ISSN (print) 0093-4666 ISSN (online) 2154-8889

MYCOTAXON

http://dx.doi.org/10.5248/119.397

Volume 119, pp. 397–403 *January–March 2012*

The first report of *Ceriporia lacerata* (*Phanerochaetaceae, Basidiomycota*) in Korea

Yeongseon Jang[1], Ha Eun Choi[1], Young Woon Lim[2], Jin Sung Lee[3] & Jae-Jin Kim[1]*

[1]*Division of Environmental Science & Ecological Engineering, College of Life Sciences & Biotechnology, Korea University 5-1 Anam-dong, Seongbuk-gu, Seoul, 136-701, Korea*
[2]*School of Biological Sciences, Seoul National University, Seoul, 151-747, Korea*
[3]*National Institute of Biological Resources, Environmental Research Complex, Incheon, 404-708, Korea*
*Correspondence to: *jae-jinkim@korea.ac.kr*

Abstract— An unrecorded *Ceriporia* species was collected during the field survey in Korea University Experimental Forests. Based on morphological characteristics and 28S, 18S, and internal transcribed spacer rDNA sequence analyses, the species was identified as *Ceriporia lacerata,* new to South Korea. A key to the Korean *Ceriporia* species is provided.

Key words— basidiomycete, polypore, taxonomy

Introduction

Ceriporia Donk is a genus of wood rotting fungi. It causes a white rot and includes species with resupinate basidiocarps with white, red, purple, orange, pink, or green pore surfaces, a monomitic hyphal system, simple septate or rarely clamped generative hyphae, lack of cystidia or other sterile hymenial elements, and subglobose to cylindric or allantoid basidiospores (Gilbertson & Ryvarden 1986).

In Korea, previously three *Ceriporia* species have been reported (Lee & Jung 2005): *Ceriporia purpurea* (Fr.) Donk, *C. reticulata* (Hoffm.) Domański, and *C. viridans* (Berk. & Broome) Donk. During our studies on diversity of indigenous fungi in Korea University Experimental Forests, two specimens of an unreported *Ceriporia* species were found. They were first identified from morphological characters, and sequence analyses of 28S, 18S and internal transcribed spacer (ITS) rDNA region supported the identification. A detailed description of the species and a key to the Korean *Ceriporia* species are provided below.

Materials & methods

Collections

The basidiocarps were collected in 2010 from one of the Korea University Experimental Forests located in Goesan-gun, Chungcheongbuk-do (36°46′13″N 127°58′57–59″E). They were dried completely overnight using an air drier at 40°C and deposited at the National Biological Resources Center (KB).

Microscopic observation

Macro- and microscopic basidiocarp features were noted from the collected specimens. Measurements and drawings were made from slide preparations mounted in 3% KOH (Largent et al. 1977) using an Olympus BX51 light microscope. Average dimensions were determined from > 20 measurements of each character. The characteristics of the four Korean *Ceriporia* listed in Table 1 are based on our observations of *C. lacerata* and descriptions of *C. purpurea*, *C. reticulata,* and *C. viridans* from previous studies (Jung 1994, Lim et al. 2000, Lee et al. 2002). A key to Korean *Ceriporia* species was constructed.

Table 1. Morphological comparison of four Korean *Ceriporia* species.

Characteristics	*C. lacerata* (this paper)	*C. purpurea* (Lim et al. 2000)	*C. reticulata* (Jung 1994)	*C. viridans* (Lee et al. 2002)
Basidiocarp	resupinate, effused, confluent	resupinate, effused, confluent	resupinate, ceraceous	resupinate, adnate
Pore surface	white, buff to ochraceous	pale to dark brownish purple	whitish to ochraceous	cream to sordid pinkish brown
Pores (per mm)	2–5	4–5	2–4	3–5
Basidia (μm)	11–16.5 × 3.5–5.5	17–21 × 5.7–6.3	15–20 × 5–6	11–15 × 4.5–6
Basidiospores (μm)	3.5–5 × 2–3	5.7–6.5 × 1.8–2.3	6–8 × 2–3	4–5 × 1.5–2

Molecular analysis

Genomic DNAs were extracted from basidiocarp hymenophores using Accuprep Genomic DNA extraction kit (Bioneer, Korea). PCR reactions were performed using Accupower PCR premix kit for 28S, 18S, and ITS rDNA, using primers LR0R/LR3 (Vilgalys & Hester, 1990), EukNS20F/EukNS1750R (Dams et al. 1988), and ITS1F (Gardes & Bruns 1993) /ITS4 (White et al. 1990), respectively. 18S PCR amplifications followed Suhara et al. (2003). 28S and ITS rDNA region conditions were as follows: initial denaturation at 95°C for 7 min, followed by 30 cycles at 95°C for 30 s, 51°C for 30 s, and 72°C for 30 s, concluded by elongation at 72°C for 7 min. DNA sequencing was performed in the DNA Engine Tetrad 2 Peltier Thermal Cycler (BIO-RAD, USA) using the ABI BigDye(R) Terminator v3.1 Cycle Sequencing Kit (Applied Biosystems, USA) with aforementioned primers and an ABI 3730XL DNA Analyzer (Applied Biosystems, USA). The sequences obtained in this study were deposited under the GenBank accession no. JN618335, JN618336, and JN641758–JN641761. Maximum parsimony (MP) and neighbor joining (NJ) analyses of each region followed Jang et al. (2011).

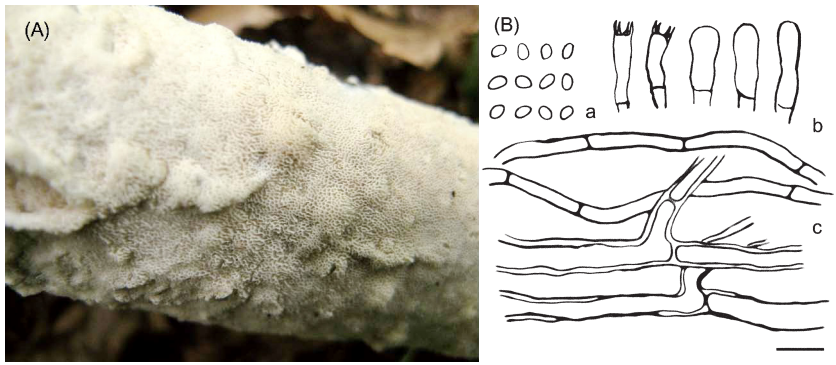

Fig. 1. *Ceriporia lacerata.* (A) Basidiocarp. (B) Microscopic features: a, basidiospores; b, basidia; c, generative hyphae. Scale bar = 10μm

Taxonomy

Ceriporia lacerata N. Maek., Suhara & R. Kondo, Mycotaxon 86: 342. 2003. Fig. 1

Basidiocarp resupinate, effused, confluent, soft when fresh, then fragile, firmly attached to the substrate; hymenophore poroid, white, buff to ochreous; dissepiments entire to lacerate; pores angular, 2–5 per mm; margin white. Hyphal system monomitic; contextual hyphae 3–5.7 μm in diameter, smooth, thin- to slightly thick-walled, simple-septate; tramal hyphae 2.3–4.6 μm in diameter, smooth, thin- to slightly thick-walled, simple-septate, cystidia lacking; basidia clavate, 11–16.5 × 3.5–5.5 μm, with 4 sterigmata; basidiospores oblong-ellipsoid to ellipsoid, 3.5–5 × 2–3 μm (ave. 3.9 ± 0.2 × 2.5 ± 0.4 μm, n = 25), smooth, thin-walled.

Specimens examined: **KOREA**, **Chungcheongbuk-do**, Goesan-gun, Korea University Experimental Forest, 36°46′13″N 127°58′57–59″E, fallen branches of *Quercus* sp. 07 July 2010, Yeongseon Jang (KB NIBRFG0000114705, GenBank JN618336, JN641758, JN641760; KB NIBRFG0000114712, GenBank JN618335, JN641759, JN641761).

Ecology & distribution — China, Korea, and Japan on gymnosperms and angiosperms.

Remarks — The characters generally match those of the holotype. However, basidiospore sizes were more variable in the Korean specimens. Suhara et al. (2003) cited 4.25–5 × 2.5–2.75 μm (ave. 4.5 ± 0.3 × 2.6 ± 0.1 μm, n = 20) for the holotype basidiospores, whereas those from our specimens measured 3.5–5 × 2–3 μm (ave. 3.9 ± 0.2 × 2.5 ± 0.4 μm, n = 25).

Phylogeny

MP and NJ analyses of the 28S, 18S, and ITS rDNA regions were conducted to confirm the morphological identification. The aligned dataset of 11 sequences

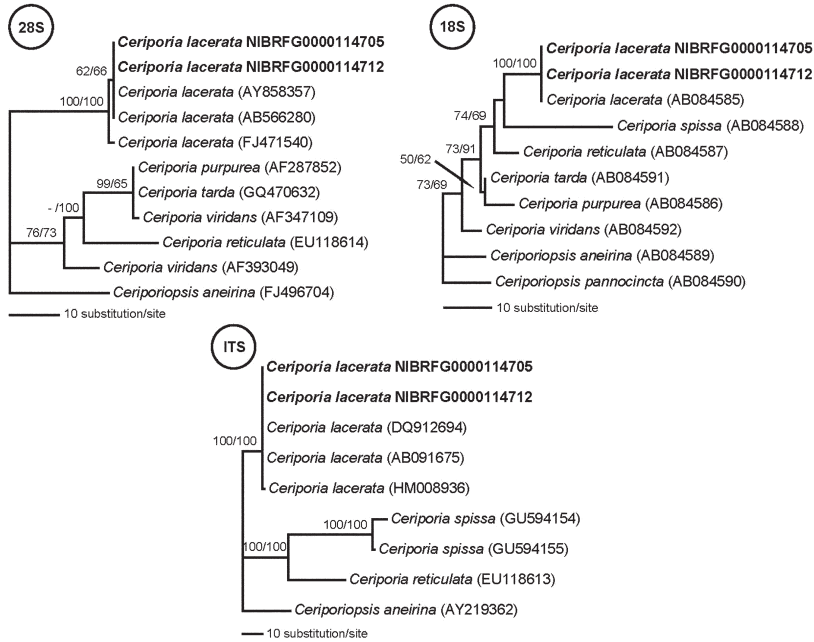

Fig. 2. 28S, 18S, and ITS rDNA region maximum parsimonious trees of *Ceriporia lacerata* and allied species. The trees were rooted by *Ceriporiopsis* species. Bootstrap values ≥ 50% are shown above branches (MP bootstrap proportions/NJ bootstrap proportions). Specimens found in this study are in bold. GenBank accession numbers in parentheses.

of 28S rDNA comprised 504 characters, of which 435 sites were constant, 24 sites variable, and 45 sites parsimony informative; tree length was 90 steps with consistency index (CI) = 0.8222 and retention index (RI) = 0.8841. The 18S rDNA dataset of 12 sequences comprised 1645 characters, of which 1578 were constant, 41 variable, and 26 parsimony informative; tree length was 79 steps with CI = 0.8608 and RI = 0.8226. The ITS rDNA dataset of 9 sequences comprised 390 characters with 281 constant, 44 variable, and 65 parsimony informative sites; tree length was 138 steps with CI = 0.9855 and RI = 0.9802. The MP and NJ analyses of all three regions clustered our sequences with previously reported sequences of *Ceriporia lacerata* with high bootstrap supports (Fig. 2). The Korean *C. lacerata* (KB NIBRFG0000114705, KB NIBRFG0000114712) showed 100% sequence similarity to a Japanese specimen (GenBank AB084585) in 18S rDNA region according to a BLAST search of GenBank. ITS rDNA region also showed 99.8% similarity (one out of 560 positions showed nucleotide difference) to a Japanese specimen (GenBank AB091675). No 28S

rDNA sequences of a Japanese specimen were available, but our specimens had 100% similarity to *C. lacerata* strains of Korea and Japan.

Discussion

Ceriporia lacerata was first described as a new species from Japan in 2003 (Suhara et al. 2003) and three years later reported from China (Cui et al. 2006, Dai 2012). In Korea, *C. lacerata* strains have been isolated from playground wood (Kim et al. 2005), CCA-treated wood (Kim et al. 2007), decayed pine tree logs (Kim et al. 2009), and decayed bamboo (Kim et al. 2011). They were also isolated from Mt. Bukhan (Seoul), Mt. Halla (Jeju), Mt. Joryeong (Chungcheongbuk-do), Mt. Mani (Incheon), Mt. Yongmun (Gyeonggi-do), and Yangpyeong Korea University Experimental Forest (Gyeonggi-do) in 2008–10 during the Korean indigenous species research project (unpublished data) and basidiocarps were found in Goesan-gun, Chungcheongbuk-do, in 2010. *Ceriporia lacerata* occurs on both angiosperm and gymnosperm wood and is widely distributed in China (Dai 2012). Our observation confirms *C. lacerata* within northeast Asia, and it is reasonable to infer that it inhabits other Asian countries in the 30–45°N latitude.

Morphologically, *Ceriporia lacerata* is similar to *C. alachuana* (Murrill) Hallenb. and *C. ferruginicincta* (Murrill) Ryvarden by having a whitish to ochreous pore surface and oblong to ellipsoid basidiospores. However, the other two species differ in having pores with entire dissepiments (3–8 per mm in *C. alachuana* and 6–8 per mm in *C. ferruginicincta*; Suhara et al. 2003), contrasting with the entire to lacerate dissepiments (2–5 per mm) of *C. lacerata.*

The 28S and ITS rDNA phylogenetic trees had similar topologies with *Ceriporia lacerata* forming a clade distinct from that of the other *Ceriporia* species (Fig. 2). On the other hand, all the analyzed *Ceriporia* species were monophyletic in 18S rDNA tree, as previously suggested by Wu et al. (2010), with *C. spissa* (Schwein.) Rajchenb. sister to *C. lacerata*. Both species occur on hardwoods and conifers, but *C. spissa* has bright orange basidiocarps (Gilbertson & Ryvarden 1986). The phylogenetic conflict represented here is probably the result of limited taxon sampling. More molecular data derived from other species are needed for the clear elucidation.

Since Kondo et al. (1999) reported that *Ceriporia lacerata* had the ability to degrade polychlorinated dibenzo-p-dioxines (PCDDs) and polychlorinated dibenzo-furans (PCDFs), its industrial potential has been investigated in pretreatment of lignocellulosic biomass for efficient hydrolysis and biofuel production (Lee et al. 2007) and PAHs degradation (Lee et al. 2010). Remarkably, Long et al. (2010) reported that *C. lacerata* had the highest decolorization ability for synthetic dyes (Congo Red, Orange II, and Reactive Blue 4) among the

white rot fungal species tested in solid media. However, information regarding this species is still limited and the abilities of this species should be investigated further.

Key to the species of *Ceriporia* in Korea

1. Pore surface pale to dark brownish purple;
   (basidiospores allantoid, 5–7 μm long) ..... *C. purpurea*
1. Pore surface white to brown 2
2. Pore surface cream to sordid pinkish-brown;
   (basidiospores cylindric to allantoid, 4-5 μm long)..... *C. viridans*
2. Pore surface white to ochraceous 3
3. Basidiospores allantoid, 6–8 × 2–3 μm ..... *C. reticulata*
3. Basidiospores oblong-ellipsoid to ellipsoid, 3.5–5 × 2–3 μm ..... *C. lacerata*

Acknowledgements

This work was carried out with the support of 'Forest Science & Technology Projects (Project No. S121010L110000) provided by Korea Forest Service. This work was also supported by the Korean indigenous species research project from the National Institute of Biological Resources (NIBR), Ministry of Environment, Republic of Korea, and by a Korea University Grant. We are grateful to Dr. Yu-Cheng Dai and Dr. Kentaro Hosaka for their valuable suggestions on the manuscript.

Literature cited

Cui B, Wei Y, Dai Y. 2006. Polypores from Zijin Mountain, Jiangsu province. Mycosystema 25: 9–14.

Dai YC. 2012. Polypore diversity in China with an annotated checklist of Chinese polypores. Mycoscience 53: 49–80. http:/dx.doi.org/10.1007/s10267-011-0134-3

Dams E, Hendriks L, Van de Peer Y, Neefs JM, Smits G, Vandenbempt I, De Wachter R. 1988. Compilation of small ribosomal subunit RNA sequences. Nucleic. Acids. Res. 16: r87–r173.

Gardes M, Bruns TD. 1993. ITS primers with enhanced specificity for basidiomycetes – application to the identification of mycorrhizae and rusts. Mol. Ecol. 2: 113–118. http:/dx.doi.org/10.1111/j.1365-294X.1993.tb00005.x

Gilbertson RL, Ryvarden L. 1986. North American polypores, Vol. 1. Fungiflora, Oslo.

Jang YS, Choi HE, Lim YW, Lee JS, Kim J-J. 2011. The first report of *Antrodia sitchensis* (*Polyporaceae, Basidiomycota*) in Korea. Mycobiology 39: 226-229. http:/dx.doi.org/10.5941/MYCO.2011.39.3.226

Jung HS. 1994. Floral studies on Korean wood-rotting fungi (II) – on the flora of the *Aphyllophorales* (*Basidiomycotina*). Kor. J. Mycol. 22: 62–99.

Kim G-H, Lim YW, Song Y-S, Kim J-J. 2005. Decay fungi from playground wood products in service using LSU rDNA sequence analysis. Holzforschung 59: 459–466. http:/dx.doi.org/10.1515/HF.2005.076

Kim G-H, Lim YW, Choi Y-S, Kim M-J, Kim J-J. 2009. Primary and secondary decay fungi on exposed pine tree logs in the forest. Holzforschung 63: 633–638. http:/dx.doi.org/10.1515/HF.2009.099

Kim J-J, Kang S-M, Choi Y-S, Kim G-H. 2007. Microfungi potentially disfiguring CCA-treated wood. Int. Biodeter. Biodegr. 60: 197–201. http:/dx.doi.org/10.1016/j.ibiod.2007.05.002

Kim J-J, Lee S-S, Ra J-B, Lee H, Huh N, Kim G-H. 2011. Fungi associated with bamboo and their decay capabilities. Holzforschung 61: 271–275. http:/dx.doi.org/10.1515/HF.2011.004

Kondo R, Mori T, Yoshimitu M, Hirose M, Wakao K, Matufuji Y, Sakai K. 1999. 10th Haikibutugakkai Youshishuu: 877–879. [In Japanese]

Largent DL, Johnson D, Watling R. 1977. How to identify mushrooms to genus, III. Microscopic features. Mad River Press, Eureka, CA, USA.

Lee H, Choi Y-S, Kim M-J, Huh N-Y, Kim G-H, Lim YW, Kang S-M, Cho S-T, Kim J-J. 2010. Degrading ability of oligocyclic aromates by *Phanerochaete sordida* selected via screening of white rot fungi. Folia Microbiol. 55: 447–453. http:/dx.doi.org/10.1007/s12223-010-0075-9

Lee JS, Jung HS. 2005. List of recorded Korean *Aphyllophorales*. Kor. J. Mycol. 33: 38–53.

Lee JS, Kim KM, Jung HS. 2002. The *Aphyllophorales* of the Kyeryoungsan National Park. Mycobiology 30: 133–138.

Lee J-W, Gwak K-S, Park J-Y, Park M-J, Choi D-H, Kwon M, Choi I-G. 2007. Biological pretreatment of softwood *Pinus densiflora* by three white rot fungi. J. Microbiol. 45: 485–491.

Lim YW, Kim YH, Jung HS. 2000. The *Aphyllophorales* of Mungyong Saejae. Mycobiology 28: 142–148.

Long Y, Kim M-J, Kim J-J, Kim G-H. 2010. Screening of white rot fungi to decolorize synthetic dyes. Abstr. B027, p. 194, in: Proc. International Meeting of the Federation of Korean Microbiological Societies.

Suhara H, Maekawa N, Kaneko S, Hattori T, Sakai K, Kondo R. 2003. A new species, *Ceriporia lacerata*, isolated from white-rotted wood, Mycotaxon 86: 335–347.

Vilgalys R, Hester M. 1990. Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. J. Bacteriol. 172: 4238–4246.

White TJ, Bruns TD, Lee S, Taylor JW. 1990. Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. 315–322, in: PCR Protocols: A Guide to Methods and Applications. Academic Press, New York.

Wu S-H, Nilsson RH, Chen C-T, Yu S-Y, Hallenberg N. 2010. The white-rotting genus *Phanerochaete* is polyphyletic and distributed throughout the phlebioid clade of the *Polyporales* (*Basidiomycota*). Fungal Divers. 42: 107–118. http:/dx.doi.org/10.1007/s13225-010-0031-7