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Research Article

Five New Wood Decay Fungi (Polyporales and Hymenochaetales) in Korea

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Abstract The wood decay fungi are a diverse taxonomic group that plays a pivotal role in forest carbon cycling. Wood decay fungi use various enzymatic pathways to digest dead or living wood in order to obtain carbon and other nutrients and these enzymatic systems have been exploited for both industrial and medical applications. Over 600 wood decay fungi species have been described in Korea; however, the recent application of molecular markers has dramatically altered the taxonomy of many of these wood decay fungi at both the genus and species levels. By combining molecular methods, specifically sequences of the internal transcribed spacer region, with traditional morphological characters, this study identified five new species records for Korea in five genera: *Aurantiporus*, *Favolus*, *Neofavolus*, *Loweomyces,* and *Hymenochaetopsis*. Three of these genera (*Aurantiporus*, *Favolus*, and *Loweomyces*) were previously unknown in Korea. The relatively simple morphology of the wood decay fungi often leads to ambiguous taxonomic assignment. Therefore, molecular markers are a necessary component of any taxonomic or evolutionary study of wood decay fungi. Our study highlights the need for a more robust and multifaceted approach in investigating new wood decay fungi in Korea.

Keywords Hymenochaetales, ITS, New record, Polyporales, Wood decay fungi

Wood decay fungi obtain their energy requirements by digesting molecules such as cellulose and lignin in moist dead or living wood and play a pivotal ecological role in forest carbon cycling (biodegradation) [1]. The decomposition of wood was first ascribed to wood decay fungi by Schacht in 1863 [2]. The majority of wood decay fungi colonize different environmental niches and produce several kinds of lignocellulolytic enzymes that break down dead wood [3]. Recently, the enzymatic systems of wood decay fungi have been recognized as potentially important natural resources. The enzymes of many species have been used in biofuel production [4, 5], bioremediation [6], and medicine [7].

Most wood decay fungi belong to several orders of class Agaricomycetes in phylum Basidiomycota. Although some wood decay fungi exhibit a characteristic agaric shape in Agaricales and Boletales, the majority of species belonging to the orders Polyporales and Hymenochaetales have simple shape of basidiocarp morphology [8-10]. Previous identification of wood decay fungi within the Polyporales was primarily based on morphological characteristics such as pileus color, pore size, basidiospore shape, hyphal system, clamp connection, and type of rot [3, 11, 12]; however, species identification based on morphology alone is insufficient due to the relatively simple characteristics and substantial morphological variation of wood decay fungi compared to other fungal groups [13-15].

Since the introduction of molecular phylogenetics, which has recently been extended to phylogenomics, to taxonomic and evolutionary studies of wood decay fungi, an abundance of DNA sequence information has accumulated and subsequently, many phylogenetic relationships have been clarified. For example, phylogenomic analysis has clarified the phylogenetic relationships in the Polyporales [16, 17]. In addition, updated evolutionary relationships within the *Polyporus*, *Favolus*, and *Neofavolus* were proposed by Sotome *et al.* [18]. An investigation of the phylogenetic

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relationships in the Hymenochaetales used two loci: the internal transcribed spacer (ITS) region and the large subunit rDNA (LSU) region [19-22]. In most recent phylogenetic studies of fungi, the ITS region has been used because there is sufficient sequence variation at this locus to resolve closely related species across the fungal tree of life. Thus, this locus has been formally proposed to be the primary fungal barcoding gene [23], and a dramatic increase in available ITS sequences have facilitated more accurate species identification across diverse fungal taxa [24, 25].

Approximately 600 wood decay fungi have been listed in the Korean fungal inventory [26]. Wood decay fungi have traditionally been identified based on the morphology of their fruiting body as well as underlying microscopic features. Recently, the combination of these morphological data with ITS sequence analysis has increased the accuracy of species identification of wood decay fungi dramatically [25, 27-29]. A recent project surveying and excavating Korean indigenous fungi has been organized by the National Institute of Biological Resources (NIBR, http://www.nibr.go.kr). Through this project, we discovered five new records of wood rot fungi from Korea. The specimens were identified to the species level using a two-step approach: phylogenetic analysis based on the ITS region and verification using morphological characters. In this paper, we document and describe these new species records using this two-step approach.

MATERIALS AND METHODS

Samples and morphological observation. Specimens of wood decay fungi were collected from various locations in Korea between 2012 and 2015. Specimens were dried and deposited in the Seoul National University Fungus Collection (SFC). The specimens were putatively identified based on fruiting body morphology and microscopic characteristics using Nikon 80i light microscope (Nikon, Tokyo, Japan) [11, 12, 18, 30]. Dried tissue was rehydrated in 3% (w/v) KOH and stained in 1% (w/v) phloxine in order to measure key features, and drawings of these macromorphological and micromorphological features were generated. Our primary focus was the measurement of basidia (30 per sample) and basidiospores (10 per sample). "Q" in our results refers to the length/width ratio of an individual basidiospore; (n = x/y) means x measurement of basidiospores from y specimens.

DNA extraction, PCR, sequencing and phylogenetic analysis. Genomic DNA was extracted using a modified cetyltrimethylammonium bromide extraction protocol and the ITS locus was amplified using the primers ITS1F and ITS4b [31, 32]. PCRs were conducted using a C1000 thermal cycler (Bio-Rad, Hercules, CA, USA) using the AccuPower PCR Premix (Bioneer Co., Daejeon, Korea) in a final volume of 20 μL containing 10 pmol of each primer and 1 μL of

Table 1. Specimen information used in this study

Species and Specimen	Substrate	Locality	Accession No.
Polyporales, Polyporaceae			
Aurantiporus fissilis (Berk. & M. A. Curtis) H. Jahn ex Ryvarden			
SFC20140626-03	Oak	Guri-si, Gyeonggi-do	KX792915
Favolus acervatus (Lloyd) Sotome & T. Hatt.			
SFC20120725-05	Oak	Boryeong-si, Chungcheongnam-do	KX792916
SFC20150707-73	Hardwood	Gwacheon-si, Gyeonggi-do	KX792917
SFC20150818-25	Hardwood	Ganghwa-gun, Incheon	KX792918
SFC20150820-03	Hardwood	Uiwang-si, Gyeonggi-do	KX792919
Neofavolus mikawai (Lloyd) Sotome & T. Hatt.			
SFC20140702-07	Hardwood	Seogwipo-si, Jeju-do	KX792920
SFC20150630-50	Hardwood	Jeju-si, Jeju-do	KX792921
Polyporales, Meruliaceae			
Loweomyces fractipes (Berk. & M. A. Curtis) Jülich			
SFC20130917-07	Hardwood	Yecheon-gun, Gyeongsangbuk-do	KX792922
SFC20140725-33	Hardwood	Jinan-gun, Jeollabuk-do	KX792923
SFC20140818-10	Hardwood	Boeun-gun, Chungcheongbuk-do	KX792924
SFC20140921-24	Hardwood	Jinan-gun, Jeollabuk-do	KX792925
SFC20150828-34	Hardwood	Muju-gun, Jeollabuk-do	KX792926
SFC20150902-80	Hardwood	Inje-gun, Gangwon-do	KX792927
Hymenochaetales, Hymenochaetaceae			
Hymenochaetopsis rigidula (Berk. & M. A. Curtis) S. H. He & Y. C. Dai			
SFC20140314-10	Hardwood	Jinan-gun, Jeollabuk-do	KX792928
SFC20140411-08	Hardwood	Jinan-gun, Jeollabuk-do	KX792929
SFC20140411-20	Hardwood	Jinan-gun, Jeollabuk-do	KX792930
SFC20140703-24	Hardwood	Jeju-si, Jeju-do	KX792931
SFC20140723-16	Hardwood	Jinan-gun, Jeollabuk-do	KX792932

DNA using the conditions described by Park *et al.* [33]. PCR products were purified using the Expin PCR Purification Kit (GeneAll Biotechnology, Seoul, Korea) according to the manufacturer's instructions. DNA sequencing was performed by Macrogen (Seoul, Korea), using an ABI3700 automated DNA sequencer.

Amplicons were aligned, proofread, and edited using MEGA 5 [34]. Representative sequences were deposited in GenBank (accession numbers presented in Table 1). Reference sequences were downloaded from GenBank and multiple alignments were performed using the default settings of MAFFT v7 [35]. Neighbor joining (NJ) trees were constructed with MEGA 5 (Kimura 2-parameter model) with 1,000 bootstrap replicates [36].

RESULTS

Phylogenetic analyses. Eighteen specimens were identified to five species in five genera: *Aurantiporus*, *Favolus*, *Neofavolus*, *Loweomyces*, and *Hymenochaetopsis*. A NJ tree was constructed for each genus, with specimens from this study highlighted in gray boxes (Figs. 1~5). One specimen (SFC20140626-03) was identified as *Aurantiporus* based on ITS sequences and a phylogram was constructed using 23 closely related species with *Rigidoporus ulmarius* as an outgroup. This specimen formed a monophyletic clade with the reference sequences of *Aurantiporus fissilis* (bootstrap support, 100%; sequence similarity, 99.7~100.0%). *A. fissilis* formed a sister clade with *Aurantiporus pulcherrimus* (HQ533012, 85.2%) and *Aurantiporus* sp. (KT156705, 88.6%) (Fig. 1).

Four specimens (SFC20120725-05, SFC20150707-73, SFC20150818-25, and SFC20150820-03) formed a monophyletic group with the reference sequences of *Favolus acervatus* with 100% bootstrap support and their sequence similarity ranged from 99.8% to 100.0% (Fig. 2). Two specimens (SFC20140702-07 and SFC20150630-50) grouped with the reference sequence of *Neofavolus mikawai* (bootstrap support, 100%; sequence similarity, 99.6~100.0%). While *N. mikawai* exhibited strong sequence similarity with both *Neofavolus alveolaris* (AB735967 and AB735968, 90.0~90.8%) and *Neofavolus cremeoalbidus* (AB735979 and AB735980, 90.5~91.1%), which are sister species, the evolutionary relationships of these three species are unclear as the cluster was not supported (Fig. 3).

Six specimens (SFC20130917-07, SFC20140725-33, SFC20140818-10, SFC20140921-24, SFC20150828-34, and SFC20150902-80) clustered into a monophyletic group with the reference sequences of *Loweomyces fractipes* (bootstrap support, 100%; sequence similarity, 97.8~100.0%) (Fig. 4).

Five *Hymenochaete*-like specimens (SFC20140314-10, SFC20140411-08, SFC20140411-20, SFC20140703-24, and SFC20140723-16) formed a monophyletic clade with the reference sequences of *Hymenochaetopsis rigidula*. The

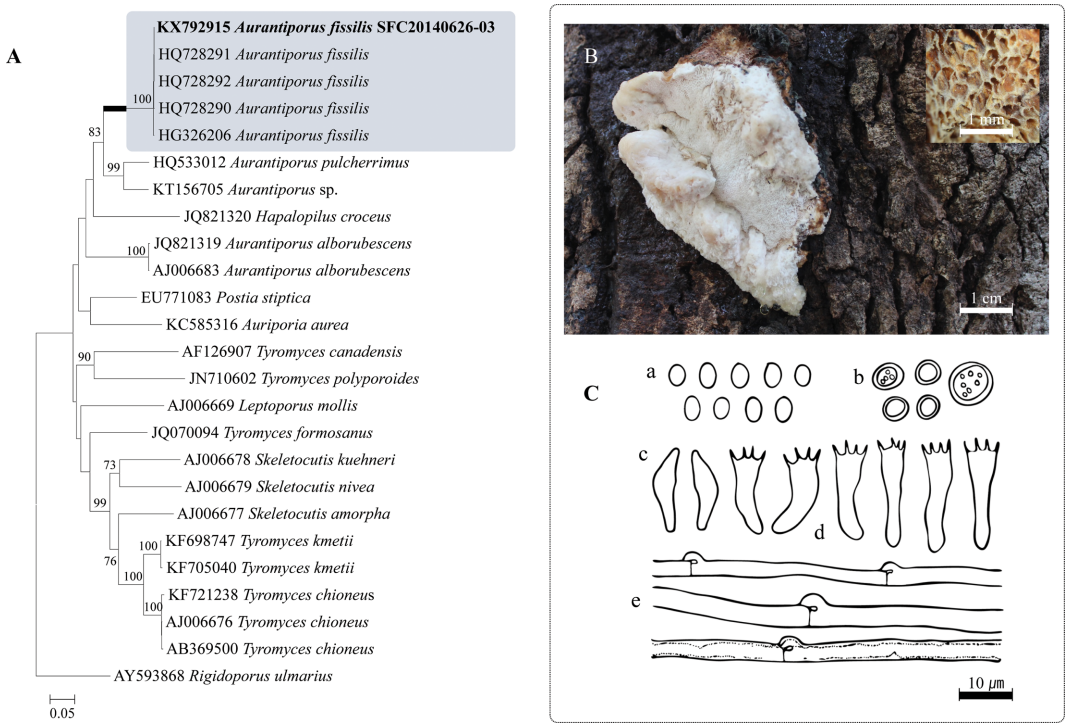

Fig. 1. Phylogenetic tree and morphological features of *Aurantiporus fissilis*. A, Neighbor joining tree based on internal transcribed spacer sequences. Bootstrap scores of > 70 are presented at the nodes. Gray box indicates focal taxon of this phylogeny; B, Fruiting body and pore size; C, Microscopic features. a, basidiospores; b, clamydospores; c, cystidiols; d, basidia; e, generative hyphae.

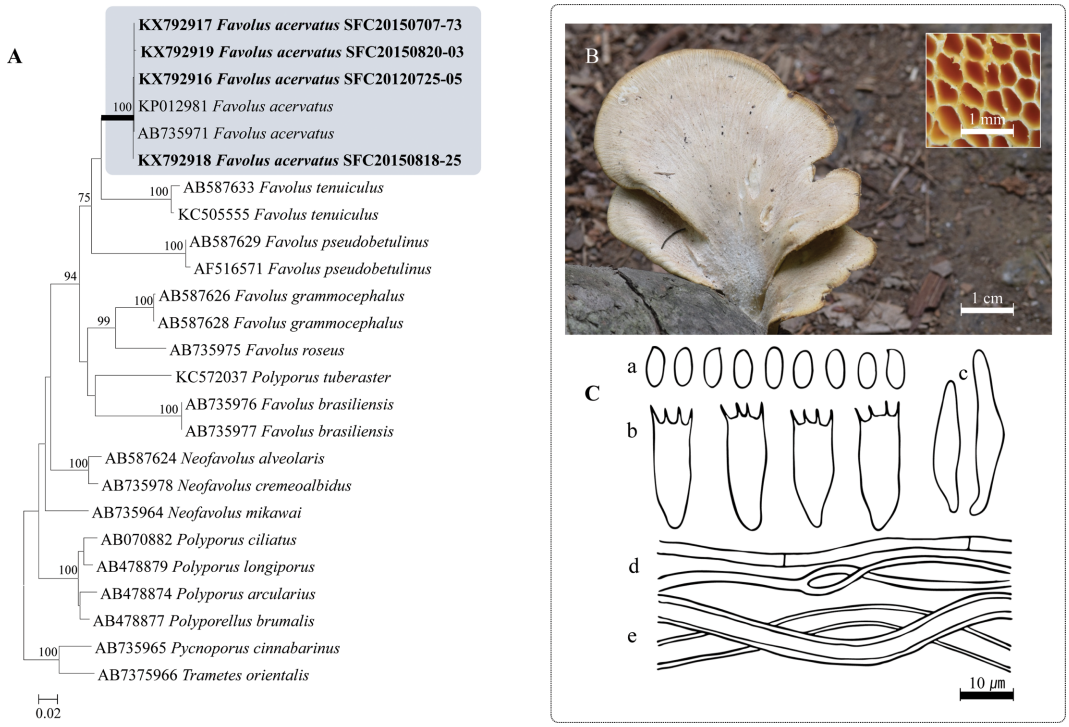

Fig. 2. Phylogenetic tree and morphological features for *Favolus acervatus*. A, Neighbor joining tree based on internal transcribed spacer sequences. Bootstrap scores of > 70 are presented at the nodes. Gray box indicates focal taxon of this phylogeny; B, Fruiting body and pore size; C, Microscopic features. a, basidiospores; b, basidia; c, cystidiols; d, generative hyphae without clamp connection; e, skeletal-binding hyphae.

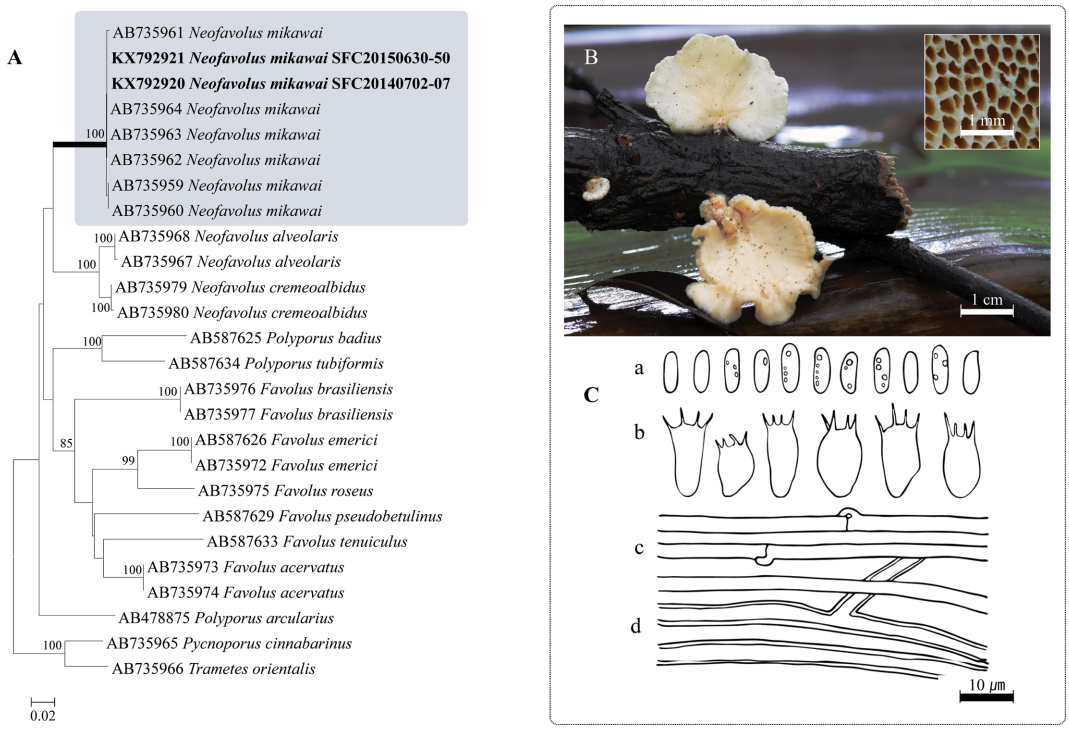

Fig. 3. Phylogenetic tree and morphological features for *Neofavolus mikawai*. A, Neighbor joining tree based on internal transcribed spacer sequences. Bootstrap scores of > 70 are presented at the nodes. Gray box indicates focal taxon of this phylogeny; B, Fruiting body and pore size; C, Microscopic features. a, basidiospores; b, basidia; c, generative hyphae; d, skeletal-binding hyphae.

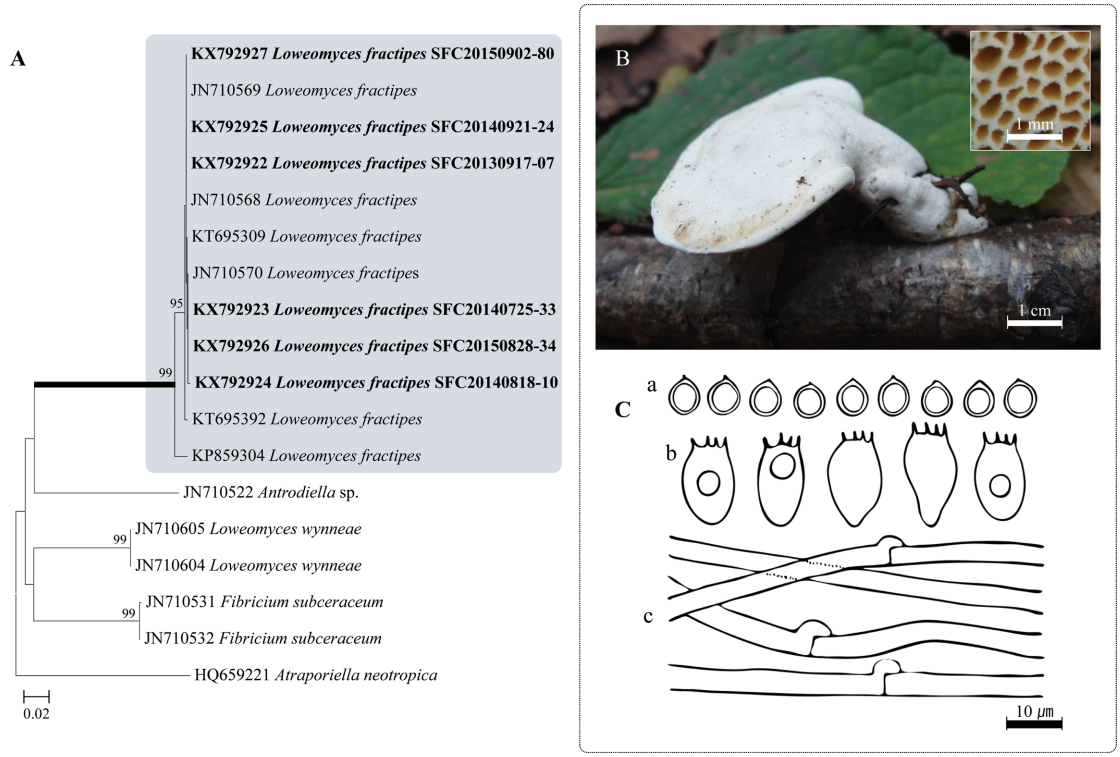

Fig. 4. Phylogenetic tree and morphological features for *Loweomyces fractipes*. A, Neighbor joining tree based on internal transcribed spacer sequences, Bootstrap scores of > 70 are presented at the nodes. Gray box indicates focal taxon of this phylogeny; B, Fruiting body and pore size; C, Microscopic features. a, basidiospores; b, basidia; c, generative hyphae.

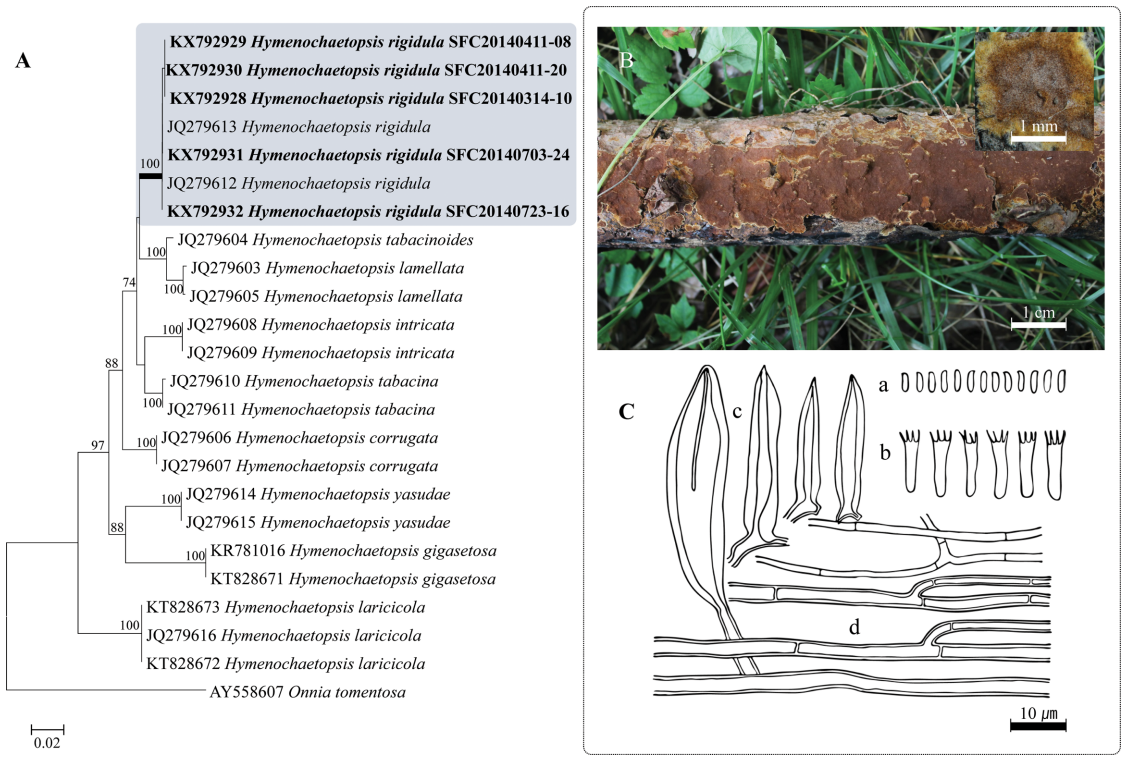

Fig. 5. Phylogenetic tree and morphological features for *Hymenochaetopsis rigidula*. A, Neighbor joining tree based on internal transcribed spacer sequences, Bootstrap scores of > 70 are presented at the nodes. Gray box indicates focal taxon of this phylogeny; B, Fruiting body; C, Microscopic features. a, basidiospores; b, basidia; c, setae; d, generative hyphae.

similarity of all the sequences in this clade was high (99.8~100.0%) and the clade was well supported (100% bootstrap value). *Hymenochaetopsis tabacinoides* and *H. lamellata* were the sister species although bootstrap support value was low (Fig. 5).

Taxonomy.

1. *Aurantiporus fissilis* (Berk. & M. A. Curtis) H. Jahn ex Ryvarden, Polyp. N. Eur. (Oslo) 2: 222 (1978).

Basidiocarps annual, pileate, broadly attached, sessile, single or imbricate, triquetrous in section, sappy to waxy and tough when fresh, drying slowly with substantial shrinking and becoming dense and hard, upper surface tomentose to pubescent, ochraceous, margin rounded or sharp. Hymenophore white, often with pinkish tint, yellowish ochraceous when dry, pores circular, 2~3 per mm, dissepiments thin, somewhat lacerate. Context slightly dark umber when dry, up to 6.5 mm thick. Tube darker than the context, up to 4 mm thick. Hyphal system monomitic; generative hyphae with clamps, thin- to thick-walled. Basidia clavate, 4-sterigmate, 17.1~22.3 × 4.5~5.7 μm. Basidiospores ellipsoid to subglobose, smooth, thin-walled, hyaline, negative in Melzer's reagent (IKI), 4.5~5.7 × 3.2~3.5 μm. L = 4.9 μm, W = 3.3 μm, Q = 2.02 (n = 20/1). Chlamydospores present in the context, globose with oil drops, thick-walled.

Habitat: White heat rot of living hardwood.

Material examined: Korea, Gyeonggi-do, Guri-si, Dongguneung, on oak, 26 Jun 2014, Y. W. Lim (SFC20140626-03).

Notes: *A. fissilis* is easily recognized by sappy and drying shrunken basidiocarps.

2. *Favolus acervatus* (Lloyd) Sotome & T. Hatt., Fungal Divers. 58: 254 (2013).

Basidiocarps annual, lateral stipitate to sessile; pileus dimidiate to flabellate, up to 10 cm long and 14 cm wide, up to 6 mm thick; pileal surface white to ivory, with age becoming light brown, radially faint striate, azonate, slightly glabrous, margin acute. Hymenophore white to cream when fresh, pores angular, 3~5 per mm; dissepiments thin. Context in pileus pale tan to ivory, corky, brittle when dry, up to 4 mm thick. Tube continuous with the context, up to 5 mm thick. Stipe lateral, white to ivory, covered with pore or glabrous, up to 30 mm long and 15 mm thick. Hyphal system dimitic; generative hyphae hyaline in KOH, thin-walled, 2.5~3.5 μm in diam., septa without clamp connection, skeletal-binding hyphae thick-walled, nonseptate, much branched, with tapering apices, up to 5.5 μm in diameter. Cystidia fusoid cystidioles present, 25~32 × 4.5~5.7 μm. Basidia clavate, 4-sterigmate (up to 3.4 μm), 23~25 × 7~7.5 μm. Basidiospores navicular to cylindric, hyaline, smooth, IKI–, 7~8 × 2.9~3.4 μm. L = 7.8 μm, W = 3.2 μm, Q = 2.46 (n = 60/5).

Habitat: Solitary to imbricate on dead wood of hardwood and conifer.

Material examined: Korea, Chungcheongnam-do, Boryeong-si, Mt. Seongju, on oak, 25 Jul 2012, Y. W. Lim (SFC20120725-05); Korea, Gyeonggi-do, Gwacheon-si, Mt. Cheonggye, on *Actinidia arguta*, 7 Jul 2015, Y. W. Lim (SFC20150707-73); Korea, Incheon-si, Ganghwa-gun, Mt. Mani, on hardwood, 18 Aug 2015, Y. W. Lim (SFC20150818-25).

Notes: *F. acervatus* has various shapes of basidiocarps, and is characterized by white to ivory basidiocarps and generative hyphae lacking clamp connections. It was treated as a synonym of *P. grammocephalus* [37-39], but can be distinguished from *P. grammocephalus* by several characteristics such as an orange to brown pileus surface, frequently flabelliform pileus, generative hyphae with clamp connections, and cylindrical basidiospores [18].

3. *Neofavolus mikawai* (Lloyd) Sotome & T. Hatt., Fungal Divers. 58: 251~253 (2013).

Basidiocarps annual, lateral stipitate to sessile; pileus dimidiate to flabellate, up to 40 mm long and 40 mm wide, up to 6 mm thick; pileal surface white to cream, azonate, slightly glabrous, margin acute, dark brown when dry. Hymenophore white to cream when fresh becoming light brown, pores angular, 2~5 per mm; dissepiments thin. Context in pileus cream to ivory, corky, brittle when dry, up to 4 mm thick. Tube continuous with the context, up to 4 mm thick. Stipe lateral or invisible, white to cream, covered with pore or glabrous. Hyphal system dimitic; generative hyphae hyaline in KOH, thin-walled, 2.8~3.4 μm in diam., septa with clamp connection, skeletal-binding hyphae thick-walled, nonseptate, highly branched, with tapering apices, up to 5.1 μm in diameter. Basidia clavate, 4-sterigmate (up to 4.5 μm), 12~17.7 × 2.8~4.5 μm. Basidiospores navicular to cylindric, hyaline, smooth, IKI–, 8~9.2 × 2.5~3.3 μm. L = 8.4 μm, W = 2.8 μm, Q = 3.02 (n = 20/1).

Habitat: Solitary to gregarious on dead wood of hardwood.

Material examined: Korea, Jeju-do, Seogwipo-si, Andeok-ri, on hardwood, 2 Jul 2014, Y. W. Lim (SFC20140702-07); Korea, Jeju-do, Jeju-si, Pyeongdae-ri, on hardwood, 30 Jun 2015, Y. W. Lim (SFC20150630-50).

Notes: *N. mikawai* was found only on Jeju Island, Korea. It was previously known only from restricted areas of warm-temperate climates in Japan and China. This species has basidiocarps similar to *F. acervatus* but can be differentiated by its short basidia (up to 17.7 μm long) and generative hyphae with clamp connection.

4. *Loweomyces fractipes* (Berk. & M. A. Curtis) Jülich, Persoonia 11: 424 (1982).

Basidiocarps annual, laterally stipitate, dimidiate with fan-shaped to reniform pilei, 2~6 cm wide, 1~5 mm thick, soft when fresh, brittle when dry; upper surface white when fresh, becoming ochraceous to straw coloured with age and drying, at first finely tomentose, with age more adpressed and semi-glabrous. Hymenophore white to cream, pores angular, 6~7 per mm, often decurrent on the stipe, but sharply delimited. Context in pileus and stipe white or beige and duplex with a hard inner layer covered with a

much looser layer. Tube layer concolorous, up to 2 mm thick. Stipe white to ochraceous, up to 40 mm long and 15 mm wide at the base, cylindric to flattened and expanded towards the pileus. Hyphal system monomitic; generative hyphae with clamps, thin-walled. Cystidia not seen. Basidia broadly clavate, 4-sterigmate, 14.9~17.5 × 7.4~9.1 µm. Basidiospores broadly ellipsoid or ovoid to subglobose, thick-walled, smooth, hyaline. IKI–, 5.8~6.9 × 5.1~5.5 µm. L = 6.5 µm, W = 5.3 µm, Q = 1.23 (n = 20/1).

Habitat: On dead hardwoods.

Material examined: Korea, Gyeongsangbuk-do, Yecheon-gun, Mt. Maebong, on hardwood, 17 Sep 2013, Y. W. Lim (SFC20130917-07); Korea, Jeollabuk-do, Jinan-gun, Mt. Cheonban, on hardwood, 25 Jul 2014, Y. W. Lim (SFC20140725-33); Korea, Chungcheongbuk-do, Boeun-gun, Mt. Songni, on hardwood, 18 Aug 2014, Y. W. Lim (SFC20140818-10); Korea, Jeollabuk-do, Jinan-gun, Mt. Unjang, on hardwood, 21 Sep 2014, Y. W. Lim (SFC20140921-24); Korea, Jeollabuk-do, Muju-gun, Mt. Deogyu, on hardwood, 28 Aug 2015, Y. W. Lim (SFC20150828-34); Korea, Gangwon-do, Inje-gun, Wondea-ri, on hardwood, 2 Sep 2015, Y. W. Lim (SFC20150902-80).

Notes: *L. fractipes* is easily distinguished by its lateral stipitate basidiocarp, two layers context, and ovoid to subglobose basidiospores.

5. *Hymenochaetopsis rigidula* (Berk. & M. A. Curtis) S. H. He & Jiao Yang, Mycol. Prog., 15: 1~8 (2016).

Basidiocarps effused or effuso-reflexed with slightly elevated margins, coriaceous to hard and brittle when dry, very thin, several centimeters to decimeters in extent reflexed part short and broad. Hymenium smooth or slightly tuberculate when old, sometimes slightly irregularly cracked, brown in fresh, with age gray-brown, resupinate margin distinct. Hyphal system monomitic, generative hyphae without clamps, thick- to thin-walled, infrequently branched, setal hyphae 4~6 µm in diam, brownish. Setae dark brown, thick-walled, fusiform, 40~57 µm. Basidia clavate, 4-sterigmate, 15.4~17.1 × 3.1~3.9 µm. Basidiospores short-cylindrical or cylindrical and slightly curved, 4.5~5.1 × 1.5~1.6 µm. L = 5.0 µm, W = 1.5 µm, Q = 3.31 (n = 20/1).

Habitat: On dead branch of hardwoods.

Material examined: Korea, Jeollabuk-do, Jinan-gun, Mt. Unjang, on hardwood, 14 Mar 2014, Y. W. Lim (SFC20140314-10); Korea, Jeollabuk-do, Jinan-gun, Mt. Unjang, on hardwood, 11 Apr 2014, Y. W. Lim (SFC20140411-08); Korea, Jeollabuk-do, Jinan-gun, Mt. Unjang, on hardwood, 11 Apr 2014, Y. W. Lim (SFC20140411-20); Korea, Jeju-do, Jeju-si, Mt. Halla, on hardwood, 3 Jul 2014, Y. W. Lim (SFC20140703-24); Korea, Jeollabuk-do, Jinan-gun, Mt. Unjang, on hardwood, 23 Jul 2014, Y. W. Lim (SFC20140723-16).

Notes: This species is easily confused with *Hymenochaetopsis corrugata* due to similar morphology and habitat. Although the slightly longer basidia (15.4~17.1 µm) of *H. rigidula* is a distinguishable character, morphological characters alone are not sufficient to accurately identify this species. Therefore, ITS sequence analysis is required to confirm the identity.

DISCUSSION

In this study, we combined macro- and microscopic morphological observations with molecular analysis of ITS sequences, and accurately identify five species (in five genera) of wood decay fungi that are new records to Korea. While BLAST searches using ITS sequences can provide valuable preliminary identification of species, incorrectly identified sequences in GenBank is an open database are not uncommon (approximately 20%) [40]. Therefore, phylogenetic analysis combined with morphological observations are critical in order to accurately identify specimens to the species level [25]. Through this two-step approach, we identified five previously unrecorded species unambiguously. Among these new records for Korea, four were classified as Polyporales and one was identified as a member of the Hymenophorales.

A. fissilis is the first recorded species in the genus *Aurantiporus* Murrill in Korea. Fruiting bodies of *A. fissilis* are characterized by an orange to pinkish brick, pubescent-strigose pileus surface. Subsequent observations of microscopic characters and comparisons with the literature [11] confirmed this identification. Morphological features of *A. fissilis* are similar to those of the genus *Tyromyces*, and previous reports identified specimens of *A. fissilis* as *Tyromyces fissilis* [11]. *Aurantiporus* species formed a sister clade with *Ceriporiopsis* and *Phlebia* [41] in the phylogenetic study using the LSU region; however, a phylogenetic tree based on ITS sequences showed that, while the genus *Aurantiporus* is closely related to *Tyromyces*, the two genera clearly separated from each other (Fig. 1).

The genus *Neofavolus* Sotome & T. Hatt. is the sister group of *Favolus* and was previously treated as one of the infrageneric groups of the genus *Polyporus* sensu lato. Recently, Sotome *et al.* [18] proposed a new genus based on phylogenetic analyses of LSU and ITS regions in tandem with morphological characteristics such as diamond shaped and radially elongated pores as well as distinct agglutinated and parallel generative hyphae. Only one species of *Neofavolus* has been reported in Korea: *N. alveolaris*. This research has added an additional species of the genus *Neofavolus* to the Korean record: *N. mikawai*. This species was previously only reported from restricted areas of warm-temperate climates in Japan and China [42, 43]. Recently, *N. mikawai* was found on Jeju Island which is located approximately 80 km off the southern coast of Korea. This suggests that the climate of Jeju Island may be changing from warm temperate to subtropic (http://www.kma.go.kr/weather/) [44].

The genus *Favolus* Fr., typified by *F. brasiliensis* (Fr.) Fr., is a wood rotting fungus within the order Polyporales. Previously, Núñez and Ryvarden [38] treated *Favolus* as one of the six infrageneric groups of the genus *Polyporus*. Recently, however, Sotome *et al.* [18] proposed the distinct genus *Favolus* based on phylogenetic analyses of LSU and

ITS regions and morphological characters such as a radially striate pileus, and lack of distinct cutis of agglutinated hyphae. The genus *Favolus* was previously unknown in Korea and thus this study reports *F. acervatus* in Korea for the first time. This is the only species of the genus with simple septated generative hyphae.

The genus *Loweomyces* (Kotl. & Pouz.) Jülich belongs to the family Meruliaceae in the order Polyporales. *Loweomyces* has historically been considered a subgenus of *Spongipellis* Pat. Jülich. However, the genus segregated from *Spongipellis* based on the larger basidia, the absence of skeletal hyphae, and smaller tubes [45]. *L. fractipes*, type species, was previously recorded in Europe [46], North America [11], and South America [47]. Both genus and species of *Loweomyces* are firstly reported in Korea. Our study is the first report of this species in Asia. However, the phylogenetic placement of this species could not be determined because little sequence information is available.

H. rigidula is classified within the Hymenochaetaceae in the order Hymenochaetales. The genus *Hymenochaetopsis* S. H. He & Jiao Yang was recently suggested to be synonymous with *Pseudochaete* [19]. Four species were recorded previously in Korea as belonging to the genus *Hymenochaete*: *H. corrugata*, *H. intricata*, *H. tabacina*, and *H. yasudae*. Through ITS sequence analysis, this study identified the species *H. rigidula* as a new record in Korea. *H. rigidula* is a cosmopolitan species that is distributed in Europe [48], North America [14], South America [49], and China [50]. The microscopic features of the *Hymenochaetopsis* are difficult to observe under a light microscope even for a skilled mycologist. *H. intricata*, *H. tabacina*, and *H. yasudae* have distinguishable fruiting body morphologies and preferred habitats. However, due to the morphological similarity of *H. rigidula* and *H. corrugata*, many specimens were previously misidentified as *H. corrugata*. For this reason, phylogenetic analyses, such as ITS based studies, are crucial for accurate identification of these closely related species.

In conclusions, the recent application of molecular markers such as the ITS has revolutionized the fields of fungal taxonomy and evolution. The morphology of the wood decay fungi is often simple and taxonomic assignments based on morphology alone are therefore suspect. Here, we add to the growing body of evidence that phylogenetic analysis based on ITS sequences, and ideally several other loci, combined with morphological observations is vital to the advancement of the taxonomic study of wood decay fungi. Our study highlights the need for a multifaceted approach to investigating new wood decay fungi in Korea.

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