

Fungal
BIOTEC

Recent Papers

Volume 1 - 2021 Special issue

1. Fomes (Polyporales, Basidiomycota): medicinal, economic and ecological importance

Wang H & Zhao CL (2021)

Volume 1 - 2021 issue 1

1. Bacteriostatic and Virostatic Activities of Mushrooms: A Mini-review

Li et al. (2021)

***Fomes* (Polyporales, Basidiomycota): medicinal, economic and ecological importance**

Wang H and Zhao CL*

College of Biodiversity Conservation, Southwest Forestry University, Kunming 650224, P.R. China

Wang H and Zhao CL 2021 – *Fomes* (Polyporales, Basidiomycota): medicinal, economic and ecological importance. Fungal Biotech 1(2), 1–9, Doi 10.5943/FunBiotech/1/2/1

Abstract

Fomes have attracted much attention because of their important ecological, economic and medical values. In forest ecosystems, *Fomes* play a core role in promoting the circulation of nutrients and the flow of energy. In the application of modern medicine and biotechnology, the effective substances extracted from *Fomes* also have a great economic value. The aims of this review are to (1) review the historical taxonomy of *Fomes*, (2) briefly describe important species of *Fomes* together with their distribution, and (3) discuss the economic value of *Fomes*.

Keywords – Health benefits – *Polyporaceae* – Taxonomy – Wood-rotting fungi

Introduction

Fungi are an ecologically important branch of the tree of life based on its distinct and diverse characteristics, in which these organisms play a vital role in ecosystems. Fungi are found in soil, forests, rocks, and ocean, but their roles are primarily enacted behind the scenes, literally as hidden layers within their substrate (James et al. 2020). Taxonomy plays a central role in understanding the diversity of life, discovering into systems of names that capture the relationships between species, and translating the products of biological exploration (Hibbett 2016, Cui et al. 2019, James et al. 2020).

Polyporales is now well accepted and strongly supported order of *Agaricomycetes* and one of the most intensively studied groups of fungi, in which fungal ecologists and applied scientists are focusing on many taxa of this order (Hibbett et al. 2014, Justo et al. 2017, James et al. 2020). These taxa play a key role as food, enzymes and medicine, based on their important and potential applications in biomedical engineering and biodegradation (Dai et al. 2009, Levin et al. 2016, Bankole et al. 2020). Among 1,589 genera and 30,000 accepted species of *Basidiomycota*, roughly 1,800 species belong to *Polyporales* and its accounts only about 1.5 % of all known species of fungi (Kirk et al. 2008). *Polyporales* were sampled extensively in phylogenetic studies using ribosomal RNA (rRNA) genes (Hibbett & Vilgalys 1993, Hibbett & Donoghue 1995, Larsson et al. 2004, Binder et al. 2005). From such analyses, four informally named clades of *Polyporales* were recognized: antrodia clade, core polyporoid clade, phlebioid clade and residual polyporoid clade. Addition of protein-coding genes, including RNA polymerase II subunit 2 (*rpb2*), and translation elongation factor 1-a (*tef1*) are necessary to achieve strong support for monophyly of *Polyporales* as a whole, and many internal nodes (Matheny et al. 2007, James et al. 2020).

The genus *Fomes* (Fr.) Fr. was proposed by Fries (1849) typified with *F. fomentarius* (L.) Fr, which was readily recognized by the non-specialist because of the layering of the tubes (Lowe

1957). The original definition of the genus *Fomes* was broad and inaccurate, but the actual concept of the genus *Fomes* s. str. includes comparatively low species diversity (Justo et al. 2017). Macromorphically, this genus is characterized by the perennial, sessile, ungulate basidiomata with a gray to blackish pileus surface (Fig. 1); a smooth, hard crust and pale brown pore surface with small pores; regular, brown tube layers, and pale brown, tough-fibrous context (Fig. 2). Micromorphically, it can be characterized by a trimitic hyphal structure with clamps on generative hyphae, in which, the skeletal hyphae show pale brownish pigment in KOH, and presence of the sclereids, and fusoid cystidioles, imbedded or projecting slightly, clavate basidia, four-celled, with a basal clamp (Fig. 3), and cylindrical basidiospores, colorless, smooth, inamyloid or negative in Melzer's reagent (Gilbertson & Ryvarden 1987). Additionally, this genus causes white rot of living or dead hardwoods (Gilbertson & Ryvarden 1987). The macroscopic characteristics most useful in identifying species in this genus are the size, shape, and comparative weight of the basidiomata, size of the pore, color and texture of context, and texture and distinctness of tube layers (Lowe 1957).

According to Index Fungorum (<http://www.indexfungorum.org/>, accessed 1st June, 2021), 48 species have been accepted in the genus worldwide. Currently, the species *F. fomentarius* is a hot topic (Grand & Vernia 2005, Júdová et al. 2012, McCormick et al. 2013).

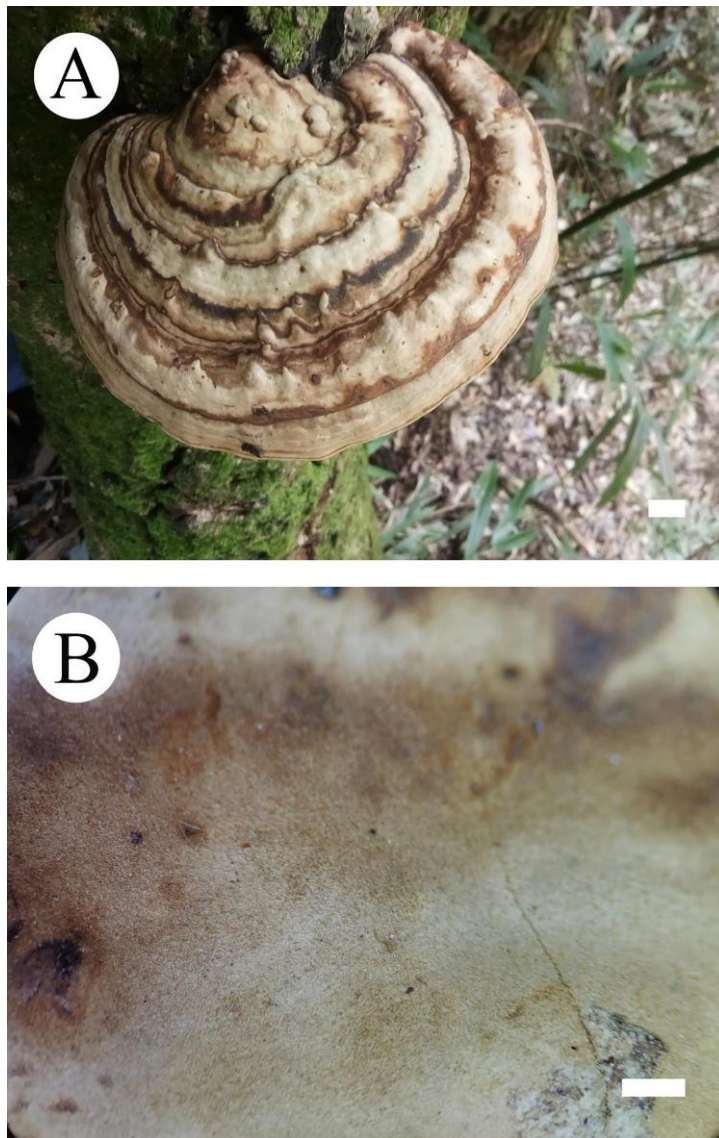


Fig 1. Basidiomata of *Fomes fomentarius* A–B. The upper surface of the basidiomata. Bars: A=1 cm; B=1 mm.

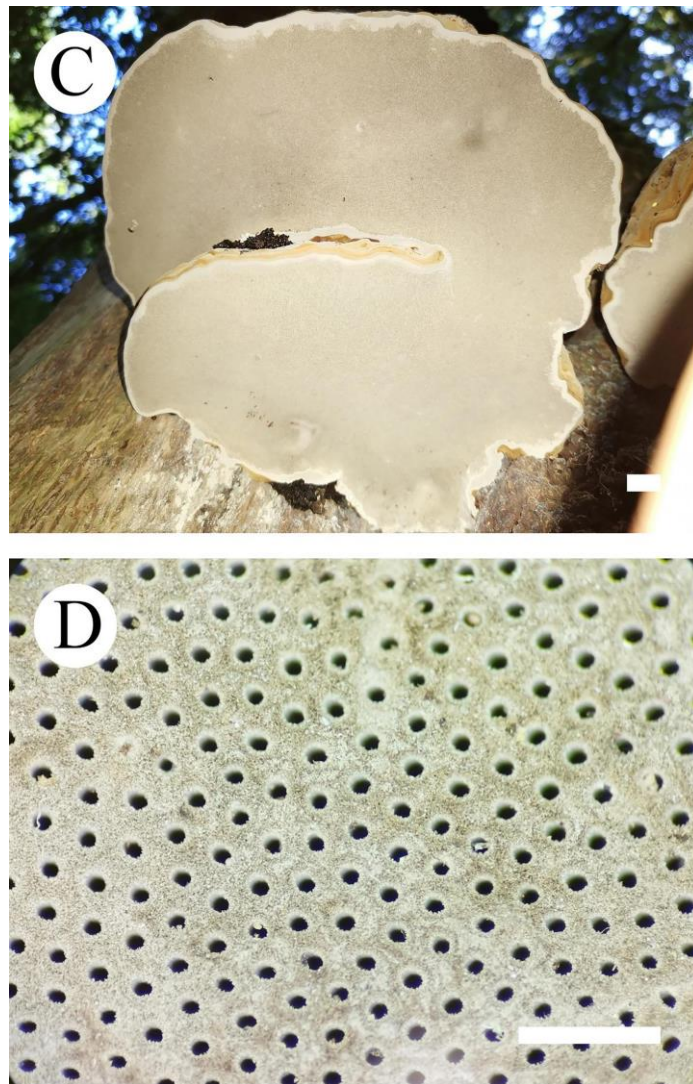


Fig 2. Basidiomata of *Fomes fomentarius* C. The lower surface of the basidiomata; D. A section of hymenophore. Bars: C=1 cm; D=1 mm.

Morphological studies of *Fomes*

Until the late 1980s, the taxa of polypores have been described mostly based on their macro-morphological and micro-morphological characteristics. The simple morphology of fungal structures (e.g., hyphae, spores, basidiomata), polypore diversity, and the lack of a useful fossil record have been major impediments to progress in this field (Júdová et al. 2012). The research showed that the genus *Fomes* was similar in its morphology to *Polyporus* P. Micheli ex Adans., *Poria* P. Browne, and *Trametes* Fr., but there can be no absolute demarcation of these genera, and three new combinations based on morphological studies: *F. johnsonianus* (Murrill) J. Lowe, *F. santic-georgii* (Pat.) J. Lowe and *F. viticola* (Schwein.) J. Lowe were proposed (Lowe 1957). In the study of Gilbertson & Ryvardeen (1986), it was found that the genus *Fomes* is well characterized by its perennial basidiomata, which have a conspicuous mycelial granular core close to the substratum, consisting of very thick-walled and irregularly shaped hyphae. The granular core instantaneously separated this genus from other similar genera that may or may not be closely related (Gilbertson & Ryvardeen 1986). In the early part of the 20th century, several hundreds of specific epithets were associated with this generic name, in which most of these species have been gradually shown to belong in other genera, thus the most recent concept of the genus was incomparably narrower and it comprised two different morphological species, *F. fomentarius* and *F. fasciatus* (Sw.) Cooke, in addition to some cryptic species within this group of strains (Ryvardeen 1991). Nevertheless, both species *F. fomentarius* and *F. fasciatus* shared many morphological traits that historically have

made species delimitation challenging (Júdová et al. 2012). Based on similarities in the basidiomata morphology of *F. fomentarius* and *F. fasciatus*, mycologists reported that basidiomata of *F. fomentarius* tended to be more consistently unguulate and typically have a concave pore surface, but *F. fasciatus* basidiomata vary greatly from applanate to unguulate and generally have a convex pore surface (Murrill 1915, Ryvarden & Gilbertson 1993). The results showed that *F. fomentarius* basidiomata produce larger basidiospores ($12\text{--}18 \times 4\text{--}7 \mu\text{m}$), whereas *F. fasciatus* has smaller basidiospores ($12\text{--}14 \times 4\text{--}4.5 \mu\text{m}$, Ryvarden & Gilbertson 1993). A few years later, research reported evidence of the conidial stages in the development of primary and dikaryotic mycelia of *F. fomentarius*, in which the experiments focused on the viability and the dynamics of basidiospore germination, primary and dikaryotic mycelia growth, conidia development of *F. fomentarius* and proposed a new model of their life cycles (Mukhin & Votintseva 2002). In recent years, the researches focused on the tinder polypore mushroom *F. fomentarius*, within medicinal fungal species and their implications for morphological variability, physiological activity, biochemical variability, and geographic ecology, in which the species epithet *F. fomentarius* had often misleadingly been used for 2 closely related species: *F. fomentarius* and *F. fasciatus* and both species were principally separated from one another by the mean basidiospore size (Gáper et al. 2016). The detailed examination of a number of different *Fomes* strains had been collected and isolated from different habitats in Italy and Austria, which confirmed the presence of distinct lineages in *F. fomentarius* clade, additionally, in their study, they also showed that physiological characteristics were species-specific properties, in which the daily mycelial growth rates or the temperature range of pure cultures and the production of VOCs could be considered as a very promising tool for fast and reliable species delimitation in the future (Peintner et al. 2019).

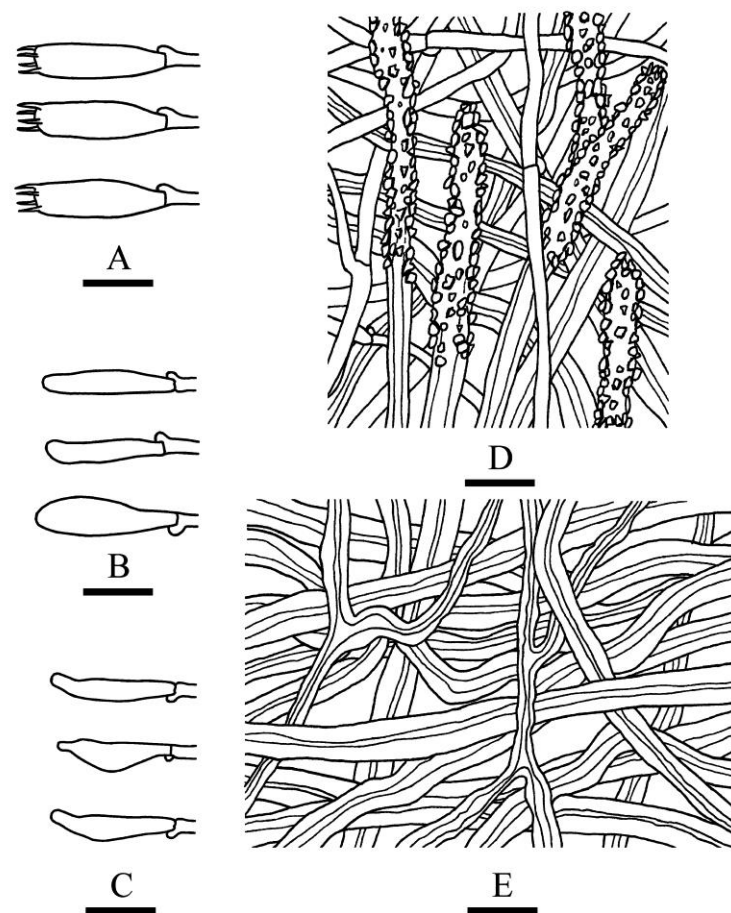


Fig 3. Microscopic structures of *Fomes fomentarius* A. Basidia; B. Basidioles; C. Cystidioles; D. Hyphae from trama; E. Hyphae from context. Bars: A–E=10 μm .

Molecular systematics of *Fomes*

In the middle of 1990s, the evolutionary based species concepts began to occur (Hibbett & Donoghue 1995, Boidin et al. 1998). The use of population tools and DNA-based methods for the identification of taxa emerged, and especially rDNA genes have been successfully used as a target for species identification in taxonomic, evolutionary, and environmental studies of fungi (Borneman & Hartin 2000, Chase & Fay 2009). Most studies focused on the internal transcribed spacer (ITS) region located between rRNA structural genes in the rDNA cistron, in which this approach was widely used for identification of many eukaryotic specimens, including fungi (Anderson & Cairney 2004, Naumann et al. 2007, Justo et al. 2017, Zhao & Zhao 2021).

In the middle of the 19th century, the genus *Fomes* was proposed as a polyphyletic group in several analyses of mitochondrial small-subunit (mt-ssu) ribosomal DNA (rDNA) or mt-ssu rDNA and nuclear small-subunit rDNA (Gáper et al. 2016). *Fomes* was determined to be monophyletic in phylogenetic analyses of nuclear and mitochondrial large- and small-subunit rDNAs, but support for this group was weak in these analyses (Gáper et al. 2016). *Fomes fomentarius* had been considered a homogeneous species, in which the existence of two lineages was revealed based on ITS sequence variability (Júdová et al. 2012). A study found evidence suggesting the presence of a third group within the North American strains of *F. fomentarius* (McCormick et al. 2013). An analysis using sequence data from nuclear and mitochondrial large- and small-subunit rDNAs from 91 species of homobasidiomycetes revealed that *Fomes* grouped with other polypores, which had a similar characteristic of the trimitic hyphal system (Hibbett et al. 2014). The phylogenetic tree distinguished a fourth group within *F. fomentarius* from China (Dresch et al. 2015). Based on the comparison of ITS sequences, three different lineages and sublineages in *F. fomentarius* were clearly identified (Gáper et al. 2016).

Economic importance

The importance of biodiversity and biogeography of fungi, especially in unique ecosystems and specific regions, was previously addressed by Grand & Vernia (2005). Fungi of the *Fomes* are the traditional morphological polypore genus, almost found on broad-leaved forest trees, and cause wood rot, and play a highly beneficial role in slash disposal (Júdová et al. 2012). On the other hand, many species under favorable conditions, attacking standing timber, causing heart rot and decaying wood products (Júdová et al. 2012, Hibbett et al. 2016, James et al. 2020). Though the economic loss from wood decay is large, it should be remembered that the harmful decay was a minor part of the indispensable and vastly beneficial cyclic process that replenishes carbon dioxide and other substances essential for green plant growth, which in turn supports all animal existence (Lowe 1957, Pozzi et al. 2020). In natural ecosystems, they have ecological functions such as nutrient cycle and providing insects with nesting holes and shelters (Gilbertson 1980, Makinen et al. 2019, Gonzalez et al. 2020).

Fomes not only act as reductors in nature, but also rely on resources of early people, and its extracted substances are of great value in modern medical treatments (Lowe 1957). The perennial bracket fungi, because of their size and persistence, have attracted attention from very early times, and the medicinal value soon brought specific recognition to *F. officinalis*, which was well-known to the Greeks and the Romans (Lowe 1957). The 5000-year-old Neolithic man was the first to apply tinder material prepared from genus *F. basidiomata* for medicinal purposes in a first aid kit (Peintner et al. 1998, Pöder & Peintner 1999). So far, the study of fungi of *Fomes* has been a hot topic, in which its extracts have remarkable efficacy on some diseases, and have great potential and economic value in modern medicine, bio-pharmaceuticals and applications (Suriya 2020, Kalitukha 2021, Liudmila & Miriam 2021).

Ecology and distribution

The genus *Fomes* are widely distributed in Africa, Asia, Europe and North America. For example, *F. fomentarius* is very common and widespread in all habitat zones of the West Siberian Plain, whose forest vegetation was shaped mainly by climate (Mukhin & Votintsevav 2002, Júdová

et al. 2012). The valid distribution records depend upon accurate determination of specimens and the species in the North Temperate Zone are usually those long known by tradition, or adequately represented by type material, the identity of each of these is clear and its distribution quite certain (Lowe 1957). Tropical species, are often known from scanty material, and are frequently represented by sterile types; in contrast, the distribution of tropical species is hazy (Lowe 1957).

Important species and applications of *Fomes*

Fomes fomentarius is the traditional morphological polypore species, and it is almost always found on broad-leaved forest trees, where it causes white rot (McDonald 1938). This very common fungus is distributed within the northern hemisphere in North America, North Africa, Asia, and all over Europe (McDonald 1938, Breitenbach & Kränzlin 1986, Kotlaba 1997). This is commonly known as the “tinder fungus”, “hoof fungus”, “tinder conk”, “tinder polypore”, or “Iceman’s fungus” (Peintner et al. 2019). Besides the widespread and important use as tinder, *F. fomentarius* was a valued medicinal polypore in European traditional medicine (Killermann 1938). The 5000-year-old Iceman probably used this polypore to make and preserve fire, as a first aid kit, an insect repellent, or for spiritual purposes (Peintner et al. 1998, Pöder & Peintner 1999). It is first mentioned date back to the times of Hippocrates, who reported its topical use for cauterizing wounds and for externally treating inflamed organs (Pöder 2005). In the medieval times, it is use in in Europe and Western Siberia as a styptic and it was prescribed as a remedy against dysmenorrhea, hemorrhoids, and bladder disorders, the active substance being “fomitin” and used as a hemostatic dressing and ban-dage to maintain body temperature and compress parts of the body (Killermann 1938). Stretched stripes or smaller pieces were used as a remedy against bleeding wounds and for various skins injures, and it therefore was called “agaric of surgeons” “Chirurgenschwamm” “Wundschwamm” or “Fungus chirurgorum” (Roussel et al. 2002). The basidiomata have been used as a traditional medicine for centuries in China and Korea in treating various diseases such as gastroenteritic disorder, hepatocirrhosis, oral ulcer, inflammation, and various cancers (Cheng et al. 2000, Chen et al. 2008, Huang et al. 2012, Gáper et al. 2016, Bari et al. 2021).

Acknowledgements

The research was funded by Yunnan Fundamental Research Project, grant number 202001AS070043 and Science Research Foundation of Yunnan Provincial Department of Education Project (Project No. 2021Y275).

References

- Anderson I, Cairney J. 2004 – Diversity and ecology of soil fungal communities: increased understanding through the application of molecular techniques. *Environmental Microbiology* 6, 769e779. Doi 10.1111/j.1462-2920.2004.00675.x
- Breitenbach J, Kränzlin F. 1986 – *Fungi of Switzerland*, vol. 2, Verlag Mykologia, Lucerne.
- Bankole PO, Adedotun AA, Jeon BH, Govindwar SP. 2020 – Novel cobiomass degradation of NSAIDs by two wood rot fungi, *Ganoderma applanatum* and *Laetiporus sulphureus*: Ligninolytic enzymes induction, isotherm and kinetic studies. *Ecotoxicology and Environmental Safety* 203, 110997. Doi 10.1016/j.ecoenv.2020.110997
- Bari E, Pizzi A, Schmidt O, Amirou S et al. 2021 – Differentiation of fungal destructive behaviour of wood by the white-rot fungus *Fomes fomentarius* by MALDI-TOF mass spectrometry. *Journal of Renewable Materials* 9, 3. Doi 10.32604/jrm.2021.015288
- Binder M, Hibbett DS, Larsson KH, Larsson E, Langer E, 2005 – The phylogenetic distribution of resupinate forms in the homobasidiomycetes. *Systematics and Biodiversity* 3, 113e157. Doi 10.1017/S1477200005001623
- Boidin J, Mugnier J, Canales R. 1998 – Taxonomie moleculaire des *Aphylllophorales*. *Mycotaxon* 66, 445e491.

- Borneman J, Hartin RJ. 2000 – PCR primers that amplify fungal rRNA genes from environmental samples. *Applied and Environmental Microbiology* 66, 4356–4360. Doi 10.1128/AEM.66.10.4356-4360.2000
- Chase M, Fay M. 2009 – Barcoding of plants and fungi. *Science* 325, 682e683. Doi 10.1126/science.1176906
- Chen W, Zhao Z, Chen S, Li Y. 2008 – Optimization for the production of exopolysaccharide from *Fomes fomentarius* in submerged culture and its antitumor effect in vitro. *Bioresour Technol* 99, 3187–3194. Doi 10.1016/j.biortech.2007.05.049
- Cheng DS, Yamaguchi T, Wang ZJ, Pan XR, 2000 – Genetic differentiation between two morphological types of *Fomes fomentarius* based on isozyme analysis. *Mycosystema* 19, 81e86.
- Cui BK, Li HJ, Ji X, Zhou JL et al. 2019 – Species diversity, taxonomy and phylogeny of *Polyporaceae* (*Basidiomycota*) in China. *Fungal Diversity* 97, 137–392. Doi 10.1007/s13225-019-00427-4
- Dai YC, Yang ZL, Cui BK, Yu CJ, Zhou LW. 2009 – Species diversity and utilization of medicinal mushrooms and fungi in China (review). *International Journal of Medicinal Mushrooms* 11, 287–302. Doi 10.1615/IntJMedMushr.v11.i3.80
- Dresch P, Aguano MN, Rosam K, Grienke U et al. 2015 – Fungal strain matters: colony growth and bioactivity of the European medicinal polypores *Fomes fomentarius*, *Fomitopsis pinicola* and *Piptoporus betulinus*. *AMB Express* 5, 1–14. Doi 10.1186/s13568-014-0093-0
- Fries E. 1849 – *Summa vegetabilium Scandinaviae*. Sectio posterior [in Latin]. Stockholm (Sweden), A Bonnier.
- Grand LF, Vernia CS. 2005 – Biogeography and hosts of poroid wood decay fungi in North Carolina: species of *Fomes*, *Fomitopsis*, *Fomitella* and *Ganoderma*. *Mycotaxon* 94, 231–234.
- Gáper J, Gáperová S, Pristaš P, Náplavová K. 2016 – Medicinal value and taxonomy of the tinder polypore, *Fomes fomentarius* (*Agaricomycetes*): A review. *International Journal of Medicinal Mushrooms* 18, 851–859. Doi 10.1615/IntJMedMushrooms.v18.i10.10
- Grand LF, Vernia CS. 2005 – Biogeography and hosts of poroid wood decay fungi in North Carolina: species of *Coltricia*, *Coltriciella* and *Inonotus*. *Mycotaxon* 91, 35–38.
- Gilbertson RL. 1980 – Wood-rotting fungi of North America. *Mycologia* 72, 1–49. Doi 10.1080/00275514.1980.12021153
- Gilbertson RL, Ryvar den L. 1986–1987 – North American polypores 1–2. *Fungifora*, Oslo. Pp. 14–33.
- Gonzalez A, Corsini G, Lobos S, Seelenfreund D, Tello M. 2020 – Metabolic specialization and codon preference of lignocellulolytic genes in the white rot *Basidiomycete Ceriporiopsis subvermispora*. *Genes* 11, 1227. Doi 10.3390/genes11101227
- Huang TZ, Du DY, Chen YQ, Yuan B et al. 2012 – Chemical constituents and antitumor activity of fruiting body of *Fomes fomentarius* [article in Chinese]. *Mycosystema* 31, 775–83.
- Hibbett DS, Vilgalys R, 1993 – Phylogenetic relationships of *Lentinus* (*Basidiomycotina*) inferred from molecular and morphological characters. *Systematic Botany* 18, 409e433.
- Hibbett DS, Donoghue MJ. 1995 – Progress toward a phylogenetic classification of the *Polyporaceae* through parsimony analyses of ribosomal DNA sequences. *Canadian Journal of Botany* 853e861. Doi 10.1139/b95-331
- Hibbett DS, Bauer R, Binder M, Giachini AJ et al. 2014 – Agaricomycetes. In: McLaughlin DJ, Spatafora RJ, editors. *The mycota: systematics and evolution part A*. VII. 2nd ed. Heidelberg (Germany), Springer. Pp. 373–429. Doi 10.1007/978-3-642-55318-9_14
- Hibbett DS. 2016 – The invisible dimension of fungal diversity. *Science* 351, 1150–1151. Doi 10.1126/science.aae0380
- Hibbett DS, Abarenkov K, Kõljalg U, Öpik M et al. 2016 – Sequence-based classification and identification of Fungi. *Mycologia* 108, 1049–1068.
- James TY, Stajich JE, Hittinge CT, Rokas A. 2020 – Toward a fully resolved fungal tree of life. *Annual Review of Microbiology* 74, 1–23. Doi 10.1146/annurev-micro-022020-051835

- Justo A, Miettinen O, Floudas D, Ortiz-Santana B et al. 2017 – A revised family-level classification of the *Polyporales* (*Basidiomycota*). *Fungal Biology* 121, 798–824. Doi 10.1016/j.funbio.2017.05.010
- Júdová J, Dubíková K, Gáperová S, Gáper J, Pristaš P. 2012 – The occurrence and rapid discrimination of *Fomes fomentarius* genotypes by ITS-RFLP analysis. *Fungal Biology* 116, 55–60. Doi 10.1016/j.funbio.2011.10.010
- Kalitikha L. 2021 – An approach to change the basic polymer composition of the milled *Fomes fomentarius* fruiting bodies. *Fungal Biology Biotechnology* 8, 5. Doi 10.1186/s40694-021-00112-9
- Killermann S. 1938 – Ehemaliger apothekerpilz. *Zeitschrift für Pilzkunde* 22, 11–13.
- Kirk PM, Cannon P.F, David JC, Minter DW, Stalpers JA. 2008 – *Ainsworth and bisby's dictionary of the fungi*, 10th edn. CAB International Press, Wallingford. Doi 10.1079/9780851998268.0000
- Kotlaba F. 1997 – Common polypores (*Polyporales s.l.*) collected on uncommon hosts. *Czech Mycology* 49, 169e188. Doi 10.1079/9780851998268.0000
- Larsson KH, Larsson E, Kõljalg U, 2004 – High phylogenetic diversity among corticioid homobasidiomycetes. *Mycological Research* 108, 983e1002. Doi 10.1017/S0953756204000851
- Levin L, Maira C, Martin H, Rene U. 2016 – Degradation of 4-nitrophenol by the white-rot polypore *Trametes versicolor*. *International Biodeterioration & Biodegradation* 107, 174–179. Doi 10.1016/j.ibiod.2015.11.023
- Liudmila K, Miriam S. 2021 – Chemical composition and ultraviolet absorption activity of an aqueous alkali extract from the fruiting bodies of the tinder conk mushroom, *Fomes fomentarius* (*Agaricomycetes*). *International Journal of Medicinal Mushrooms* 23, 23–37. Doi 10.1615/IntJMedMushrooms.2021038160
- Lowe JL. 1957 – *Polyporaceae* of North America the genus *Fomes*. State University College of Forestry at Syracuse University, No. 80.
- Matheny PB, Wang Z, Binder M, Curtis JM et al. 2007 – Contributions of *rpb2* and *tefl* to the phylogeny of mushrooms and allies (*Basidiomycota*, *Fungi*). *Molecular Phylogenetics and Evolution* 43, 430e451. Doi 10.1016/j.ympev.2006.08.024
- Makinen M, Kuuskeri J, Laine P, Smolander OP et al. 2019 – Genome description of *Phlebia radiata* 79 with comparative genomics analysis on lignocellulose decomposition machinery of phlebioid fungi. *BMC Genomics* 20, 430. Doi 10.1186/s12864-019-5817-8
- McCormick MA, Grand FL, Post BJ, Cubeta MA. 2013 – Phylogenetic and phenotypic characterization of *Fomes fasciatus* and *Fomes fomentarius* in the United States. *Mycologia* 105, 24–34. Doi 10.3852/12-336
- McDonald JA, 1938 – *Fomes fomentarius* (Linn) Gill (*Ungulina fomentaria*) on birch in Scotland. *Transactions of the British Mycological Society* 32, 396e408. Doi 10.1080/13594863809441531
- Murrill WA. 1915 – Southern polypores. New York, Murril. Doi 10.5962/bhl.title.22920
- Mukhin VA, Votintsevav AA. 2002 – Basidiospore germination and conidial stages in the life cycles of *Fomes fomentarius* and *Fomitopsis pinicola* (*Fungi*, *Polyporales*). *Polish Botanical Journal* 47, 265–272.
- Naumann A, Navarro-González M, Sánchez-Hernández O, Hoegger PJ, Kües U. 2007 – Correct identification of wood-inhabiting fungi by ITS analysis. *Current Trends in Biotechnology and Pharmacy* 1, 41e61.
- Peintner U, Pöder R, Pümpel T. 1998 – The Iceman's fungi. *Mycological Research* 102, 1153–1162. Doi 10.1017/S0953756298006546
- Peintner U, Kuhnert-Finkernagel R, Wille V, Biasioli F, Shiryaev A, Perini C. 2019 – How to resolve cryptic species of polypores: an example in *Fomes*. *IMA Fungus* 10, 17. Doi 10.1186/s43008-019-0016-4

- Pozzi C, Rajchenberg M, Ojeda V. 2020 – Decay fungi associated with cavity excavation by a large South American woodpecker. *Forest Pathology* 50, e12634.
- Pöder R, Peintner U. 1999 – Laxatives and the ice man. *The Lancet* 353, 926–926. Doi 10.1016/S0140-6736(05)75032-7
- Pöder R. 2005 – The Ice Man’s fungi: facts and mysteries. *Int J Med Mushrooms* 7, 37–59. Doi 10.1615/IntJMedMushr.v7.i3.190
- Ryvarden L. 1991 – *Genera of polypores, nomenclature and taxonomy*. Synopsis Fungorum 5, Oslo, Fungiflora.
- Ryvarden L, Gilbertson RL. 1993 – *European polypores. Part 1*. Synopsis Fungorum 5, Oslo, Fungiflora.
- Roussel B, Rapior S, Charlot C, Masson CL, Boutié P. 2002 – History of the therapeutic uses of the tinder polypore, *Fomes fomentarius* (L.): Fr. [article in French]. *Revue Histoire de la Pharmacie* 50, 599–614. Doi 10.3406/pharm.2002.5432
- Suriya R, Romana F, Rabindran J, Sarah Mousa A et al. 2020 – A wild *Fomes fomentarius* for biomediation of one pot synthesis of titanium oxide and silver nanoparticles for antibacterial and anticancer application. *Biomolecules* 10, 622. Doi 10.3390/biom10040622
- Zhao W, Zhao CL. 2021 – The Phylogenetic relationship revealed three new wood-inhabiting fungal species from genus *Trechispora*. *Frontiers in Microbiology* 12, 650195. Doi 10.3389/fmicb.2021.650195