2012, Miettinen et al. 2011, Binder et al. 2013) which is also the same as in the authors’ study (Fig. 1). *Phlebiporia* is similar to *Mellipora* by having the poroid hymenophore and the generative hyphae bearing both simple septa and clamp connections, but it is separated from *Elaphroporia* by having dextrinoid generative hyphae, tissues becoming brownish in KOH and presence of thin-walled quasi-binding hyphae in the subiculum (Chen and Cui 2014).

Polypores are an extensively studied group of Basidiomycota (Gilbertson and Ryvarden 1987, Núñez and Ryvarden 2001, Dai 2012, Ryvarden and Melo 2014), but the Chinese polypore diversity is still not well known, especially in subtropics and tropics, from where many recently described taxa of polypores were discovered (Song et al. 2014, 2016, Zhou et al. 2015, 2016, Nie et al. 2017, Yuan et al. 2017). The new genus in the present study, *Elaphroporia*, is also from the subtropics. It is possible that new polypore taxa will be found after further investigations and molecular analyses.

**Acknowledgments**

We express our gratitude to Yong-He Li (Yunnan Academy of Biodiversity, Southwest Forestry University, P.R. China) for his support on molecular work. The research is supported by the National Natural Science Foundation of China (Project No. 31700023) and the Science Foundation of Southwest Forestry University (Project No. 111715) and the Science and Technology Talent Support Programme of Three Areas in Yunnan Province (Project No. 21700329).

**References**

Bernicchia A, Gorjón SP (2010) Fungi Europaei 12: Corticiaceae l. Edizioni Candusso, Lomazzo, 1–1007.

Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, Langer G (2005) The phylogenetic distribution of resupinate forms across the major clades of mushroom-forming fungi (Homobasidiomycetes). Systematics and Biodiversity 3: 113–157. https://doi.org/10.1017/S1477200005001623
Parmasto E, Reeb V, Rogers JD, Roux C, Ryvarden L, Sampaio JP, Schüssler A, Sugiyama J, Thorn RG, Tibell L, Untereiner WA, Walker C, Wang Z, Weir A, Weiss M, White MM, Winka K, Yao YJ, Zhang N (2007) A higher-level phylogenetic classification of the Fungi. Mycological Research 111: 509–547. https://doi.org/10.1016/j.mycres.2007.03.004

Hibbett DS, Abarenkov K, Köljalg U, Öpik M, Chai B, Cole J, Wang Q, Crous P, Robert V, Helgason T, Herr JR, Kirk P, Lueschow S, O'Donnell K, Nilsson RH, Oono R, Schoch C, Smyth C, Walker DM, Porras-Alfaro A, Taylor JW, Geiser DM (2016) Sequence-based classification and identification of Fungi. Mycologia 108: 1049–1068. https://doi.org/10.3852/16-130

Jia BS, Zhou LW, Cui BK, Rivoire B, Dai YC (2014) Taxonomy and phylogeny of Ceriporia (Polyporales, Basidiomycota) with an emphasis of Chinese collections. Mycol Prog 13: 81–93. https://doi.org/10.1007/s11557-013-0895-5

Kim KM, Lee JS, Jung HS (2007) Fomitopsis incarnatus sp. nov. based on generic evaluation of Fomitopsis and Rhodofomes. Mycologia 99: 833–841. http://dx.doi.org/10.3852/mycologia.99.6.833

Kirk PM, Cannon PF, David JC, Minter DW, Stalpers JA (2008) Ainsworth and bisby’s dictionary of the fungi. 10th ed. CAB International Press, Wallingford, Oxon, UK.

Larsson KH (2007) Re-thinking the classification of corticioid fungi. Mycological Progress 111: 1040–1063. https://doi.org/10.1016/j.mycres.2007.08.001

Levin L, Maira C, Martin H, Rene U (2016) Degradation of 4-nitrophenol by the white-rot polypore Trametes versicolor. International Biodeterioration and Biodegradation 107: 174–179. https://doi.org/10.1016/j.ibiod.2015.11.023

Li HJ, Cui BK (2013) Taxonomy and phylogeny of the genus Megasporoporia and its related genera. Mycologia 105: 368–383. https://doi.org/10.3852/12-114

Miettinen O, Larsson KH (2011) Sidera, a new genus in Hymenochaetales with poroid and hydnoid species. Mycological Progress 10: 131–141. https://doi.org/10.1007/s11557-010-0682-5

Miettinen O, Larsson KH, Sjökvist E, Larsson KL (2011) Comprehensive taxon sampling reveals unaccounted diversity and morphological plasticity in a group of dimitic polypores (Polyporales, Basidiomycota). Cladistics 28: 251–270. https://doi.org/10.1111/j.1096-0031.2011.00380.x

Miettinen O, Rajchenberg M (2012) Obba and Sebipora, new polypore genera related to Cinereomyces and Gelatoporia (Polyporales, Basidiomycota). Mycological Progress 11: 131–147. https://doi.org/10.1007/s11557-010-0736-8

Miettinen O, Spirin V, Vlasák J, Rivoire B, Stenroos S, Hibbett D (2016) Polypores and genus concepts in Phanerochaetaceae (Polyporales, Basidiomycota). MycoKeys 17: 1–46. https://doi.org/10.3897/mycokeys.17.10153

Miller MA, Holder MT, Vos R, Midford PE, Liebowitz T, Chan L, Hoover P, Warnow T (2009) The CIPRES Portals. CIPRES. http://www.phylo.org/sub_sections/portal [Archived by WebCite(r) at http://www.webcitation.org/5imQlJeQa]

Murrill WA (1905) The Polyporaceae of North America: XI. A synopsis of the brown pileate species. Bulletin of the Torrey Botanical Club 32: 353–371.

Nie T, Tian Y, Liu SL, Yang J, He SH (2017) Species of Hymenochaete (Hymenochaetales, Basidiomycota) on bamboos from East Asia, with descriptions of two new species. MycoKeys 20: 51–65. https://doi.org/10.3897/mycokeys.20.11754
Núñez M, Ryvarden L (2001) East Asian polypores 2. Polyporaceae s. lato. Synopsis Fungorum 14: 165–522.

Nylander JAA (2004) MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University.

Petersen JH (1996) Farvekort. The Danish Mycological Society’s color-chart. Foreningen til Svampekundskabens Fremme, Greve.

Posada D, Crandall KA (1998) Modeltest: Testing the model of DNA substitution. Bioinformatics 14:817–818. https://doi.org/10.1093/bioinformatics/14.9.817

Robledo GL, Amalfi M, Castillo G, Rajchenberg M, Decock C (2009) Perenniporia eachenia sp. nov. and further notes on Perenniporia and its relationships with Perenniporia (Poriales, Basidiomycota). Mycologia 101: 657–673. https://doi.org/10.3852/08-040

Ronquist F, Huelsenbeck JP (2003) MRBAYES 3: bayesian phylogenetic inference under mixed models. Bioinformatics 19: 1572–1574. https://doi.org/10.1093/bioinformatics/btg180

Ryvarden L, Melo I (2014) Poroid fungi of Europe. Synopsis Fungorum 31: 1–455.

Song J, Chen YY, Cui BK, Liu HG, Wang YZ (2014) Morphological and molecular evidence for two new species of Laetiporus (Basidiomycota, Polyporales) from southwestern China. Mycologia 106: 1039–1050. https://doi.org/10.3852/13-402

Song J, Chen JJ, Wang M, Chen YY, Cui BK (2016) Phylogeny and biogeography of the remarkable genus Bondarzewia (Basidiomycota, Russulales). Scientific Reports 6: 34568. https://doi.org/10.1038/srep34568

Swofford DL (2002) PAUP*: phylogenetic analysis using parsimony (*and other methods). Version 4.0b10. Sinauer Associates, Massachusetts.

Tomšovský M, Menkis A, Vasaitis R (2010) Phylogenetic relationships in European Ceriporiopsis species inferred from nuclear and mitochondrial ribosomal DNA sequences. Fungal Biology 114: 350–358. http://dx.doi.org/10.1016/j.funbio.2010.02.004

White TJ, Bruns T, Lee S, Taylor J (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols: a guide to methods and applications. Academic Press, San Diego, 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1

Yuan Y, Ji XH, Chen JJ, Dai YC (2017) Three new species of Megaspora (Polyporales, Basidiomycota) from China. MycoKeys 20: 37–50. https://doi.org/10.3897/mycokeys.20.11816

Zhao CL, Cui BK, Song J, Dai YC (2015) Fragiliporiaceae, a new family of Polyporales (Basidiomycota). Fungal Diversity 70: 115–126. https://doi.org/10.1007/s13225-014-0299-0

Zhou JL, Zhu L, Chen H, Cui BK (2016) Taxonomy and phylogeny of Polyporus group Melanopus (Polyporales, Basidiomycota) from China. PLoS ONE 11(8): e0159495. https://doi.org/10.1371/journal.pone.0159495

Zhou LW (2015) Fulvifomes imbricatus and F. thailandicus (Hymenochaetales, Basidiomycota): Two new species from Thailand based on morphological and molecular evidence. Mycological Progress 14: 89. https://doi.org/10.1007/s11557-015-1116-1