Lentinoid and Polyporoid Fungi, Two Generic Conglomerates Containing Important Medicinal Mushrooms in Molecular Perspective

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ABSTRACT: Polyporoid and lentinoid fungi contain the important producers of substances having immunomodulatory, antitumoral, antiviral, and antihyperlipidemic effects. The discovery of several phylogenetic lines within the lentinoid-polyporoid continuum will help with target metabolomic analysis of species still not studied in pharmacological respects. The purpose of the present work was to increase a resolution in the lentinoid-polyporoid phylogenetic zone by means of selection of both the main representatives of Lentinus-related genera and poorly known/intermediate taxa such as Lentinus suavissimus, Neofavolus spp., and the resupinate part of Polyporus (genera Perenniporia and Pachykytospora) in the context of the basic structure of the Polyporales tree. The molecular phylogeny of highlighting all the polyporoid and lentinoid nodes was reconstructed using nLSU ITS rDNA and TEF datasets. The data obtained from ITS, TEF, and LSU coincide in support of core Polyporaceae of 10 clades corresponded to the generic level and 7 of these (Cerioporus, Cladomeris, Favolus, Lentinus, Neofavolus, Picipes, and Polyporus s.str.) contain generic units characterized by polyporoid or lentinoid morphotypes. The other 2 clades containing lentinoid taxa are outside the core Polyporaceae, namely Panus (Meruliaceae, Polyporales) and Neolentinus (Gloeophyllaceae, Gloeophyllales). A new genus, Picipes, is described and 25 new combinations are proposed.

KEY WORDS: medicinal mushrooms and fungi, Polyporus s.l., Lentinus s.l., molecular phylogeny, Polyporaceae, taxonomy

ABBREVIATIONS: BA, Bayesian; ML, maximum likelihood; MP, maximum parsimony

I. INTRODUCTION

Along with the widely distributed term polyporoid fungi, the term lentinoid fungi has been recently introduced into the current literature.1-4 This applies to genera segregated from Lentinus in Pegler’s sense. Both groups contain the important producers of substances having immunomodulatory, antitumoral, antiviral, and antihyperlipidemic effects (Table 1).5-11 Further search for active producers of pharmacologically meaningful metabolites within these generic conglomerates represents a sufficient issue in medicinal mushroom science.

Beginning with Fries,12 who described the Lentinus genus, the relationships of lentinoid and polyporoid fungi were obvious for various authors. Friesian establishment of Lentinus was based on his subtribe Lentoscyphi of the Omphalina tribe of the Agaricus genus.13 Despite the declaration of affinity between Lentinus, Favolus, and Polyporus (Favoli very absolute agaricini, Polypori autem favoloidei ab hoc genere neutiquam separari debent14), a formal taxonomical position of Polyporus was far from Lentinus in the Friesian system because its large units were based on the hymenophore configuration—poroid or cellar-like in the first and truly lamellate in the second ones.

Torrend15 was the first to adapt the Lloydian genus Lentus for segregation of the lentinoid element of Polyporus, namely Polyporus brumalis. Kühner16 has emphasized the close relationships between Lentinus variabilis (modern name Neolentinus cyathiformis)
and the *Polyporus squamosus* group. Singer\textsuperscript{17-19} has united *Polyporus*, *Lentinus*, and *Panus* in the family Polyporaceae, restricted to 3 polyporoid (*Polyporus*, *Pseudovafolus*, and *Mycobonia*) and 4 lamellate (*Phyllotopsis*, *Pleurotus*, *Panus*, and *Lentinus*) genera. The genus *Lentinus* this author has typified by *Lentinus lepideus* (the widely accepted typification is connected to *L. crinitus*), whereas the small-spored velutinate element of this genus he left in the *Panus*. Pouzar\textsuperscript{20} reported that squamules at the basal portion of the stipe are amyloid both in *Polyporus* species and *Lentinus suavissimus*. Basing on Singer’s classification, Stankovicová\textsuperscript{21} showed some intermediate morphological phenomena between polyporoid and lentinoid taxa.

Concerning *Lentinus* splitting, the first related entity was the genus *Panus* described by Fries\textsuperscript{22} with type *Panus conchatus*. A perfectly elaborated differentiation of *Lentinus* and *Panus* was made by Corner,\textsuperscript{23} who limited the genus *Lentinus* to species with ligative skeletals, separating species with fibroid skeletals into *Panus*. In parallel, Pegler\textsuperscript{24} re-established a large *Lentinus* with 2 subgenera, *Lentinus* and *Panus*, based on Cornerian principles. The further segregation was made by Redhead and Ginn,\textsuperscript{25} who split from *Lentinus* 2 brown-rot genera, *Heliocybe* (the type *H. sulcata*) and *Neolentinus* (the type *N. kauffmanii*).

Furthermore, a sufficient distance between *Lentinus*, *Panus*, and *Neolentinus* was supported by karyological observation\textsuperscript{26} and molecular studies.\textsuperscript{3,27} Beginning with Krüger and Gargas,\textsuperscript{28} a congeneric nature of *Lentinus* s. str. with some representatives of large *Polyporus*, such as *P. arcularius*, *P. brumalis*, and *P. tricholoma*,\textsuperscript{29-31} becomes obvious. Zmitrovich\textsuperscript{32} has proposed some corresponding combinations into the genus *Lentinus*. Subsequent molecular tests of large *Polyporus*,\textsuperscript{33,34} however, did not involve any lentinoid element; even in such a foreshortening, they allow for allocation of an independent status of the *Neofavolus* entity.\textsuperscript{34} The molecular phylogeny shows the position of the *Panus* within merulioid lineage, not the polyporoid one.\textsuperscript{31,35}

The purpose of the present work is to increase a resolution in the lentinoid-polyporoid phylogenetic zone by means of selection both of main section representatives of *Lentinus*-related genera and poorly known/intermediate taxa such as *L. suavissimus*, *Neofavolus* spp., and the resupinate part of *Polyporus* (genera *Perenniporia* and *Pachykytospora*) in the context of the basic structure of the *Polyporales* tree. Identification of the polyporoid-lentinoid phylogenetic zone should help researchers with target metabolomics analysis of species still not studied in pharmacological respects.

### II. MATERIALS AND METHODS

#### A. Taxon Sampling

A total of 54 specimens of polyporoid and lentinoid fungi were selected for molecular analysis. We generated a total of 17 ITS, 16 nLSU, and 16 TEF sequences for this study; 34 additional ITS sequences, 26 additional LSU sequences, and 1 additional TEF sequence of other polyporoid/merulioid genera were retrieved from GenBank based on BLAST results (http://www.ncbi.nlm.nih.gov/BLAST/). The final

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**TABLE 1: Key Representatives of Medicinal Mushrooms within Lentinoid and Polyporoid Fungi**

<table>
<thead>
<tr>
<th>Species</th>
<th>Medicinal Properties</th>
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</thead>
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<tr>
<td><em>Polyporus umbellatus</em></td>
<td>Immune-modulation\textsuperscript{5,6}</td>
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<tr>
<td><em>Lentinus tuber-regium</em></td>
<td>Immune-modulatory, antiviral\textsuperscript{7}</td>
</tr>
<tr>
<td><em>Lentinus crinitus</em></td>
<td>Anti-inflammatory, direct antitumor\textsuperscript{8,9}</td>
</tr>
<tr>
<td><em>Lentinus strigosus</em> (= <em>Panus lecomtei</em>)</td>
<td>Anti-inflammatory, direct antitumor\textsuperscript{8,9}</td>
</tr>
<tr>
<td><em>Lentinus lepideus</em> (= <em>Neolentinus lepideus</em>)</td>
<td>Antihyperlipidemic\textsuperscript{10}</td>
</tr>
<tr>
<td><em>Lentinus conchatus</em> (= <em>Panus conchatus</em>)</td>
<td>Direct antitumor\textsuperscript{11}</td>
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</tbody>
</table>
data set consisted of 51 ITS sequences, 17 TEF sequences, and 43 nLSU sequences. For all analyses, the sequences of *Exidia glandulosa* retrieved from GenBank were chosen as the outgroup based on BLAST homology. An overview of all taxa studied is given in Table 2, which shows the names of species, GenBank accession numbers, herbarium numbers, and collection particulars.

**B. DNA Extraction, PCR, and Sequencing**

DNA was extracted from herbarium material using 2% cetyl trimethylammonium bromide extraction buffer with the following steps of consecutive addition of the chloroform-isomyl alcohol mixture (24:1), then isopropyl alcohol and 3 M sodium acetate solution for precipitation, 70% ethanol for washing, and finally water for dissolution. The NucleoSpin Plant II Kit (Macherey-Nagel) was used as an alternative method of DNA extraction. The ribosomal ITS1-5.8S-ITS2 region was amplified by PCR with the fungal specific primers ITS1F and ITS4B and the 28S region was amplified by PCR with the fungal specific primers LROR and LR7 (Vilgalys Laboratory; http://www.biology.duke.edu/fungi/mycolab/primers). The 1000-bp fragment of TEF1 was amplified using the primer pair EF1-983F and EF1-2212R.

For rDNA regions, the following PCR protocol was used: 1) initial denaturation at 95°C for 2 min, 2) denaturation at 94°C for 40 s, 3) annealing at 50°C for 1 min, 4) extension at 75°C for 2 min, 5) repeat for 35 cycles starting at step 2, and 6) leave at 75 °C for 10 min. For TEF1, the PCR protocol included the following steps: 1) initial denaturation at 95°C for 2 min, 2) denaturation at 95°C for 40 s, 3) annealing at 60°C for 40 s, 4) extension at 70°C for 2 min, 5) repeat for 9 cycles starting at step 2, 6) denaturation at 95°C for 45 s, 7) annealing at 50°C for 1.5 min, 8) extension at 70°C for 2 min, 9) repeat for 36 cycles starting at step 6, and 10) leave at 70°C for 10 min.

The PCR products were purified using the Fermentas Genomic DNA Purification Kit (Thermo Scientific).

Sequencing of this strand was performed with an ABI model 3130 Genetic Analyzer (Applied Biosystems) using the BigDye Terminator Cycle Sequencing Ready Reaction Kit (Applied Biosystems) with the same primers. The raw data were processed using Sequencing Analysis 5.3.1 (Applied Biosystems).

**C. Alignments and Phylogenetic Analysis**

The sequences were aligned with the web tools MAFFT (http://align.bmr.kyushu-u.ac.jp/mafft/online/server/) with Q-INS-i strategy and default settings for other options. The final alignment was corrected manually using MEGA 5.36

Phylogenetic reconstructions were performed with maximum parsimony (MP), maximum likelihood (ML), and Bayesian (BA) analyses.

A MP analysis was performed using PAUP*4.0.b10.37 One-hundred heuristic searches were conducted by stepwise addition with random sequence addition and a tree bisection-reconnection branch-swapping algorithm. One tree was held at each step during stepwise addition and the number of trees retained was limited to 100. Parsimony bootstrap analysis was performed with 1000 replicates. Gaps were treated as missing characters. Clades with only a support ≥50% were retained.

ML was run in the RAxML server (version 7.2.8; http://phylobench.vital-it.ch/raxml-bb),38 under a GTR model with 100 rapid bootstrap replicates.

Bayesian analysis was performed using MrBayes 3.139 for 2 independent runs, each with 10,000,000 generations with sampling every 100 generations, with a GTR model and 4 chains. Posterior probability values ≥0.95 are considered significant.

**D. Morphological Elaboration**

Microscopical study of basidiomata was carried out as described by Gilbertson and Ryvarden.40 Freehand sections and squash mounts of basidiomata were examined in Melzer’s reagent, 5% KOH, and 2% Cotton Blue. Basidiome morphotypes recognized after Zmitrovich et al.41 (see Supplement 1; http://www.researchgate.net/publication/279447216).
### TABLE 2: Collections Used in This Study of ITS, nLSU, and TEF 1-Alpha Data Sets and Their Herbarium and GenBank Accession Numbers

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III. RESULTS AND DISCUSSION

A. Ten Clades in the Polyporoid-Lentinoid Continuum

The results of molecular taxonomical analysis of the lentinoid-polyporoid taxonomical continuum are presented in Figs. 1–3 (in which ITS and combined ITS+TEF+LSU phylogenies are given) and Table 3 (where all of the molecular entities are characterized).

All of the data obtained from ITS, TEF, and LSU coincide in support within core Polyporaceae of 10 clades corresponded to generic levels, and 7 of these clades contain a generic units characterized by polyporoid or lentinoid morphotypes. The remaining 2 clades containing lentinoid taxa lie outside of core Polyporaceae, namely *Panus* (Meruliaceae, Polyporales) and *Neolentinus* (Gloeophyllaceae, Gloeophyllales) (Table 3).

The consequences of molecular resolution of phylogenetic pathways in the polyporoid-lentinoid continuum seem to be sufficient. The LSU data set appears the most informative for resolution of clade interrelationships. The clade *Cerioporus* seems to be an ancient lineage in core polyporoid radiation. This unit contains fungi of polyporoid morphotype characterized by more or less inflated axial element of skeleto-binding dendrite. Such inflation can be interpreted as a residual phenomenon of physalohyphae sclerification in basically a tyromycetoid-scutigeroid morphotype. The basidiospores in all representatives included are characterized by subfusoid to subnavicular appearance. The tendency to trametization is obvious within this line (*C. varius*, *C. stereoides*, *C. mollis*).

The further phylogenetic radiation is based on *Lentinus* (including *Polyporellus*) lineage. Their representatives keep an inflation of axial element of skeleto-binding dendrite, but hyphal

<table>
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FIG. 1: The best tree obtained from the ML analysis of combined LSU data set. Bootstrap values (%) from MP and posterior probability from BY analyses are shown under and above the branches, respectively.

Ramification here is more regular having dichotomous appearance as a result. The hymenophore configuration in *Lentinus* representatives varies from poroid or radially poroid in various representatives of *Polyporellus* sublineage to true lamellate with lamellae and lamellulose (in *Lentinus* and *Tigrini* sublineage representatives). Numerous superficial adaptations are characteristic to tropical taxa (e.g., an upperside pillar development). The main morphogenetic tendency in tropical taxa is the substitution of protoplasm-bearing hyphae by sclerified dendrites in all tissues of basidiome. The basal *Polyporellus* sublineage can be morphogenetically connected to derivative trametoid (*Dichomitus*) and fibroporioid (*Pachykytospora, Perenniporia*) morphotypes. *Dichomitus* keeps micromorphological identity with the *Lentinus* lineage, whereas the *Perenniporia* lineage is characterized by basidiospore wall sclerification. The verrucose basidiospores of *Pachykytospora* represent a result of partial exospore degradation of basidiospores of the *Perenniporia* type.42

The crown group is presented by independent lineages *Polyporus* s. str., *Neofavolus, Cladomeris, Picipes*, and *Favolus*. It is possible that more ancient lineage of the crown group is *Cladomeris* represented by one sclerotium-forming species of grifoloid morphotype (*C. umbellatus*). This species is characterized by predominance of protoplasm-bearing hyphae with inflated axial segments. The substitution of protoplasm-bearing hyphae by sclerified dendrites with inflated axial element is characteristic to *Picipes* lineage (=*Polyporus melanopus* group), uniting fungi of the polyporoid morphotype with small pores, blackish stipe cuticle, and tendency to trametization. Generative hyphae in *P. badius* are devoid of clamps, whereas all of the other representatives bear the fibulate hyphae. The basidiospores in both *Cladomeris* and *Picipes* lines are cylindric. The lineage *Polyporus* s. str. (*P. tuberaster*) is connected...
FIG. 2: The best tree obtained from the ML analysis of ITS data set. Bootstrap values (%) from MP and posterior probability from BY analyses are shown under and above the branches, respectively.

to Cladomeris by other way: this is sclerotium-forming polypore with sclerified dichophytic skeletal and elongated spores due to large subcellular pores. The characters’ patterns of Favolus and Neofavolus allow characterize them as certain scraps of lines to tramaetization (Favolus) and lentination (Neofavolus suavissimus) of Picipes-like morphotypes. Some Favolus representatives are devoid of clamps. The basidiospores in Neofavolus and Favolus are cylindric, like those of Picipes representatives.
The consensus dataset indicates multiple origins of polyporoid and lentinoid morphotypes, the phylogenetically derivative nature of lentinoid and resupinate poroid morphotypes, as well as the tendency of transformation of skeleto-binding dendrites into fibrohyphae massifs in long-lived basidiomes. The taxonomical consequences of such a resolution are also diverse. In particular, the genus *Lentinus* s. str. has to include the *Polyporus arcularius* group. The corresponding combinations were made by Zmitrovich\(^3\); however, the name *Lentinus ciliatus* (Fr.) Zmitr. would be rejected as invalid and replaced by the new correct name. Another matter is final recognition of heterogeneity of the remaining *Polyporus*. Until now, the *Polyporus* conglomerate has been kept as widely known and corresponding
### Table 3: Phylogenetic Overview of the Polyporoid-Lentinoid Continuum

<table>
<thead>
<tr>
<th>Clade Name</th>
<th>Phylogeny Supporting Characteristics</th>
<th>Morphological Characterization</th>
</tr>
</thead>
<tbody>
<tr>
<td><strong>Core polyporoid phylogenetic radiation</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><em>Cerioporus</em></td>
<td>ITS (‒/0.98); LSU (53/‒); combined (94/1)</td>
<td>Polyporoid to trametoid; dimitic with inflated axial skeletals and arboriform branching; basidiospores fusoid, with navicular tendency, or humpbacked</td>
</tr>
<tr>
<td><em>Cladomeris</em></td>
<td>Combined (100/1)</td>
<td>Polyporoid – grifoloid; subdimitic with inflated axial hyphae and ±dichophytic branching; basidiospores subcylindric</td>
</tr>
<tr>
<td><em>Dichomitus</em></td>
<td>Combined (100/1)</td>
<td>Trametoid to fibroporioid; dimitic with inflated axial skeletals and dichophytic branching; basidiospores fusoid, smooth, thin-walled</td>
</tr>
<tr>
<td><em>Favolus</em></td>
<td>ITS (71/‒); LSU (97/1); combined (99/1)</td>
<td>Polyporoid – favoloid; dimitic with uninflated axial element and arboriform branching; basidiospores with fusoid or navicular tendency</td>
</tr>
<tr>
<td><strong>Lentinus</strong>*</td>
<td>ITS (87/1); LSU (93/1); combined (95/1)</td>
<td>Lentinoid or polyporoid; dimitic with inflated axial element ±dichophytic branching; basidiospores subcylindric</td>
</tr>
<tr>
<td><strong>Neofavolus</strong>*</td>
<td>LSU (91/‒); combined (94/1)</td>
<td>Polyoporoid (favoloid) or lentinoid; dimitic with uninflated axial element and rare; ±dichophytic branching; basidiospores subcylindric</td>
</tr>
<tr>
<td><em>Pachykytospora</em></td>
<td>combined (96/0.99)</td>
<td>Fibroporioid; dimitic with inflated axial skeletals and arboriform branching; basidiospores fusoid-elliptical, with ridged exosporium</td>
</tr>
<tr>
<td><em>Perenniporia</em></td>
<td>ITS (86/0.98); combined (99/1)</td>
<td>Trametoid to fibroporioid; dimitic with inflated axial skeletals and arboriform branching; basidiospores truncate, smooth, thick-walled</td>
</tr>
<tr>
<td><em>Picipes</em></td>
<td>ITS (88/1); LSU (89/0.98); combined (98/1)</td>
<td>Polyoporoid without sclerotium; dimitic or trimitic with uninflated axial skeletals and active dichophytic branching; basidiospores cylindric, &lt;10 μm long</td>
</tr>
<tr>
<td><em>Polyporus s.str.</em></td>
<td>Combined (100/1)</td>
<td>Polyoporoid arising from sclerotium; dimitic with uninflated axial skeletals and moderate dichophytic branching; basidiospores fusoid, &gt;10 μm long</td>
</tr>
<tr>
<td><strong>Merulioid phylogenetic radiation</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Panus</strong></td>
<td>ITS (98/1); LSU (98/1); combined (100/1)</td>
<td>Lentinoid; dimitic with fibrohyphae (uninflated with collapsed appendages); basidia &lt; 30 μm long; basidiospores subcylindric; white-rot fungi</td>
</tr>
<tr>
<td><strong>Gloeophyllales phylogenetic radiation</strong></td>
<td></td>
<td></td>
</tr>
<tr>
<td><strong>Neolentinus</strong></td>
<td>ITS (96/1); LSU (93/0.95); combined (98/1)</td>
<td>Lentinoid; dimitic with fibrohyphae (uninflated with collapsed appendages); basidia &gt; 30 μm long; basidiospores with navicular or fusoid tendency; brown-rot fungi</td>
</tr>
</tbody>
</table>

Bootstrap values (%) from MP and posterior probability from BY analyses are shown below and above the slash, respectively.

*Entity unites species of polyporoid (including favoloid) morphotype.*

**Entity unites species of lentinoid morphotype.*

*/**Entity unites species both of polyporoid and lentinoid morphotypes.*
Table 4: Diagnostic Key to Genera of Polyporoid and Lentinoid Fungi

I. Sclerohyphae unbranched at the maturity (fibrohyphae) – uninflated with collapsed appendages; their abundant terminations in the hymenium are recognized as pseudocystidia. Hymenophore lamellate.

A. Basidia <30 μm at maturity. Basidiospores cylindrical. Cause a white rot. ... Panus.

B. Basidia >30 μm at maturity. Basidiospores with navicular or fusoid tendency. Cause brown-rot. ... Neolentinus.

II. Sclerohyphae sympodially branched. Pseudocystidia none. Hymenophore lamellate, cellular, or poroid.

A. Axial element of skeleto-binding dendrite is recognizable owing to its inflation.


2. Hyphal system dimitic, sclerohyphae present in hymenophoral trama. Basidiomes of polyporoid, trametoid, or lentinoid morphotypes.

   α. Basidiomes of polyporoid or trametoid morphotype. Basidiospores fusoid, with navicular tendency, or humpbacked. ... Cerioporus.

   β. Basidiomes of lentinoid or polyporoid morphotype. Basidiospores subcylindric. ... Lentinus.

B. Axial element of skeleto-binding dendrite uninflated.


   α. Sclerohyphae moderately branched. Basidiospores fusoid, >10 μm long. Basidiomata arising from sclerotium. ... Polyporus.

   β. Sclerohyphae strongly branched. Basidiospores cylindric, <10 μm long. Sclerotium absent. ... Picipes.

2. Sclerohyphae arboriform. Basidiomes of polyporoid, favoloid, or lentinoid morphotype.

   α. Sclerohyphae regularly branched. Basidiospores with fusoid or navicular tendency. Basidiomes of polyporoid or favoloid morphotype. ... Favolus.

   β. Sclerohyphae rarely branched. Basidiospores subcylindric. Basidiomes of favoloid or lentinoid morphotype. ... Neofavolus.

The catalog presented in Table 5 reflects the view of the Polyporus s.l.-Lentinus s.l. conglomerate on a molecular perspective. Therefore, some nomenclatural innovations are given here. An enlarged version of the taxonomical catalogue of polyporoid and lentinoid fungi, which includes a synonymy of all of the taxa, is presented in Supplement 2 (http://www.researchgate.net/publication/279447065).

B. Diagnostic Key to Genera of Polyporoid and Lentinoid Fungi

A diagnostic key to genera of polyporoid and lentinoid fungi is presented in Table 4.

C. Taxonomical Catalogue of Polyporoid and Lentinoid Fungi

To the everyday patrimonial generic concept, although the micromorphological diversity within this genus was discussed by some authors. The discovery of an independent lineage, which includes the Polyporus type (Polyporus tuberaster), raised a problem of restoration of old and establishing of new names for remaining lineages: Cerioporus (type P. squamosus), Cladomeris (type P. umbellatus), Favolus (type P. brasiliensis), and Neofavolus (type P. alveolaris). The last lineage also includes lentinoid elements such as L. suavissimus. Such rearrangement successfully solves a problem of Datronia. This trametoid unit joins in polyporoid Cerioporus.

The revealing of several phylogenetic lines within the lentinoid-polyporoid continuum undoubtedly will help with target metabolomic analysis of species still not studied in pharmacological respects.
### TABLE 5: Taxonomical Catalogue of Polyporoid and Lentinoid Fungi

#### POLYPORALES

#### POLYPORACEAE

**Cerioporus** Quél., Ench. Fung.: 167, 1886.

- **Cerioporus leptocephalus** (Jacq.) Zmitr. et Kovalenko comb. nov. (MB 812037). – Bas.: *Boletus leptocephalus* Jacq., Miscell. austriac. 1: 142, 1778 [*Polyporus leptocephalus* Jacq.: Fr., 1821].
- **Cerioporus mollis** (Sommerf.) Zmitr. et Kovalenko comb. nov. (MB 812039). – Bas.: *Daedalea mollis* Sommerf., Suppl. Fl. Lapp.: 271, 1826.
- **Cerioporus rhyzophilus** (Pat.) Zmitr. et Kovalenko comb. nov. (MB 812040). – Bas.: *Polyporus rhyzophilus* Pat., J. Bot. 8: 219, 1894.
- **Cerioporus squamosus** (Huds.) Quél., Enchir. Fung.: 166, 1886.
- **Cerioporus stereoides** (Fr.) Zmitr. et Kovalenko comb. nov. (MB 812041). – Bas.: *Polyporus stereoides* Fr., Observ. mycol. 2: 258, 1818.
- **Cerioporus varius** (Pers.) Zmitr. et Kovalenko comb. nov. (MB 812042). – Bas.: *Boletus varius* Pers., Observ. mycol. 1: 85, 1796 [*Polyporus varius* Pers.: Fr., 1821].

#### Provisonal position:


#### CLADOMERIS

**Cladomeris** Quél., Enchir. fun.: 167, 1886.

- **Cladomeris umbellata** (Pers.) Zmitr. et Kovalenko comb. nov. (MB 812043). – Bas.: *Boletus umbellatus* Pers., 1801.

#### Favolus

**Favolus** Fr., Elench. 1: 44, 1828.

- **F. brasiliensis** (Fr.) Fr., Linnaea 5: 511, 1830 [*Daedalea brasiliensis* Fr., 1821].
**TABLE 5:** (Continued)

| F. roseus Lloyd, Mycol. Writ. 7: 1157, 1922. |

**LENTINUS** Fr., Syst. Orbis Veg. 1: 77, 1825.  
Type: Agaricus crinitus L., 1763.  
Lentinus anastomosans Rick, Lilloa 2: 310, 1938.  
Lentinus araucariae Har. et Pat., J. Bot. 17: 11, 1903.  
Lentinus badius (Berk.) Berk., London J. Bot. 6: 491, 1847.  
Lentinus bertieri (Fr.) Fr., Syst. Orbis Veg. 1: 77, 1825.  
Lentinus concavus (Berk.) Henn. in Engler et Prantl, Nat. Pflfam. 1: 224, 1900.  
Lentinus crinitus (L.) Fr., Syst. Orbis veg. 1: 77, 1851.  
Lentinus flexipes (Fr.) Zmitr. et Kovalenko comb. nov. (MB 812268). – Bas.: Polyporus flexipes Fr., Linnaea 5: 515, 1830.  
Lentinus glabratus Mont. in La Sagra, Cuba Pl. Cell.: 424, 1842.  


Lentinus sajor-caju (Fr.) Fr., Epicr.: 393, 1838.


Lentinus stupeus Klotzsch, Linnaea 8: 480, 1833 [ut 'stupens'].


Lentinus tigrinus (Bull.) Fr., Syst. Orbis Veg.: 78, 1825.

Lentinus tuber-regium (Fr.) Fr., Syn. generis Lentinus: 3, 1836.


Lentinus villosus Klotzsch, Linnaea 8: 479, 1833.


Type: Merulius alveolaris DC., 1815.


Neofavolus suavissimus (Fr.) Zmitr. et Kovalenko comb. nov. (MB 812026). – Bas.: Lentinus suavissimus Fr., Meth. Grund. Mod. Pflanzensoziol.: 13, 1836.


PICIPES Zmitr. et Kovalenko gen. nov. (MB 812027)

= Melanopus Pat., 1887 in Donk’s (1960) typification. Nomen ambiguum.

Basidiomata annual, stipitate, of polyporoid morphotype. Pilei infundibiliform, covered with hard cuticle, without scales, smoke gray to castaneous or deeply brown. Stipe covered with brownish to black cuticle. Pores small (more than 5 per mm). Hyphal system dimitic with uninflated both corioloid and fibrous skeletals; the last ones are subsolid. Clamps present or absent. Basidiospores cylindric, smooth, hyaline. On wood of frondose and coniferous trees causing a white rot.

Type: Boletus badius Pers., 1801.

Etymology: piceus – covered by tar, pes – stipe. This term refers to Polyporus picipes Fr. and substitutes the name Melanopus Pat. nom. ambig. based on Polyporus melanopus Sw.: Fr.

A numerous branched skeletals with uninflated axial elements, numerous subsolid fibrohyphae in combination with small pores and dark-colored stipe cuticle are characteristic for the genus.

TABLE 5: (Continued)


Type: *Polyporus tuberaster* Jacq. ex Pers. per Fr., 1821.

**MERULIACEAE**

**PANUS** Fr., Syst. Mycol. 1: 396, 1821.
Type: *Agaricus conchatus* Bull., 1787.
*Panus conchatus* (Bull.: Fr.), Epicr.: 397, 1838.
*Panus lecomtei* (Fr.) Corner, Beih. Nova Hedw. 69: 90, 1981.
*Panus velutinus* (Fr.) Overh., J. Dept Agric. Porto Rico 14: 353, 1930 non Fr., 1838.

**GLOEOPHYLLALES**

**GLOEOPHYLLACEAE**

Type: *Lentinus kaufmannii* A. H. Sm., 1946.
*Neolentinus cyathiformis* (Schaeff.) Della Maggiora et Trassinelli, Index Fungorum 171: 1, 2014.

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