Diversity of *Trametes* (Polyporales, Basidiomycota) in tropical Benin and description of new species *Trametes parvispora*

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**Academic editor:** M.-A. Neves | Received 28 October 2019 | Accepted 22 December 2019 | Published 10 March 2020

**Citation:** Olou BA, Krah F-S, Piepenbring M, Yorou NS, Langer E (2020) Diversity of *Trametes* (Polyporales, Basidiomycota) in tropical Benin and description of new species *Trametes parvispora*. MycoKeys 65: 25–47. https://doi.org/10.3897/mycokeys.65.47574

**Abstract**

*Trametes* is a globally distributed genus of white-rot polypores and well sampled in temperate and boreal areas. However, the diversity, taxonomy, and phylogenetic positions of *Trametes* spp. are poorly known in tropical Africa. This study aims at documenting the diversity of *Trametes* species in Benin (tropical Africa) and their phylogenetic positions with a focus on the *T. elegans* species complex. Therefore, we collected specimens of *Trametes* from different forest types across Benin. To infer phylogenetic relationships between *Trametes* species, we investigated sequences of five gene regions and added available sequences from GenBank. Using Maximum likelihood and Bayesian phylogeny inference methods, we found eight supported species clades. For the *T. elegans* species complex, we re-establish the name *Trametes palisotii* for species previously known as *T. elegans* in tropical Africa. Furthermore, we propose *Trametes parvispora* as a species new to science and provide the description of this species. Our molecular phylogeny of *Trametes* with a focus on tropical Benin contributes to taxonomic clarity of an important wood-decay fungal genus, which is the basis for biodiversity assessments of *Trametes* in the tropics.

**Keywords**

Africa, morphology, new taxa, phylogeny, Polyporales, taxonomy, tropics, white rot
Introduction

The genus *Trametes* Fr. (Polyporales, Basidiomycota) consists of wood-decay fungi with a distribution covering all continents and all major climatic zones (Gilbertson and Ryvarden 1987; Ryvarden 1991). Species of *Trametes* are characterized by a combination of a pileate basidioma, a poroid hymenophore, a trimitic hyphal system, and non-amyloid, thin-walled basidiospores (Gilbertson and Ryvarden 1987). They are saprotrophs causing white rot during the decay of woody substrates (Wong and Wilkes 1988). Species of the genus *Trametes* have a long ethnobotanical history as medicinal fungi in many cultures (Cui et al. 2011; Ss and Pandey 2012; Ueitele et al. 2017) and some species are studied in the context of cancer research (Zmitrovich et al. 2012; Cruz et al. 2016; Blagodatski et al. 2018). Despite the global-scale distribution, importance for wood decomposition, and medicinal properties, the taxonomic and phylogenetic knowledge of *Trametes* spp. worldwide is still incomplete (Carlson et al. 2014).

Since the first formal description of the genus *Trametes* by Fries (1835), based on the type species *Trametes suaveolens* (L.) Fr., the concept of this genus was interpreted in different ways, resulting in different numbers of species attributed to the genus (Karsten 1881; Murrill 1905; Kavina and Pilát 1936; Kotlaba and Pouzar 1957; Gilbertson and Ryvarden 1987; Corner 1989). Recently, based on phylogenetic analyses, the concept of *Trametes* was re-delimited and circumscribed (Justo and Hibbett 2011). Here, we apply the broad concept of *Trametes* as proposed by Justo and Hibbett (2011). This concept includes in addition to species of *Trametes* sensu stricto, species of *Artolenzites* Falck, *Coriolopsis* Murrill, *Lenzites* Fr., and *Pycnoporus* P. Karst.

Previous studies on *Trametes* spp. mainly concentrated on specimens from temperate and boreal regions (David 1967; Gilbertson and Ryvarden 1987; Hattori 2005; Tomšovský et al. 2006; Pieri and Rivoire 2007; Ryvarden et al. 2009; Gomes-Silva et al. 2010; Hattori and Sotome 2013), and thus most *Trametes* spp. have been described from these regions. By contrast, little is known on *Trametes* spp. in tropical Africa (Fig. 1A), and most known specimens of *Trametes* spp. from this area are missing in most phylogenetic analyses.

For Benin, seven species of *Trametes*, namely *T. cingulata* Berk., *T. elegans* (Spreng.) Fr., *T. flavida* (Lév.) Zmitr., Wasser & Ezhov (cited as *Leiotrametes flavida*), *T. polyzona* (Pers.) Justo, *T. sanguinea* (L.) Lloyd (cited as *Pycnoporus sanguineus*), and *T. socotrana* Cooke were reported by Olou et al. (2019). Taking a closer look at these species, we noticed that sequence data are lacking for specimens from tropical Africa and that the knowledge on taxonomical and phylogenetic placements is incomplete.

Additional to these known species in Benin, we recently found a putatively new species of *Trametes* (Olou et al. 2019), but morphological and phylogenetic analyses were outstanding. In the same study, we reported the occurrence of *T. elegans* in Benin.

*Trametes elegans* was found to be a species complex and has therefore recently been split into three distinct species, namely *T. aesculi* (Fr.) Justo, *T. elegans* s.str., and *T. repanda* (Pers.) Justo (Carlson et al. 2014). However, this study did not include tropical African specimens although *T. elegans* exists in this area.
Diversity and Phylogeny of *Trametes* in tropical Africa

Our study thus aims to report the diversity of *Trametes* species in Benin and their phylogenetic positions, with a focus on a new species of *Trametes* and the *T. elegans* species complex.

**Material and methods**

**Specimens sampling and preservation**

A total of 37 specimens of *Trametes* were collected in three different macroclimatic zones and different forests of Benin (Fig. 1A, C) from July to September in 2017 (Olou et al. 2019) and in 2018 (another series of surveys). Small pieces of fresh fruit bodies were placed in plastic bags half-filled with silica gel for DNA extraction. The rest of fruit bodies were air- or oven-dried at 45–50 °C for 1–2 days depending on the consistency of the fruit body. The dried fruit bodies were then preserved in plastic bags for morphological investigation. Specimens are deposited at the mycological herbaria of the University of Parakou (UNIPAR; Thiers 2019) and the University of Kassel (KAS).
DNA extraction, amplification, sequencing and alignment

**DNA extraction.** Genomic DNA of all specimens classified into nine morphotypes was extracted using the microwave DNA extraction method (Dörnte and Kües 2013) or the NucleoSpin Plant II DNA extraction kit (Macherey, Nagel, Germany).

**Amplifications and sequencing.** The extracted genomic DNA was amplified targeting two nuclear ribosomal DNA (nrDNA) regions, internal transcribed spacer (ITS) and ribosomal large subunit-coding DNA (28S rRNA) for all specimens. Additionally, three protein-coding genes, RNA polymerase II largest subunit (RPB1), RNA polymerase II second largest subunit (RPB2), and translation elongation factor 1-alpha (TEF1) were amplified for specimens forming part of the *T. elegans* species complex and specimens of *Trametes* sp. The amplification of the 5.8S rRNA gene region, including ITS were performed in Mastercycler nexus gradient (Eppendorf, Germany), using the primer pair ITS-1F/ITS4 (White et al. 1990; Gardes and Bruns 1993). The Polymerase Chain Reaction (PCR) procedure for the ITS region, was as follows: initial denaturation at 95 °C for 3 min, followed by 35 cycles at 95 °C for 30 s, 52 °C for 30 s and 68 °C for 1 min, and a final extension at 68 °C for 3 min. Amplifications of LSU and three protein-coding genes were performed in 96-well TGradient Thermocycler (Biometra, Göttingen, Germany). PCR procedure for amplifying partial LSU rDNA using the primer pair LR0R/LR5 (Vilgalys and Hester 1990) approximately 964 bp differed to the ITS only by the annealing temperature (55 °C instead of 52 °C) and increased cycle extension time (90 s per cycle). The primer pairs EF1-983F/EF1-1567R (Rehner and Buckley 2005), RPB1-Af/RPB1-Cr (Stiller and Hall 1997; Matheny et al. 2002), and RPB2-b6F/RPB2-b7.1R (Liu et al. 1999; Matheny 2005) were used to amplify approximately 500 bp of TEF1, 1000 bp of RPB1, and 800 bp of RPB2. To amplify the protein-coding genes RPB1 and RPB2, the touchdown PCR protocol following Justo and Hibbett (2011) was used. PCR products were checked on 1% agarose gel stained with GelRed fluorescence dye (Biotium, Hayward, California, USA) in the Transilluminator Biometra Ti5 equipped with BioDocAnalyze software (Biometra GmbH, Göttingen, Germany). They were further cleaned up with QIAquick PCR Purification Kit according to manufacturer’s instructions (QIAGEN GmbH, Hilden, Germany). Thereafter, Sanger sequenced at GATC Biotech in Germany.

At least one sequence per specimen was generated for each morphotype except for the morphotype named *T. aff. versicolor* (Fig. 2N; Suppl. material 1). All newly generated sequences composed of 25 ITS, 20 LSU, two RPB1, four RPB2, and three TEF1 were deposited in GenBank (for accession numbers, see Table 1).

**Sequence alignment and phylogenetic analyses.** To place all the 25 generated ITS sequences of specimens of *Trametes* spp. in a phylogenetic context, we aligned them in addition to 66 ITS sequences retrieved from GenBank (Benson et al. 2011). Further, 48 LSU sequences were aligned with 20 LSU sequences generated here. For the
Table 1. Taxa names with collection details and GenBank accession numbers of all sequences of *Trametes* spp.

| Species name | Voucher or strain | Origin | GenBank N° | Reference |
|--------------|-------------------|--------|------------|-----------|
| *Dentocorticium sulphurellum* | FP11801 | | JN165018 | Justo and Hibbett 2011 |
| *Lopharia cinerascens* | FP105043sp USA: Mississippi | JN165019 | JN164813 | Justo and Hibbett 2011 |
| *T. aesculi* (T. elegans species complex) | HHB4626sp USA | JN164950 | KF573173 | Justo and Hibbett 2011, Carlson et al. 2014 |
| *T. betulina* (Lenzites betulinus) | FP105038sp USA: Mississippi | JN164951 | KF573174 | Justo and Hibbett 2011 |
| *T. cinnabarina* (cited as *Pycnoporus cinnabarinus*) | Dai 14386 China | KX880629 | KX880667 | unpublished |
| *T. coccinea* (cited as *Pycnoporus coccineus*) | Cui-7096 | KC848350 | KC848414 | unpublished |
| *T. conchifer* | FP106793sp USA: Mississippi | JN164924 | JN164797 | Justo and Hibbett 2011 |
| *T. cubensis* | TJV93_213sp USA: Mississippi | JN164923 | JN164798 | Justo and Hibbett 2011 |
| *T. cingulata* | MUC1L40167 Malawi | JN694075 | | Wölti et al. 2012 |
| *T. ectypa* | FP103976sp USA: Florida | JN164905 | | Justo and Hibbett 2011 |
| *T. flavida* | FP106037T USA | JN164929 | JN164803 | Justo and Hibbett 2011 |
| *T. gibbosa* | DMC341 Cameroon | KC859144 | KC859164 | unpublished |
| *T. hirsuta* | DMC341 Cameroon | KC859146 | KC859166 | unpublished |
| *T. junipericola* | 145295(0) USA: New York | JN164941 | JN164801 | Justo and Hibbett 2011 |
| *T. lactuca* | DMC346 Cameroon | KC589126 | KC589152 | unpublished |

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| Species name | Voucher or strain | Origin | GenBank N° | Reference |
|--------------|------------------|--------|------------|-----------|
| *T. lactinea* (cited as *Leiotrametes lactinea*) | CBS 109427 | Taiwan | MH862825 | Vu et al. 2019 |
| *T. lactinea* | LIP:GUY09-110 | French Guiana | JN645069 | Welti et al. 2012 |
| OAB0232 | Benin | MK736983, MK736948 | this study |
| BCC 35266 | Thailand | GQ982888, GQ982881 | unpublished |
| Yuan5493 | | KC848320, KC848404 | |
| *T. ljubarskyi* | Wei1653 | | KC848352, KC848416 | unpublished |
| Li286 | | | KC848331, KC848415 | |
| *T. maxima* | OH189sp | Venezuela | JN164957, JN164804, JN164816, JN164864 | Justo and Hibbett 2011 |
| *T. membranacea* | PRSC82 | Puerto Rico | JN164945, JN164805, JN164832, JN164857 | Welti et al. 2012 |
| FBM-FRA:1368 | Martinique | JN645103 | Justo and Hibbett 2011 |
| Dai682 | | | KC848289, KC848374 | unpublished |
| *T. meyenii* | CBS:453.76 | India | JN164945, JN164805, JN164832, JN164857 | Justo and Hibbett 2011 |
| *T. meyenii* | PRSC95 | Puerto Rico | JN164936 | Welti et al. 2012 |
| CBSA53.76 | | | JN164933, MF73179, MF73145 | Justo and Hibbett 2011 |
| HHH13445sp | USA/Michigan | JN164954, JN164812, JN164826, JN164852 | Justo and Hibbett 2011 |
| Dai2005 | China | | KC848272, KC848357 | unpublished |
| *T. palisotii* (T. elegans species complex) | OAB0118 | Benin | MK736980, MK736956, MK802884, MK802882, MK802886 | this study |
| OAB0153 | Benin | MK736981, MK736957, MK802885, MK802883, MK802887 | |
| OAB0198 | Benin | MK736982, MK736958, MK802888 | |
| *T. palisotii* | DMC360 | Cameroon | KC589139, KC589160 | unpublished |
| DMC817 | Cameroon | KC589142, KC589163 | |
| DMC816 | Cameroon | KC589141, KC589162 | |
| *T. parvipora* | OAB0022 | Benin | MK736989, MK736964, MN127965 | this study |
| OAB0023 | Benin | MK736990, MK736965, MN127964 | |
| *T. pavonia* | FP103990sp | USA/Florida | JN164958, JN164806, JN164835, JN164862 | Justo and Hibbett 2011 |
| *T. polyzona* | DMC370 | Cameroon | KC589125, KC589151 | unpublished |
| Cui 11040 | China | KX880647, KX880836, KR610849 | |
| BKW004 | Ghana | JN164978, JN164790 | Justo and Hibbett 2011 |
| OAB0092 | Benin | MK736984, MK736959 | this study |
| OAB0128 | Benin | MK736985, MK736960 | |
| OAB0195 | Benin | MK736986, MK736961 | |
| *T. punicea* (cited as *Pycnoporus puniceus*) | FP101414sp | USA/Wisconsin | JN164963, JN164811, JN164827, JN164851 | Justo and Hibbett 2011 |
| *T. punicea* | BCC26408 | Thailand | FJ372685, FJ372707 | unpublished |
| *T. repanda* (T. elegans species complex) | FRI437T | | JN164985, JN164806, JN164835, JN164862 | Justo and Hibbett 2011, Carlson et al. 2014 |
| FPRI390 | Philippines | JN164921, JN164798, JN164790 | |
| OH271sp | Venezuela | JN164936, JN164812, JN164826, JN164852 | Justo and Hibbett 2011 |
| M0138339 | Papua New Guinea | KF573029, KF573078 | |
| *T. sanguinea* (cited as *Pycnoporus sanguineus*) | OAB0088 | Benin | MK736969, MK736949 | this study |
| OAB0095 | Benin | MK736986, MK736961 | |
| *T. sanguinea* | PRSC95 | Puerto Rico | JN164982, JN164795, JN164842, JN164858 | justo and Hibbett 2011 |
| BCC 36861 | Thailand | GQ982885, GQ982878 | unpublished |
| 8R_1_2 | Thailand | FJ372672, FJ372694 | |
| CBS6164.73 | Sri Lanka | MH860781, MH862513 | |
| *T. venusta* | BFC12724 | China | KC848313, KC848397 | unpublished |
| OAB0131 | Benin | MK736987, MK736962 | this study |
| OAB0162 | Benin | MK736988, MK736963 | |
| *Trametes* sp. (cited as *Leiotrametes* sp.) | LIP:GUY08-156 | French Guiana | JN645062 | Welti et al. 2012 |
T. elegans species complex, seven newly generated sequences of protein-coding genes were aligned in addition to sequences used by Carlson et al. (2014). Each marker was aligned separately using MAFFT version 7, with the algorithm L-INS-i (Katoh et al. 2017) and standard settings as default. The resulting multiple species alignments were slightly adjusted and trimmed at both ends a bit from incomplete sequences in Geneious 5.6.7 (Kearse et al. 2012). Eight different datasets were assembled for the phylogenetic analyses: (i) ITS dataset with 91 sequences of Trametes spp., (ii) combined ITS-LSU dataset with 91 sequences Trametes spp., (iii) combined RPB1-RPB2 dataset with 23 sequences of Trametes spp., (iv) ITS dataset with 17 sequences of T. elegans species complex, (v) RPB1 dataset with ten sequences of the T. elegans species complex, (vi) RPB2 dataset with 12 sequences of T. elegans species complex, (vii) TEF1 dataset with 14 sequences of T. elegans species complex, and (viii) combined dataset of four genes (ITS, RPB1, RPB2, TEF1) of T. elegans species complex. The combined datasets were concatenated using Geneious 5.6.7 (Kearse et al. 2012). For the phylogenetic analyses, the partitioning of the combined datasets of Trametes spp. was considered. Lopharia cinerascens (Schwein.) G. Cunn., and Dentocorticium sulphurellum (Peck) M.J. Larsen & Gilb., were chosen as the outgroup in all datasets (Justo and Hibbett 2011). Two phylogenetic tree inference methods, Maximum likelihood (ML) and Bayesian (BY) were performed in each dataset. The ML of all datasets were performed using RAxML 8.2.10 (Stamatakis 2014) and the BY of all individual genes and combined dataset of T. elegans species complex were performed using MrBayes 3.2.6 (Ronquist et al. 2012) at the Cipres Science Gateway V.3.3. (Miller et al. 2010). The BY of the partitioned datasets of Trametes spp. were run independently using MrBayes 3.2.7 (Ronquist et al. 2012). The parameters in BY inference were set as follows: lset applyto = (all), nst = 6, rates = invgamma, ngammacat = 4, sampling frequency = 1000, and the command “unlink” was used to unlink parameters across characters on partitioned datasets. Two independent Markov Chain Monte Carlo (MCMC) processes were run, each in 4 chains, for 5 million generations, and 0.2 fraction were discarded as burn-in. The Phylogenetic Tree Summarization (SumTrees) program within DendroPy 4.3.0. (Sukumaran and Holder 2010) was used to build the consensus tree with branch supports (posterior probabilities). Further, by using IQ-Tree (Trifinopoulos et al. 2016), we assigned the bootstrap values (BS) of ML to the consensus tree of BY. The resulting phyloge-
Figure 2. Macromorphology of *Trametes* species in Benin and specimen numbers in parentheses. A *Trametes cingulata* B hymenophore of *Trametes cingulata* (10) C *Trametes flavida* D hymenophore of *Trametes flavida* (05) E *Trametes lactinea* F hymenophore of *Trametes lactinea* (01) G *Trametes palisotii* H hymenophore of *Trametes palisotii* (04)
Figure 2. (Continued) **I** *Trametes parvispora* **J** hymenophore of *Trametes parvispora* (04) **K** *Trametes polyzona* **L** hymenophore of *Trametes polyzona* (06) **M** *Trametes sanguinea* (04) **N** *Trametes aff. versicolor* (01) **O** *Trametes socotrana* **P** hymenophore of *Trametes socotrana* (02). Scale bar corresponds to 1cm except in **E, F** where it corresponds to 2 cm.
netic trees were inspected in FigTree v. 1.4.2 (Rambaut 2014). All sequence alignments and phylogenetic trees generated in the study were deposited in TreeBASE: http://purl.org/phylo/treebase/phylows/study/TB2:S24354. The topologies of the consensus trees obtained from BY are presented in all figures throughout the document. Posterior probabilities (PP) and bootstrap values (BS) on or below branches as followed (PP/BS).

Microscopic analyses of specimens of the new species of Trametes

Macro-morphological descriptions were based on fresh and dried herbarium specimens. Microstructures are described using dried herbarium specimens. Fine sections through the basidiomata were prepared for observation using a razor blade under a stereomicroscope Leica EZ4 and mounted in 5% aqueous solution of potassium hydroxide (KOH) mixed with 1% aqueous solution of Phloxine. Melzer’s reagent (to test for dextrinoid or amyloid reactions), Cotton Blue (to test for cyanophilic reaction) were used and then examined at a magnification of 1000× using a Leica DM500 light microscope. Measurements were done with the software “Makroaufmaßprogramm” from Jens Rüdigs (https://ruedig.de/tmp/messprogramm.htm) and analysed with the software “Smaff” version 3.2 (Wilk 2012). In total, 135 basidiospores were measured from the sequenced specimen OAB0022 and additional examined specimen OAB0268. The basidiospore size is given as length and width of the spore. As measurements we present the mean with standard deviation and minimum and maximum values in parentheses (see below). The length (L), arithmetic average of all spore lengths, and the width (W), arithmetic average of all spore widths, were calculated. In addition, the ratio of length/width (Q) was calculated.

Availability of data and materials

All alignments and phylogenetic trees generated in this study are available in TreeBASE under this link: http://purl.org/phylo/treebase/phylows/study/TB2:S24354. Newly generated sequences are available in GenBank, and the accession numbers are given in Table 1. Alignments, phylogenetic trees, and accession numbers of newly generated sequences will be public after the paper is published. Collected specimens are available at the mycological herbarium of the University of Parakou (UNIPAR). The new species was registered in mycoBank, and the registration number is given in the taxonomy section of this paper.

Abbreviations

a.s.l. above sea level
BS Bootstrap values
BY Bayesian
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Results

Phylogenetic analyses of sequences of Trametes species from Benin

**ITS dataset.** The 25 ITS sequences obtained from Trametes spp. from Benin clustered in eight distinct clades (Suppl. material 2). All sequences of Trametes spp. from Benin fell into the monophyletic corresponding clades except the clade of Trametes lactinea (Berk.) Sacc., which, besides sequences of T. lactinea, accommodated also sequences of Trametes cubensis (Mont.) Sacc. with a very high support (BP = 1.00/BS = 100). Sequences of specimens of Trametes sp. (OAB0022 and OAB0023) from Benin formed a separated and well-supported clade within the Trametes clade (BP = 0.73/BS = 66).

**ITS-LSU dataset.** Results of ML and of BY show higher congruency, higher support values, and a higher number of resolved nodes than the results obtained with ITS data only. As evident by the ITS dataset, the sequence of T. lactinea from Benin clustered in addition to other sequences of T. lactinea retrieved from GenBank with sequences of T. cubensis with high support (BP = 1.00/BS = 92). Like in the analysis of the ITS dataset, sequences of Trametes sp. from Benin formed a distinct clade (Fig. 3). The two sequences of the new species of Trametes from Benin clustered in a distinct lineage within the Trametes clade (Figs 2I, J; 4). The clade of the T. elegans species complex is presented in the section below.

Phylogenetic placement of Trametes elegans from tropical Africa within the Trametes elegans species complex

The phylogenetic trees generated from individual gene regions ITS, RPB1, RPB2, and TEF1 (Suppl. material 3) and the combined datasets (Fig. 5) show similar results for phylogenetic relationships within the T. elegans species complex. Four distinct and
Figure 3. ML phylogeny of *Trametes* spp. based on combined ITS-LSU dataset. Branch support values given as PP/BS. All clades where newly generated sequences clustered are highlighted in grey and bars with names are given beside for more readability. Taxon names are followed by voucher or stain number and country of origin.
well-supported clades were evident in all datasets. The clade highlighted in grey (Fig. 5; Suppl. material 3) is distinct from all other clades within *T. elegans* species complex and highly supported in all individual gene and combined dataset. This clade contains only sequences of *T. elegans* from Benin and Cameroon.
Figure 5. ML phylogeny of *Trametes elegans* species complex based on combined dataset of four-gene regions (ITS, RPB1, RPB2, TEF1). Branch support values given as PP/BS. Sequences of *T. elegans* from tropical Africa investigated in this study are highlighted in grey.

**Taxonomy**

*Trametes parvispora* Olou, Yorou & Langer, sp. nov.
MycoBank No: 830395
Figures 2I, J, 4

**Diagnosis.** *Trametes parvispora* differs from known species of *Trametes* in the combination of the following characteristics: daedaleoid hymenophore, context whitish, thin 1–1.5 mm, homogeneous, without black lines, small spores 3.2–4.6 × 2.1–2.8 μm, regular hyphal pegs 25–30 μm long, cystidia absent, abundance of basidioles, and basidia 12–15 × 3–5 μm.

**Type.** BENIN. Atlantic province, dry dense forest of Pahou in Ouidah, 6°23′2.97″N, 2°9′15.90″E, altitude: 33.1 m, on dead part of living tree of Dialium guineense Willd., leg. Boris A. Olou, sampling date: 21.07.2017, OAB0022 (dried specimen, holotype in UNIPAR and isotype in KAS). Holotype Sequences: ITS MK736989, LSU MK736964, and RPB2 MN127965

**Etymology.** *parvispora* (Lat.): referring to the small size of the spores.
**Description.** Basidiomata probably perennial, sessile, pileate, applanate, semicircular, up to 13 cm long and 8 cm wide, up to 2.5 cm thick at the base, coriaceous to woody and hard when dry, without odour or taste when fresh. Pileus surface dull, glabrous, and whitish, zonate, margin thick, obtuse. Pore surface whitish, daedaleoid. Context whitish, thin (1–1.5 mm), homogeneous, without black lines.

Hyphal system trimitic, generative hyphae hyaline branched with clamp connections, thin-walled, 1.5–2.0 μm in diameter, acyanophilous; skeletal hyphae solid to thick-walled, hyaline, non-septate, 3–4 μm in diameter, totally dominating in the context, acyanophilous, tissues unchanged in KOH, unbranched; binding hyphae very common in both the context and trama, hyaline, thick-walled, acyanophilous, and much branched.

Cystidia absent, but the branches of the binding hyphae may easily be mistaken for thick-walled cystidia in the hymenium unless a careful examination is undertaken. Hyphal pegs present, especially at the base of pores, and regular, 25–30 μm long.

Basidia 12–15 × 3–5 μm, clavate, tetrasterigmatic, sterigmata 3 μm long; Basidioles numerous, similar in shape to basidia but slightly smaller than basidia, up to 4 μm in diameter.

Basidiospores broadly ellipsoid, hyaline, thin-walled, smooth, usually with one guttule each, negative in Melzer’s reagent, acyanophilous, (2.9)3.2–4.6(4.9) × 2.1–2.8(2.9) μm, L = 3.88 μm, W = 2.48 μm; Q = (1.17)1.24–1.91(2.05), Q = 1.57.

**Ecology and distribution.** Saprotrophic, on dead part of living tree *Dialium guineense* and only known from dry dense forest of Pahou in southern Benin.

**Additional materials examined.** BENIN. Atlantic province, dry dense forest of Pahou/ Ouidah, leg. Boris A. Olou, on dead wood of *D. guineense*, 21.07.2017, 6°23’3.07”N, 2°9’16.32”E, altitude 18.4 m a.s.l., OAB0023 (UNIPAR); on dead part of living tree of *D. guineense*, 6°23’2.49”N, 2°9’16.27”E, altitude 33.1 m a.s.l., 20.07.2018, OAB0267 (UNIPAR); at the same locality, 26.09.2018, OAB0268 (UNIPAR).

**Discussion**

**Trametes spp. diversity in Benin**

In Benin, seven species of *Trametes* were previously reported (Olou et al. 2019). By the present, study two additional species, namely *T. lactinea* and *T. aff. versicolor* (Fig. 2E, F, N), were recorded in addition to previous species. Thus, to our knowledge, nine species of *Trametes* are currently known for Benin. Of these nine species, only two species, *T. elegans* and *T. sanguinea*, were reported in Benin until 2002 (Yorou and De Kesel 2002). The remaining seven species, namely *T. cingulata, T. flavida, T. lactinea, T. parvispora, T. polyzona, T. socotrana*, and *T. aff. versicolor*, were recorded between 2017 and 2018. Given this history, it is most likely that more species will be found. Nonetheless, this number is significant when compared to the total diversity of 9–14 species of *Trametes* reported for Europe (Ryvarden and Gilbertson 1994; Ryvarden and Melo 2014). Further studies are needed to document the overall diversity of species of *Trametes* in Benin.
Phylogenetic positions of Trametes species of Benin

To place specimens of Trametes spp. from Benin in a larger phylogenetic context, we generated sequences of several genes. Generated sequences were placed into the phylogeny of the genus Trametes as established by Justo and Hibbett (2011). Eight distinct clades corresponding to eight different species were obtained from these sequences.

Our phylogenetic analyses from ITS and combined ITS-LSU datasets reveal sequence similarities and taxonomic misplacement within the clades of T. flavida and T. lactinea (Fig. 3; Suppl. material 2). The clade of T. flavida accommodated, in addition to sequences of T. flavida, sequences of Trametes sp. from French Guiana which is known as Leiotrametes sp. (Welti et al. 2012). This species was proposed as a new species by Welti et al. (2012). Here, Trametes sp. clustered together with T. flavida with high support in the ITS dataset (PP = 0.84/BS = 89) and the combined ITS-LSU datasets (PP = 0.98/BS = 99). Both species share also high morphological similarity (Welti et al. 2012; Fig. 2C, D) and a tropical distribution. We therefore suggest that Trametes sp. from French Guiana should not be considered as a new species but should be referred to as T. flavida. In addition to the T. flavida clade, our phylogenetic analyses showed that the T. lactinea clade contains not only sequences of T. lactinea, but also sequences of T. cubensis with high support in the ITS and ITS-LSU datasets (Fig. 3; Suppl. material 2). This result is similar to previous phylogenetic analyses on Trametes using the ITS marker (Justo and Hibbett 2011; Carlson et al. 2014). Trametes lactinea and T. cubensis are still valid names and both species share quite similar morphological characters. They are characterized by an applanate, broadly attached to dimidiate, white to cream basidiomata and a white to cream pore surface (Ryvarden and Johansen 1980; Gilbertson and Ryvarden 1987). Nevertheless, although both species are sharing quite similar morphological characters, they also differ in some characters. Trametes cubensis is characterized by an annual basidioma, small pores, almost invisible to the naked eye, 5–7 per mm, and cylindrical basidiospores 7–9 × 3–3.5 μm (Gilbertson and Ryvarden 1987), while T. lactinea has an annual to perennial basidioma and large pores, which are visible to the naked eye, mostly 1.5–2 per mm, but can reach up to 3–4 (5) per mm in some specimens with cylindrical-ellipsoid basidiospores 4–7.5 × 2.2–3 μm (Ryvarden and Johansen 1980). Our specimen of T. lactinea (Fig. 2E, F) matches the morphological description of T. lactinea with 3–4 pores per mm, but we did not observe any spore despite numerous attempts. Thus, considering the result of our phylogenetic analyses, absence of spores in our T. lactinea specimen, and the high morphological similarity between species within Trametes (Gilbertson and Ryvarden 1987), we cannot reasonably distinguish T. lactinea from T. cubensis. Further morphological, chemotaxonomic, and molecular studies integrating proteins coding genes (e.g. RPB1, RPB2, and TEF1) are therefore needed to confirm whether T. lactinea and T. cubensis refer to the same species.

Previously the phylogenetic resolution of T. cingulata was problematic due to low sequence availability. Here we generated a total of 17 de novo sequences and show that T. cingulata appears as a monophyletic group within Trametes with high support in ITS
and combined ITS-LSU datasets respectively (PP = 1.00/BS = 97) and (PP = 1.00/BS = 100) (Fig. 3; Suppl. material 2). Thus, contrary to the uncertain position of *T. cingulata* within the genus *Trametes* (Welti et al. 2012), our results revealed that the latter does not belong to *Trametes* sensu stricto in the sense of Justo and Hibbett (2011) and Welti et al. (2012) (Fig. 3; Suppl. material 2) but rather to *Trametes* sensu lato.

Species diversity in the *Trametes elegans* species complex

The specimens from Benin identified as members of the *T. elegans* species complex correspond to the morphological descriptions of *T. elegans* by Gilbertson and Ryvarden (1987) and Ryvarden and Johansen (1980). The clades evident in all datasets within the *T. elegans* complex (Figs 3, 5; Suppl. material 2, 3) represent three clades previously attributed to three different species by Carlson et al. (2014), and a new clade highlighted in grey (Fig. 5; Suppl. material 3) represents specimens of *T. elegans* from Benin and Cameroon (Tropical Africa). This new clade contains only sequences of *T. elegans* from Benin and Cameroon due to the non-publication of most *T. elegans* sequences from tropical Africa (Olusegun 2015; Awala and Oyetayo 2016; Ueitele et al. 2018). Thus, prior to this study, only sequences of *T. elegans* from Cameroon and Gabon are available in GenBank for Africa. However, the sequences of *T. elegans* from Gabon (GenBank accession number: KY449397, KY449398) were not considered because they fell outside the *T. elegans* species complex and were instead closely related to *T. lactinea*. We, therefore, excluded these sequences from our analyses. All in all, since the sequences of *T. elegans* from tropical Africa investigated in this study are demarcated from sequences of *T. elegans* s. str., the adoption of another correct name for specimens of *T. elegans* from this area is necessary.

Specimens belonging to the *T. elegans* species complex have been reported in the past for tropical African countries (Ryvarden and Johansen 1980), with the first name applied to such specimens being *Daedalea amanitoides* P. Beauv., which was based on a specimen from Nigeria (cited as kingdom of Oware) (Palisot-Beauvois 1804). The morphological characteristics evident in the very short description and illustration of a fruiting body of *D. amanitoides* match the characteristics of the specimens examined in this study. However, for reasons that we ignore, Fries (1821) replaced this name (*D. amanitoides*) by the name *Daedalea palisotii* Fr., which is sanctioned and therefore must be used. The combination *Trametes palisotii* (Fr.) Imazeki (Imazeki 1952) is available and must be used for African specimens known previously as *T. elegans* (Fig. 5).

Phylogenetic position and taxonomy of the new species *Trametes parvispora*

The sequences belonging to the new species named *T. parvispora* form a distinct and well-supported clade in the ITS and the combined ITS-LSU datasets (Fig. 3; Suppl. material 2). This species forms a sister clade with the still formally undescribed *Tram-
etes sp. (KT896651) from Finland. However, unlike *T. parvispora* where fruiting bodies were available for morphological characterization (Fig. 2I, J), the Finnish specimen was isolated as mycelium from the bark beetle *Ips typographus* L. (Linnakoski et al. 2016). Thus, anatomical and morphological comparisons are currently not possible. Furthermore, both sequences of *T. parvispora* share a clade with *Trametes meyenii* (Klotzsch) Lloyd. This clade was confirmed by phylogenetic analyses including two additional markers RPB1 and RPB2 (Suppl. material 4). *Trametes meyenii* has hispid and cream-yellow pilei, irpicoid and white to ochraceous hymenophore, pores 1–3 per mm, 4.5–6 × 2–2.5 μm basidiospores (Zmitrovich et al. 2012), whereas *T. parvispora* has glabrous and whitish pilei, a daedaleoid and white hymenophore, 3.2–4.6 × 2.1–2.8 μm basidiospores, and the presence of regular hyphal pegs (Figs 2I, J, 4). These morphological differences confirm that *T. parvispora* and *T. meyenii* are distinct species as shown by the phylogenetic analyses (Fig. 3; Suppl. material 2, 4). However, some species lacking DNA sequences, namely *Trametes barbulata* Corner, *Trametes daedaleoides* Corner, and *Trametes rugosituba* Corner (Corner 1989; Hattori 2005; Hattori and Sotome 2013), share with *T. parvispora* a quite similar spore size range. But the latter species differs from each other species by the combination of macro- and microscopic characteristics outlined above. Thus, the rare anatomic features of the regular hyphal pegs and the small size of the basidiospores together with the phylogenetic placement within the *Trametes* clade, provide enough evidence for *T. parvispora* as a distinct new species.

**Acknowledgements**

The research grant “Bi-nationally Supervised Doctoral Degrees” from the German Academic Exchange Services (DAAD) allowed for the stay of Boris Armel Olou in Germany while carrying out this study.

**References**

Awala SI, Oyetayo VO (2016) The Phytochemical and Antimicrobial Properties of the Extracts Obtained from *Trametes Elegans* Collected from Osengere in Ibadan, Nigeria. Jordan Journal of Biological Sciences 8(4): 289–99. https://doi.org/10.12816/0027065

Benson DA, Karsch-Mizrachi I, Clark K, Lipman DJ, Ostell J, Sayers EW (2011) GenBank. Nucleic Acids Research 40(D1): D48–D53. https://doi.org/10.1093/nar/gkq1079

Blagodatski A, Yatsunskaya M, MikhailovaV, Tiasto V, Kagansky A, Katanaev VL. (2018) Medicinal mushrooms as an attractive new source of natural compounds for future cancer therapy. Oncotarget 9(49): 29259–29274. https://doi.org/10.18632/oncotarget.25660

Carlson A, Justo A, Hibbett DS (2014) Species delimitation in *Trametes*: a comparison of ITS, RPB1, RPB2 and TEF1 Gene Phylogenies. Mycologia 106(4): 735–745. https://doi.org/10.3852/13-275

Corner EJH (1989) Ad Polyporaceas VI. The genus *Trametes*. Beilhete zur Nova Hedwigia 97: 1–197.
Diversity and Phylogeny of *Trametes* in tropical Africa

Cruz A, Pimentel L, Rodríguez-Alcalá LM, Fernandes T, Pintado M (2016) Health benefits of edible mushrooms focused on *Coriolus versicolor*: a review. Journal of Food and Nutrition Research 4(12): 773–781. https://doi.org/10.1155/2016/9827369

Cui DZ, Zhao M, Yang HY, Wang Cl, Dai HB (2011) Molecular phylogeny of *Trametes* and related genera based on Internal Transcribed Spacer (ITS) and Nearly Complete Mitochondrial Small Subunit Ribosomal DNA (Mt SSU RDNA) sequences.” African Journal of Biotechnology 10(79): 18111–18121. https://doi.org/10.5897/AJB10.1830

David A (1967) Caractères mycéliens de quelques *Trametes* (Polyporacées). Les Naturalistes Canadiens 94: 557–572.

Dörnte B, Kües U (2013) Fast microwave-based DNA extraction from vegetative mycelium and fruiting body tissues of Agaricomycetes for PCR amplification. Current Trends in Biotechnology and Pharmacy 7(4): 825–836.

Fries EM (1821) Systema Mycologicum, sistens Fungorum ordines, genera et species huc usque cognitas quas ad normas methodi naturalis deter- minavit, disposuit atque descriptis. vol. 1: Ex Officina Berlingiana, Greifswald, 520 pp. https://doi.org/10.5962/bhl.title.5378

Fries EM (1835) Corpus Florarum provincialium Sueciae I. Floram Scanicam. Typis Palmblad, Upsala, 349 pp. https://doi.org/10.5962/bhl.title.47083

Gardes M, Bruns TD (1993) ITS primers with enhanced specificity for Basidiomycetes—application to the identification of mycorrhizae and rusts. Molecular Ecology 2(2): 113–118. https://doi.org/10.1111/j.1365-294X.1993.tb00005.x

Gilbertson RL, Ryvarden L (1987) North American polypores: Megasporoporia – Wrightoporia. Vol. 2. Fungiflora, Oslo, 434–885.

Gomes-Silva AC, Ryvarden L, Giberonti TB (2010). Notes on *Trametes* from the Brazilian Amazonia. Mycotaxon 113(1): 61–71. https://doi.org/10.5248/113.61

Hattori T (2005) Type studies of the polypores described by E.J.H. Corner from Asia and West Pacific areas. VII. Species described in *Trametes* (1). Mycoscience 46(5): 303–312. https://doi.org/10.1016/j.myc.2012.10.008

Hattori T, Sotome K (2013) Type studies of the polypores described by E.J.H. Corner from Asia and West Pacific areas VIII. Species described in *Trametes* (2). Mycoscience 54(4): 297–308. https://doi.org/10.1016/j.myc.2012.10.008

Imazeki R (1952) A contribution to the fungous flora of Dutch New Guinea. Bulletin of the Government Forest Experimental Station Meguro 57: 87–128.

Justo A, Hibbett DS (2011) Phylogenetic classification of *Trametes* (Basidiomycota, Polyporales) based on a five-marker dataset. Taxon 60(6): 1567–1583. https://doi.org/10.1002/tax.606003

Karsten PA (1881) Enumeratio Boletinearum et Polyporearum Fennicarum, systemate novo dispositarum. Revue mycologique, Toulouse 3(9): 16–19.

Katoh K, Rozewicki J, Yamada KD (2017) MAFFT online service: multiple sequence alignment, interactive sequence choice and visualization. Briefings in Bioinformatics 20(4): 1160–1166. https://doi.org/10.1093/bib/bbx108

Kavina C, Pilát A (1936) Atlas des champignons de l’Europe. Töme III, Polyporaceae I. Chez les éditeurs, Praha, 624 pp.

Kearse M, Moir R, Wilson A, Stones-Havas S, Cheung M, Sturrock S, Buxton S, Cooper A, Markowitz S, Duran C, Thierer T, Ashton B, Meintjes P, Drummond A (2012) Geneious
Basic: an integrated and extendable desktop software platform for the organization and analysis of sequence data. Bioinformatics 28 (12): 1647–1649. https://doi.org/10.1093/bioinformatics/bts199

Kotlaba F, Pouzar Z (1957) On the classification of European pore fungi. Ceska Mycol 11: 152–170.

Linnakoski R, Mahilainen S, Harrington A, Vanhanen H, Eriksson M, Mehtatalo L, Pappinen A, Wingfield MJ (2016) Seasonal succession of fungi associated with Ips typographus beetles and their phoretic mites in an outbreak region of Finland. PLoS ONE 11(5): 1–14. https://doi.org/10.1371/journal.pone.0155622

Liu YJ, Whelen S, Hall BD (1999) Phylogenetic relationships among ascomycetes: evidence from an RNA polymerase II subunit. Molecular Biology and Evolution 16: 1799–1808. https://doi.org/10.1093/oxfordjournals.molbev.a026092

Matheny PB (2005) Improving phylogenetic inference of mushrooms with RPB1 and RPB2 nucleotide sequences (Inocybe, Agaricales). Molecular Phylogenetics and Evolution 35: 1–20. https://doi.org/10.1016/j.ympev.2004.11.014

Matheny PB, Liu YJ, Ammirati JF, Hall BD (2002) Using RPB1 sequences to improve phylogenetic inference among mushrooms (Inocybe, Agaricales). American Journal of Botany 89: 688–698. https://doi.org/10.3732/ajb.89.4.688

Miller MA, Pfeiffer W, Schwartz T (2010) Creating the CIPRES Science Gateway for inference of large phylogenetic trees. In: 2010 Gateway Computing Environments Workshop, GCE 2010, IEEE, 1–8. https://doi.org/10.1109/GCE.2010.5676129

Murrill WA (1905) The Polyporaceae of North America: XI. A synopsis of the brown pileate species. Bulletin of the Torrey Botanical Club 32: 353–371. https://doi.org/10.2307/2478499

Olou BA, Yorou NS, Striegel M, Bässler C, Krah FS (2019) Effects of macroclimate and resource on the diversity of tropical wood-inhabiting fungi. Forest Ecology and Management 436: 79–87. https://doi.org/10.1016/j.foreco.2019.01.016

Olusegun OV. (2015) Molecular identification of Trametes species collected from Ondo and Oyo states, Nigeria. Jordan Journal of Biological Sciences 7: 165–169. https://doi.org/10.12816/0008234

Palisot-Beauvois AMFJ (1804) Flore d’Oware et de Benin en Afrique (2nd edn). Imprimerie de Fain et Compagnie, Paris, 464 pp. https://doi.org/10.5962/bhl.title.101798

Pieri M, Rivoire B (2007) Autour du genre Trametes. Bulletin de la Société Mycologique de France 123(1): 49–66.

Rambaut A (2014) FigTree, a graphical viewer of phylogenetic trees. http://tree.bio.ed.ac.uk/software/figtree

Rehner SA, Buckley E (2008) A Beauveria phylogeny inferred from nuclear ITS and EF1-sequences: evidence for cryptic diversification and links to Cordyceps teleomorphs. Mycologia 97: 84–98. https://doi.org/10.3852/mycologia.97.1.84

Ronquist F, Teslenko M, Van Der Mark P, Ayres DL, Darling A, Höhna S, Larget B, Liu L, Suchard MA, Huelsenbeck JP (2012) Mrbayes 3.2: efficient bayesian phylogenetic inference and model choice across a large model space. Systematic Biology 61: 539–542. https://doi.org/10.1093/sysbio/sys029

Ryvarden L (1991) Genera of polypores, nomenclature and taxonomy. Synopsis Fungorum. 5: 1–373.
Diversity and Phylogeny of *Trametes* in tropical Africa

Ryvarden L, Johansen I (1980) A preliminary polypore flora of East Africa. Fungiflora, Oslo, 636 pp.

Ryvarden L, Gilbertson RL (1994) European polypores. Part 2. Synopsis Fungorum 7: 394–743 pp.

Ryvarden L, Melo I (2014) Poroid Fungi of Europe. Fungiflora, Oslo, 431 pp.

Ryvarden L, Aime MC, Baroni TJ (2009) Studies in neotropical polypores 26. A new species of *Trametes* and revisitation of an old. Synopsis Fungorum 26: 27–32.

Stiller JW, Hall BD (1997) The origin of red algae: Implications for plastid evolution. Proceedings of the National Academy of Sciences 94: 4520–4525. https://doi.org/10.1073/pnas.94.9.4520

Ss V, Pandey M (2012) Physiological and cultivation requirements of *Trametes versicolor*, a medicinal mushroom to diversify Indian mushroom industry. Indian Journal of Agricultural Sciences 82: 672–675.

Stamatakis A (2014) RAxML Version 8: A tool for phylogenetic analysis and post-analysis of large phylogenies. Bioinformatics 30(9): 1312–1313. https://doi.org/10.1093/bioinformatics/btu033

Sukumaran J, Holder MT (2010) DendroPy: a python library for phylogenetic computing. Bioinformatics 26(12): 1569–1571. https://doi.org/10.1093/bioinformatics/btq228

Thiers B (2019) Index Herbariorum: a global directory of public herbaria and associated staff. New York Botanical Garden’s Virtual Herbarium. http://sweetgum.nybg.org/ih [Accessed on: 2019-03-14; continuously updated]

Tomšovský M, Kolářík M, Pažoutová S, Homolka L (2006) Molecular phylogeny of European *Trametes* (Basidiomycetes, Polyporales) species based on LSU and ITS (nrDNA) sequences. Nova Hedwigia 82: 269–280. https://doi.org/10.1127/0029-5035/2006/0082-0269

Trifinopoulos J, Nguyen LT, von Haeseler A, Minh BQ (2016) W-IQ-TREE: a fast online phylogenetic tool for maximum likelihood analysis. Nucleic Acids Research 44: W232–W235. https://doi.org/10.1093/nar/gkw256

Ueitele IS, Kadhila-Muandingi NP, Chimwamurombe PM (2017) Ethnomycology of indigenous trametes mushrooms from northern Namibia. International Science Technology Journal of Namibia 9: 26–36.

Ueitele ISE, Chimwamurombe PM, Kadhila NP (2018) Molecular phylogeny of trametes and related genera from Northern Namibia. Jordan Journal of Biological Sciences 11: 99–105.

Vilgalys R, Hester M (1990) Rapid genetic identification and mapping of enzymatically amplified ribosomal DNA from several *Cryptococcus* species. Journal of bacteriology 172: 4238–4246. https://doi.org/10.1128/JB.172.8.4238-4246.1990

Vu D, Groenewald M, de Vries M, Gehrmann T, Stielow B, Eberhardt U, Al-Hatmi A, Groenewald JZ, Cardinali G, Houbraken J, Boekhout T, Crous PW, Robert V, Verkley GJM (2019) Large-scale generation and analysis of filamentous fungal DNA barcodes boosts coverage for kingdom fungi and reveals thresholds for fungal species and higher taxon delimitation. Studies in Mycology 92: 135–154. https://doi.org/10.1016/j.simyco.2018.05.001

Welti S, Moreau PA, Favel A, Courtecuisse R, Haon M, Navarro D, Taussac S, Lesage-Meessen L (2012) Molecular phylogeny of *Trametes* and related genera, and description of a new genus *Leiotrametes*. Fungal Diversity 55: 47–64. https://doi.org/10.1007/s13225-011-0149-2

White TJ, Bruns S, Lee S, JT (1990) Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. In: Innis MA, Gelfand DH, Sninsky JJ, White TJ (Eds) PCR Protocols: A Guide to Methods and Applications. Academic Press, New York: 315–322. https://doi.org/10.1016/B978-0-12-372180-8.50042-1
Wilk J (2012) Smaff – “Statistische Messreihen-Auswertung für Fungi v3.1.” Südwestdeutsche Pilzrundschau 48: 49–56.

Wong AHH, Wilkes J (1988) Progressive changes in cell wall components of *Pinus radiata* during decay. International Biodeterioration 24: 481–487. https://doi.org/10.1016/0265-3036(88)90036-X

Zmitrovich IV, Ezhov ON, Wasser SP (2012) A survey of species of genus *Trametes* Fr. (Higher Basidiomycetes) with estimation of their medicinal source potential. International Journal of Medicinal Mushrooms 14: 307–319. https://doi.org/10.1615/IntJMedMushr.v14.i3.70

Yorou SN, De Kesel A (2002) Connaissances ethnomycologiques des peuples Nagot du centre du Bénin (Afrique de l’Ouest). Proceedings of XVI the AETFAT congress, Brussels 2000. Systematic and Geographic of Plants 71: 627–637. https://doi.org/10.2307/3668707

**Supplementary material 1**

*Names, voucher numbers, and substrates of specimens of *Trametes* spp. collected in Benin*

Authors: Boris Armel Olou, Franz-Sebastian Krah, Meike Piepenbring, Nourou Soulemane Yorou, Ewald Langer

Data type: species data

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Link: https://doi.org/10.3897/mycokeys.65.47574.suppl1

**Supplementary material 2**

*ML phylogeny of *Trametes* spp. based on a single gene region ITS*

Authors: Boris Armel Olou, Franz-Sebastian Krah, Meike Piepenbring, Nourou Soulemane Yorou, Ewald Langer

Data type: phylogeny data

Explanation note: Support values are given as PP/BS. Newly generated sequences are highlighted in bold italic. Taxon names are followed by the voucher or stain numbers and the country of origin.

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Link: https://doi.org/10.3897/mycokeys.65.47574.suppl2
Supplementary material 3

ML phylogeny of *Trametes elegans* species complex as recovered from four individual gene regions
Authors: Boris Armel Olou, Franz-Sebastian Krah, Meike Piepenbring, Nourou Soulemane Yorou, Ewald Langer
Data type: phylogeny data
Explanation note: Support values are given as PP/BS. Taxon names are followed by the voucher or stain numbers and the country of origin. The clade formed by the sequences of *T. elegans* from tropical Africa are highlighted in grey.
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Supplementary material 4

ML phylogeny of *Trametes parvispora*, based on two-gene dataset (RPB1, RPB2)
Authors: Boris Armel Olou, Franz-Sebastian Krah, Meike Piepenbring, Nourou Soulemane Yorou, Ewald Langer
Data type: phylogeny data
Explanation note: Support values given as PP/BS. Taxon names are followed by the voucher or stain numbers and the country of origin.
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