



Laetiporus lobatus (Basidiomycota, Polyporales), a new fungal species from Costa Rica

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Abstract

A new species of *Laetiporus*, *L. lobatus*, is described. The species is closely related to *L. caribensis*, having similar ITS sequence and morphology. *L. lobatus* has smaller pores than *L. caribensis* and also has a distinctively lobed edge on its basidiocarps. To date, this species has only been found in Costa Rica. Taxonomic issues associated with *Laetiporus* are briefly discussed.

Keywords: brown-rot fungi, taxonomy, tropical distribution, wood-inhabiting fungi

Introduction

The genus *Laetiporus* Murrill (1904: 607) with one species, *Laetiporus speciosus* Battarra ex Murrill (1904: 607), was erected by Murrill (1904) for a common and very distinct wood-rotting fungus characterized by a poroid hymenophore, dimidiate to flabellate pilei of bright orange to yellow colour, soft and fleshy context, functionally dimitic simple septate hyphal system with thin-walled generative hyphae and thick-walled branched binding hyphae, and causing a brown rot (Ryvarden & Melo 2017). Based on these characteristics, Murrill ascribed also *Boletus sulphureus* Bull. to *Laetiporus* in 1920 and *L. sulphureus* (Bull.) Murrill subsequently came to be considered a species with worldwide distribution (Gilbertson & Ryvarden 1986, Núñez & Ryvarden 2001, Ryvarden & Gilbertson 1993, Ryvarden & Johansen 1980, Ryvarden 2015). However, incompatibility studies performed by Banik & Burdsall (1999, 2000) revealed 5–6 incompatibility groups/species in the USA alone, and this result was confirmed by molecular studies (Lindner & Banik 2008). Several new North American species have been described: *L. conifericola* Burds. & Banik (2001: 47), *L. gilbertsonii* Burds. (2001: 48), and *L. huroniensis* Burds. & Banik (2001: 50)—all often very similar to *L. sulphureus* but differing by DNA sequence, ecology and geographical distribution, and showing also slight differences in basidiospore size and shape.

Similarly, more species were described from Asia (Ota *et al.* 2009, Song *et al.* 2014, Song *et al.* 2018). In the study of Vasaitis *et al.* (2009), broader sampling over the whole world and analysis based on ITS rDNA sequence revealed 11 clades, named consecutively A–K. Five were of already known USA species and another six were of specimens from other countries. Emerging new clades A2, D, G were later (Banik *et al.* 2012) formally acknowledged as *Laetiporus* species *L. montanus* Černý ex Tomšovský & Jankovský (2009: 292) and *L. cremeiporus* Y. Ota & T. Hatt. in Ota *et al.* (2009: 1289). Banik *et al.* (2012) also described *L. caribensis* Banik & D.L. Lindner (2012: 17) forming a new clade J and added some more of Central and South American collections to their phylogeny, showing additional clades L and M; clade L was represented by only one collection from Costa Rica. We have recently collected and studied another specimen falling within clade L based on ITS sequence, and because this and the original clade L specimen have common morphological traits, different from other *Laetiporus* species, we describe below clade L specimens as a new species.

Materials and Methods

Specimens studied are deposited in international herbaria (Center for Forest Mycology Research (CFMR) and National Museum, Prague (PRM); duplicates in private herbarium of Josef Vlasák (JV) and the Mycological Herbarium of the Department of Biology, University of West Bohemia (abbreviated CBG here). The specimens were microscopically examined in Melzer's reagent (IKI) and 5% KOH. Tissue sections were studied at a magnification of 1000× with Olympus BX 51 light microscope. 20 spores were measured from sections cut from the tubes and 5% of measurements were excluded from each end of the range. L = mean spore length (arithmetic average), W = mean spore width (arithmetic average), Q = variation in the L/W ratios between specimens studied, n (a/b) = number of spores (a) measured from a given number of specimens (b).

DNA extraction and nuclear ribosomal DNA ITS region sequencing follow Vlasák & Kout (2011). Sequences generated for this study (see Fig. 1) were aligned with additional sequences downloaded from GenBank using Clustal X in MEGA6 (Tamura *et al.* 2013) and ambiguous terminal sequences were trimmed. Maximum likelihood analysis of ITS sequences was conducted in MEGA6 using the Kimura 2-parameter model with gamma distribution, which was determined as the best-fit model with "Model testing for estimation of distances" option (Tamura *et al.* 2013). *Wolfiporia dilatohypha* Ryvarden & Gilb. was used as outgroup to root the tree (Banik *et al.* 2010, Banik *et al.* 2012, Lindner & Banik 2008, Ota *et al.* 2009).

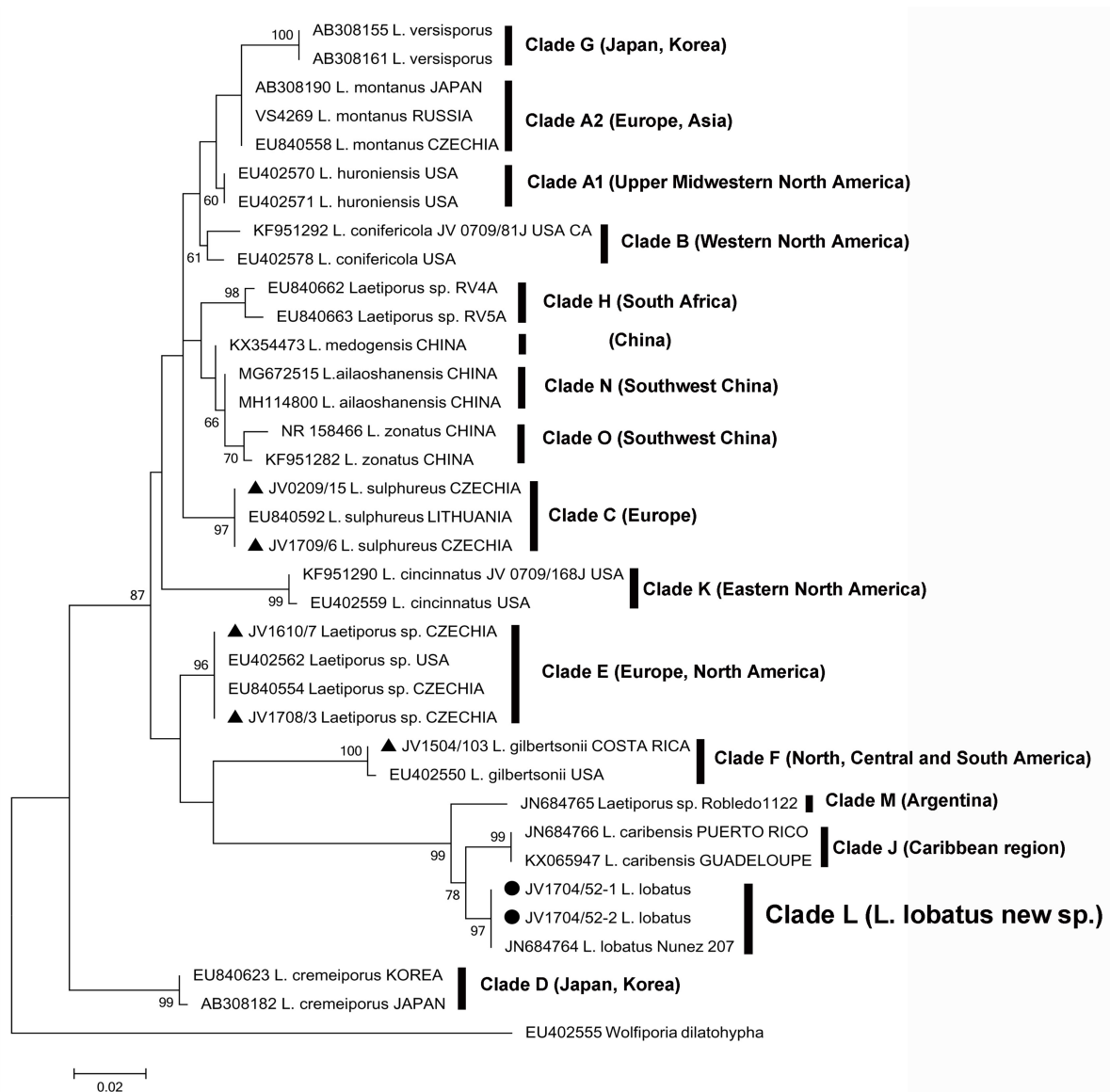


FIGURE 1. Maximum likelihood phylogeny of known *Laetiporus* clades based on ITS rDNA sequences. Species clades are indicated with vertical black lines. Clade names A–K follow Vasaitis *et al.* (2009), J, K, L Banik *et al.* (2012), N, O are from Song *et al.* (2014). Bootstrap values from 500 replicates are shown. Sequences generated for this study are indicated by triangles, sequences of the new species by circles.

Results

The analyzed dataset included ITS sequences of 34 *Laetiporus* specimens representing 16 taxa. The dataset had an aligned length of 559 characters including gaps, of which 418 are constant, 56 are variable and parsimony uninformative and 85 are parsimony informative. In the consensus tree inferred from Maximum likelihood (ML) analysis, the specimens of the new species formed a well-supported lineage (Fig. 1).

Taxonomy

Laetiporus lobatus J. Vlasák, J. Kout & D.L. Lindner, *sp. nov.* (Figs. 1–4)

Mycobank MB828335

Diagnosis:—Differs from other *Laetiporus* species by its small pores, 7–8 per mm, small spores, $3.9\text{--}4.4 \times 2.8\text{--}3.2 \mu\text{m}$, strikingly lobed pileus margin, and unique ribosomal ITS sequence. Known only from Costa Rica.

Etymology:—*lobatus* (Lat.): referring to the strikingly lobed pileus margin.

Type:—COSTA RICA. Guanacaste Prov.: Guanacaste conservation Area, Pitilla Biological Station, 5 August 1993, leg. J. Stockland, det. M. Núñez as *L. sulphureus* (CFMR Núñez 207, GenBank JN684764).

Basidiomata annual, with dimidiate pilei in imbricate clusters, 10–15 cm broad and wide and 0.5 cm thick, upper surface indistinctly zonate with pale orange/yellow transitions when young; zonation fading when dry; mature surface dull, tuberculate; margin strikingly lobed or dentate; context soft, easily broken, white, up to 3.5 mm thick; pore surface pale yellow, without bright yellow colours; pores minute, subangular, 6–8 per mm, up to 1.5 mm deep. Odour not distinctive; taste none.

Hyphal system functionally dimitic; generative hyphae thin-walled, hyaline, simple septate, with rare branching; vegetative hyphae of similar character, thick-walled, IKI–, dissolving in KOH. In the context, generative hyphae are infrequent, up to 9 μm in diam; binding hyphae are dominant, 6.3–12 μm diameter with walls 1.4–2.7 μm thick, much branched, hyaline. Tramal generative hyphae subparallel, thin-walled, with occasional branching, simple septate, 2.5–4 μm in diam.; tramal (pseudo) skeletal hyphae similar but thick-walled, 3–6 μm in diam. Basidia 9–15 \times 5–8 μm , clavate, hyaline, thin-walled, 4-sterigmate, lacking a basal clamp. Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, guttulate, IKI–, $3.9\text{--}4.4 \times 2.8\text{--}3.2 \mu\text{m}$, $L = 4.22 \mu\text{m}$, $W = 3.10 \mu\text{m}$, $Q = 1.40\text{--}1.43$ ($n = 40/2$).

Ecology: causing a brown heart rot of undetermined tropical hardwoods. Basidiocarps appear on the base of living trees. One collection is from tropical dry forest (type), the other from tropical rain forest close to the coast.

Distribution: known only from Costa Rica, Pacific side.

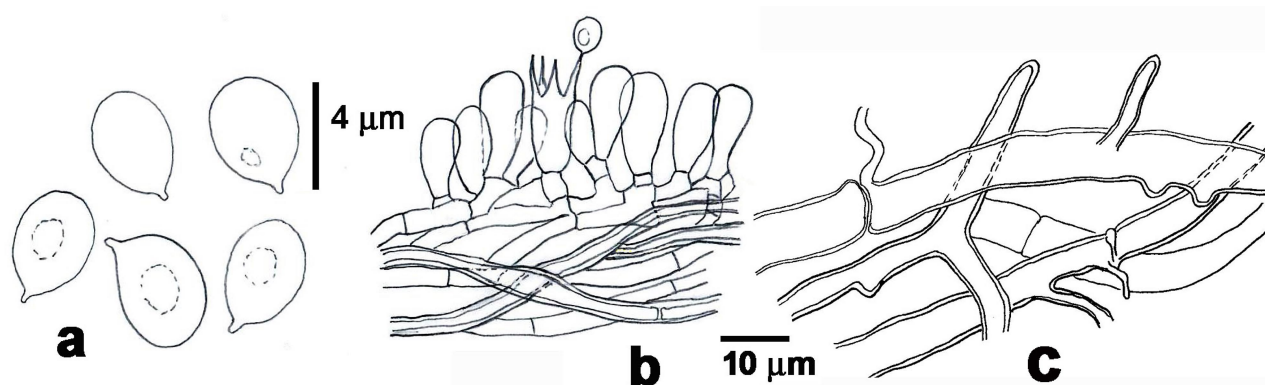


FIGURE 2. Microscopic structure of *Laetiporus lobatus* (drawn from the holotype). a. Basidiospores. b. Basidia, basidioles and hyphae from trama. c. Hyphae from context.

Additional material examined: *L. lobatus*—COSTA RICA. Puntarenas Prov.: Golfito, Playa Nicuesa, unknown living hardwood tree, 19 April 2017, *Vlasák 1704/52* (CBG, JV, PRM, GenBank MK098490, MK098491). *L. gilbertsonii*—COSTA RICA. Alajuela Prov.: Santa Elena, hardwood, 24 April 2015, *Vlasák 1504/103* (JV, GenBank MK098492). *L. sulphureus* (clade C)—CZECHIA. South Bohemia: Hluboká nad Vltavou, Old deerfield, *Quercus* sp., 14 September 2002, *Vlasák 0209/15* (JV, GenBank MK09849); Štěpánovice, *Robinia pseudacacia*, *Vlasák 1709/6*



FIGURE 3. A part of basidiocarp of *Laetiporus lobatus* (Núñez 207, holotype). Photo J. Vlasák.

(JV, GenBank MK098494, MK098495). *Laetiporus* sp. (Clade E)—CZECHIA. South Bohemia: Hluboká nad Vltavou, Šnekl pond dam, *Quercus* sp., Oct 2016, *J. Souček 2016/196*, 27 August 2018, *J. Souček 2018/117* (JV 1610/7, JV 1808/155, GenBank MK098496), Bezdrev pond dam, *Quercus* sp., 28 August 2017, *Vlasák 1708/3* (JV, GenBank MK098497).



FIGURE 4. A basidiocarp of *Laetiporus lobatus* (Vlasák 1704/52), showing lobed margin. Photo J. Vlasák.

Discussion

The specimen *Vlasák 1704/52* of *L. lobatus* shows the same ITS sequence as the type collection (Núñez 207), but it contains also a minor allele with 10b deletion in ITS2 sequence (1704/52-2 in Fig. 1). The sequences are distinctly different from all other *Laetiporus* species, but they group together with South American species *L. caribensis* (Clade J), *Laetiporus* sp. (Clade M) and *L. gilbertsonii* (Clade F). The most similar, *L. caribensis* differs also in having larger pores (4–5 per mm) and a mostly entire pileus margin (Banik *et al.* 2012). *L. gilbertsonii*, the most common *Laetiporus* species in Central America, differs by larger spores (Burdsall & Banik 2001). Specimen Robledo 1122 from Argentina (Clade M undescribed species) is also close but it shows a divergent sequence and slightly longer spores (4.5–5.4 μm according to our measurements). Other *Laetiporus* species have all distinctly larger spores (Song & Cui 2017, Table 2).

In the past, the variation of some features of *Laetiporus* specimens was interpreted as *L. sulphureus* varieties, which notion was probably promoted by the cosmopolitan abundance and morphological uniqueness of *Laetiporus* s. lato. Nevertheless, sequence and incompatibility studies showed that a number of distinct species are present. Many new species have been described in *Laetiporus* s. lato (see Introduction), but some of the clades still await formal species description. The most interesting problem represents the genus type, *L. sulphureus*, which used to be assigned to two very distant clades C and E, which overlap geographically, ecologically, and show hardly any morphological differences. We have here tentatively assigned the name *L. sulphureus* to clade C, occurring only in Europe, and called clade E *Laetiporus* sp. (Fig. 1). However, solving nomenclature in this complex requires its own paper.

Acknowledgments

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