Polyphyletic genera in Xylariaceae (Xylariales): Neoxylaria gen. nov. and Stilbohypoxylon

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Abstract

Several genera in Xylariaceae are polyphyletic in phylogenetic trees and represent more than one distinct genus. However, it is challenging to resolve these genera that are often phylogenetically distantly related, because many taxa have never been recollected and sequenced. Those that have been named and sequenced often lack documented characters or herbarium material. In this paper, we use descriptive morphology of fresh collections, and molecular data to resolve some taxonomic problems in Xylariaceae. During the of microfungi on palms in Thailand, we collected several novel xylariaceous taxa. Herein, we introduce a new genus Neoxylaria which is distantly related to Xylaria sensu stricto and a new species Stilbohypoxylon elaeidis. Neoxylaria is characterized by relatively small stromata with conspicuously exposed perithecial contours under a narrowly striped outer layer. Neoxylaria accommodates a species morphologically similar to Xylaria juruensis, which was also collected from palm material in Brazil and X. queenslandica collected from Archontophoenix alexandri in Australia. As no molecular data exists for these old collections, we have linked them with morphology to our fresh collection and use both molecular data and morphology to introduce the new genera. Neoxylaria juruensis (Henn.) Konta & K.D. Hyde, comb. nov. and N. queenslandica (Joanne E. Taylor, K.D. Hyde & E.B.G. Jones) Konta & K.D. Hyde, comb. nov. are therefore established. Multigene phylogenetic analysis shows that our new species (S. elaeidis) clusters with Stilbohypoxylon sensu stricto (Stilbohypoxylon clade II) and
clarifies the nature of the genus. The new species differs from other species in having solitary, smooth stromata and forms synnemata-like structures on the host, but not on the stroma. The novel taxa introduced here are supported by multigene phylogeny and morphology. Comprehensive morphological descriptions, illustrations and a phylogenetic tree to show the placement of new taxa are provided.

**Keywords** – 3 new taxa – palmicolous fungi – phylogeny – Sordariomycetes – taxonomy – Thai fungi

**Introduction**

Xylariaceae has a long history of study and is one of the largest and most diverse families of Ascomycota (Fröhlich & Hyde 2000, Tang et al. 2009, Stadler et al. 2013, Koyani et al. 2016, Daranagama et al. 2018). Most xylariaceous species are saprobes or endophytes, while a few are considered to be plant pathogens (Rogers 2000, Okane et al. 2008, Stadler et al. 2013, Husbands & Aime 2018, Pourmoghadam et al. 2018). Xylariaceous taxa exhibit high diversity in tropical regions and produce a high number of bioactive secondary metabolites (Fröhlich & Hyde 2000, Stadler & Hellwig 2005, Senanayake et al. 2015, Adnan et al. 2018a, Chen et al. 2018, Elias et al. 2018, Cedeño-Sanchez et al. 2020). Over time, several genera have either been included or excluded from Xylariaceae and the family limits remain unstable (Daranagama et al. 2016, 2018, Tibpromma et al. 2017, Fournier et al. 2018a, Voglmayr et al. 2018, Wendt et al. 2018). The evolutionary relationships of Xylariaceae with other related families using molecular clock evidence have been studied by Samarakoon et al. (2016), Hongsanan et al. (2017) and Hyde et al. (2017, 2020). Samarakoon et al. (2016) estimated that the crown node ages of Xylariaceae and Microdochiaeae were during the Late Mesozoic (66–100 Mya). Hongsanan et al. (2017) and Hyde et al. (2017) also concluded that the divergence times of familial ranks in Sordariomycetes should be around 50–150 Mya. Hyde et al. (2020) confirmed the familial status of Xylariaceae in the subclass Xylariomycetidae and estimated the divergence time for Xylariomycetidae at 278 Mya. Wijayawardene et al. (2018) listed 44 genera in Xylariaceae based on the updated phylogenetic relationships of Daranagama et al. (2018) and Wendt et al. (2018). Hyde et al. (2020) redefined the families of Sordariomycetes based on phylogenetic analyses and divergence estimates coupled with morphology. They accepted 32 genera for Xylariaceae, and this was followed by Wijayawardene et al. (2020).

*Xylaria* was introduced by Schrank (1789) as the generic type of Xylariaceae. *Xylaria* is the largest genus of Xylariaceae with *X. hypoxylon* as the type species (Greville 1824, Persoh et al. 2009). *Xylaria* species are saprobes on dead wood and endophytes occurring in living plants and are sometimes associated with termites (Hsieh et al. 2010, Daranagama et al. 2018). The important characteristics of this genus are stromata that are extremely variable in size, colour, and shape; subglobose perithecia, immersed to slightly exposed in perithecia mounds; 8-spored asci that are unitunicate, cylindrical, long-pedicellate, with J+, apical ring and uniseriate ascospores, that are ellipsoid-inequilateral, medium to dark brown, containing two large guttules and with a germ slit. The asexual morph is geniculosporium-like, with hyaline-light brown, smooth, branched conidiophores bearing hyaline, roughened or smooth-walled, ellipsoidal conidia (Stadler et al. 2013, Maharachchikumbura et al. 2016, Daranagama et al. 2018).

*Stilbohypoxylon* was introduced by Hennings (1902) with the type species *S. moelleri*. The genus is characterized by globose to pulvinate black stromata, with scales or blunt spines on the surface, cylindrical asci, with a J+, apical ring, brown, ellipsoidal ascospores, often with a thin mucilaginous sheath, with a straight or spiral germ slit and geniculosporium-like asexual morphs (Hennings 1902, Rogers & Ju 1997, Petrini 2004, Daranagama et al. 2018). Rogers & Ju (1997) re-described the type species and introduced a new species, *S. samuelsii*. Hladki & Romero (2003) accommodated two new species in this genus viz. *S. macrosorum* and *S. minus*. A key to the species was provided by Petrini (2004). Recently, a new record of *S. quisquiliarum* was reported from Argentina (Esteban et al. 2013). DNA sequence data are available for only two species in
GenBank, *S. elaedicola* and *S. quisquiliarum*. These two *Stilbohypoxylon* species did not resolve as a monophyletic group (Ju et al. 2007, Tang et al. 2007, 2009, Peláez et al. 2008, Hsieh et al. 2010, Daranagama et al. 2018, Wendt et al. 2018).

Both *Stilbohypoxylon* and *Xylaria* are unresolved lineages and much lumping and splitting of species has occurred over time. For example, Fröhlich & Hyde (2000) lumped numerous collections under *S. moelleri*, both from palms and dicotyledonous wood. Thus, researchers must strictly consider the type when comparing genera and species. However, since few types have sequence data and only few species have been epitypified, comparison of species is rather difficult. Phylogenetic studies indicated that *Stilbohypoxylon* and *Xylaria* do not form monophyletic groups, even though they clustered within Xylariaceae (Lee et al. 2000, Hsieh et al. 2010, Senanayake et al. 2015, Maharachchikumbura et al. 2016, Hongsanan et al. 2017, Daranagama et al. 2018, Wendt et al. 2018). Daranagama et al. (2018) and Wendt et al. (2018) discussed the phylogenetic affinities of xylariaceous genera based on morphology, phylogeny, and chemotaxonomic concepts. Wendt et al. (2018) found that *Xylaria* clustered in three main clades within Xylariaceae, while *Stilbohypoxylon* formed a clade with some *Xylaria* species and other genera viz. *Amphirosellinia*, *Astrocystis*, and *Collodiscula* but without statistical support. Daranagama et al. (2018) also confirmed that *Xylaria* is polyphyletic in Xylariaceae; for *Stilbohypoxylon*, *S. quisquiliarum* clustered within one subclade and *S. elaedicola* clustered within another subclade.

This study is a continuation of the series on palmicolous fungi in Thailand (Konta et al. 2016, 2020). The combined sequence data of ITS, RPB2 and TUB2 is used to investigate the placement of *Neoxylaria* and *Stilbohypoxylon* and their phylogenetic relationships.

**Materials & Methods**

**Collection, isolation, and identification**

Dead palm materials were collected from two locations in Krabi and Phang-nga Provinces, Thailand, in 2014 (Fig. 1). Fungal isolates were obtained from dead petioles of palm and primary identification of the fungi was performed based on the presence of fruiting bodies, asci, and ascospores. Pure cultures were obtained using single spore isolation on a petri-dish containing malt extract agar (MEA) medium and incubated at 25–28°C overnight (Konta et al. 2016). Culture characteristics were recorded after incubation at 25–28°C for 14 days.

Morphological characteristics were examined using a Motic SMZ 168 series stereomicroscope and photographed using an Axio camera fitted on the Zeiss Discover V8 stereomicroscope. Micro-morphological structures were photographed using a Canon 600D camera on Nikon ECLIPSE 80i microscope. Distilled water, lactic acid and/or lacto glycerol were used as mounting agents, Meltzer’s reagent was used for testing amyloid reaction of the apical ring structures. Fungal structures were measured using Image Framework software (IFW v. 0.9.7). Photo plates were processed using Adobe Photoshop CS6 (Adobe Systems, USA). The holotype specimens were deposited in the herbarium of Mae Fah Luang University (Herb. MFLU) and ex-type cultures in Mae Fah Luang Culture Collection (MFLUCC), Chiang Rai, Thailand. Facesoffungi and Index Fungorum numbers are registered as outlined in Jayasiri et al. (2015) and Index Fungorum (2020).

**DNA extraction and PCR amplification**

The DNA was extracted from the mycelia of 14 days old fungal cultures using the Biospin Fungus Genomic DNA Extraction Kit (BioFlux®, P.R. China) following the manufacturer’s protocol. The internal transcribed spacer (ITS), partial RNA polymerase II second largest subunit (RPB2) and partial β-tubulin (TUB2) loci were subjected to PCR amplification and sequencing using specific primers and PCR conditions (Table 1). The total volume of PCR mixtures for amplifications were carried out in a 25 μl reaction volume containing, 8.5 μl of ddH₂O, 12.5 μl of 2× Easy Taq PCR Super Mix (mixture of Easy Taq TM DNA Polymerase, dNTPs and optimized buffer (Beijing Trans Gen Biotech Co., Chaoyang, Beijing, P.R. China), 2 μl of DNA template, and
1 μl of each forward and reverse primers (10 pM). The quality of PCR products was checked on 1% agarose gel electrophoresis stained with 4S green nucleic acid (Life Science Products & Services Cat. Songjiang, Shanghai, P.R. China). Purification and sequencing of PCR products were carried out by Sangon Biotech Co., Shanghai, China. Consensus sequences were generated using SeqMan software (DNASTAR). The newly generated sequences were deposited in GenBank (Table 2).

**Table 1** Details of genes/loci with PCR primers and PCR conditions.

| Genes/loci | Primers | PCR conditions | References |
|------------|---------|----------------|------------|
| ITS        | ITS5/ITS4 | a; 95°C: 30 s, 55°C: 50 s, 72°C: 30 s (35 cycles); c | White et al. (1990) |
| RPB2       | fRPB2-5f/fRPB2-7cR | b; 95°C: 1 min, 54°C: 2 min, 72°C: 1.5 min (35 cycles); c | Liu et al. (1999) |
| TUB2       | T1/ T22 | b; 94°C: 1 min, 52°C: 1 min, 72°C: 1.5 min; c | O’Donnell & Cigelnik (1997) |

a Initiation step of 94°C: 3 min. b Initiation step of 95°C: 5 min. c Final elongation step of 72°C: 10 min and final hold at 4°C

**Phylogenetic analyses**

Consensus sequences were subjected to BLAST searches in the NCBI GenBank database (http://blast.ncbi.nlm.nih.gov/). Sequence data were retrieved from GenBank following recent studies (Hsieh et al. 2010, Daranagama et al. 2018, Ju et al. 2018, Wendt et al. 2018). Sequences of the ITS, RPB2 and TUB2 were analyzed individually and in combination. Alignments were processed with MAFFT v. 7.372 (Katoh et al. 2017) and manually improved where necessary. The sequence datasets were combined using MEGA7 (Kumar et al. 2016). Maximum likelihood analyses (ML) were performed with RAxML GUI v.1.0. (Stamatakis 2006, Silvestro & Michalak 2012) and Bayesian inference (BI) analysis were performed with MrBayes v3.1.2 (Huelsenbeck & Ronquist 2001). MrModeltest v. 2.2 (Nylander 2004) was used to estimate the best fit substitution model for each locus; which resulted in GTR+I+G (ITS, RPB2) and HKY+I+G (TUB2) substitution models under the Akaike Information Criterion (AIC). Bayesian posterior probabilities (BYPP) were determined by Markov Chain Monte Carlo sampling (MCMC) in MrBayes v3.1.2 (Huelsenbeck & Ronquist 2001). Six simultaneous Markov chains were run for 3,000,000 generations and trees were sampled every 100th generation. MCMC heated chain was set with a “temperature” value of 0.20. All sampled topologies beneath the asymptote (25%) were discarded as part of a burn-in procedure; the remaining trees were used for calculating posterior probabilities.
in the majority rule consensus tree. The phylogenetic tree was visualized in FigTree v1.4.0 (Rambaut 2006) and edited using Microsoft Office PowerPoint 2010 and Photoshop CS6. The alignments and respective phylogenetic tree were deposited in TreeBASE (submission number: 25775).

Table 2 GenBank accession numbers of the sequences used in phylogenetic analyses.

| Species                          | Isolate No.       | RPB2     | TUB2     | ITS         | References                      |
|----------------------------------|-------------------|----------|----------|-------------|---------------------------------|
| *Amphirosellinia fushanensis*    | 9111209 (HAST)    | GQ848339 | GQ495950 | GU339496    | Hsieh et al. 2010               |
| *Astrocystis bambusae*           | 89021904 (HAST)   | GQ844836 | GQ495942 | GU322449    | Hsieh et al. 2010               |
| *Astrocystis concavispora*       | MFLUCC 14-0174    | KP340532 | KP406615 | KP297404    | Daranagama et al. 2015          |
| *Astrocystis mirabilis*          | 94070803 (HAST)   | GQ844835 | GQ495941 | GU322448    | Hsieh et al. 2010               |
| *Astrocystis sublimbata*         | 89032207 (HAST)   | GQ844834 | GQ495940 | GU322447    | Hsieh et al. 2010               |
| *Barrmaelia rappazii*            | CBS 142771        | MF488998 | MF489017 | MF488989    | Voglmayr et al. 2018            |
| *Barrmaelia rhamnicola*          | CBS 142772        | MF488999 | MF489018 | MF488990    | Voglmayr et al. 2018            |
| *Brunneiperidium gracilentum*    | MFLUCC 14-0011    | KP340528 | KP406611 | KP297400    | Daranagama et al. 2015          |
| *Brunneiperidium involucratum*   | MFLUCC 14-0009    | KP340527 | KP406610 | KP297399    | Daranagama et al. 2015          |
| *Clypeosphaeria mammilana*       | CBS 140735        | MF489001 | MH704637 | KT949897    | Jaklitsch et al. 2016, Voglmayr et al. 2018 |
| *Collodiscula bambusae*          | GZUH 0102         | KP276675 | KP276674 | KP045279    | Li et al. 2015b                 |
| *Collodiscula fangjiingshansensis* | GZUH0109        | KR002592 | KR002589 | KR002590    | Li et al. 2015a                 |
| *Collodiscula leigongshanensis*  | GZUH0107         | KR002588 | KR002587 | -           | Li et al. 2015a                 |
| *Daldinia loculatoides*          | CBS 113279        | KY624247 | KX271246 | MH862918    | Wendt et al. 2018, Vu et al. 2019 |
| *Entoleuca mammata*              | 100 JDR           | GQ470230 | GQ470230 | GU300072    | Hsieh et al. 2010               |
| *Entosordaria perfidiosa*        | EPE = CBS 142773  | MF489003 | MF489021 | MF488993    | Voglmayr et al. 2018            |
| *Euepixylon sphaeriostoma*       | 261 JDR           | GQ44774  | GQ470224 | GQ292821    | Hsieh et al. 2010               |
| *Hypocoeckendorphon sanguineum*  | 169 JDR           | GQ484819 | GQ487710 | GQ322433    | Hsieh et al. 2010               |
| *Hypoxyylon fragiforme*          | MUCL 51264        | KM186296 | KX271282 | KC477229    | Stadler et al. 2013, Daranagama et al. 2015, Wendt et al. 2018 |
| *Hypoxyylon monticulosum*        | MUCL 54604        | KY624305 | KX271273 | KY610404    | Wendt et al. 2018               |
| *Kretzschmaria deusta*           | CBS 163.93        | KY624227 | KX271251 | KC477237    | Stadler et al. 2013             |
| *Kretzschmaria guyanensis*       | 89062903 (HAST)   | GQ44772  | GQ478214 | GU300079    | Hsieh et al. 2010               |
| *Kretzschmaria culmorum*         | 88 (JDR)          | KX430045 | KX430046 | KX430043    | Johnston et al. 2016           |
| *Nemania abortiva*               | 467 BISH          | GQ44768  | GQ470219 | GU292816    | Hsieh et al. 2010               |
| *Nemania beaumontii*             | 405 (HAST, JF)    | GQ44772  | GQ470222 | GU292819    | Hsieh et al. 2010               |
| *Nemania bipapillata*            | 90080610 (HAST)   | GQ44771  | GQ470222 | GU292818    | Hsieh et al. 2010               |
| *Nemania primoluate*             | 91102001 (HAST)   | GQ44776  | EF025607 | EF026121    | Ju et al. 2007, Hsieh et al. 2010 |
| *Nemania serpens*                | CBS 679.86        | KU684284 | KU684188 | KU683765    | U’Ren et al. 2016               |
| *Neoxylaria arengae*             | MFLUCC 15-0292    | MT502418 | -        | MT496747    | This study                      |
| *Neoxylaria ’Xylaria’ juruensis* | 92042501 (HAST)   | GQ844825 | GQ495932 | GU322439    | Hsieh et al. 2010               |

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| Species                     | Isolate No. | RPB2  | TUB2  | ITS         | References                        |
|-----------------------------|------------|-------|-------|-------------|-----------------------------------|
| *Podosordaria mexicana*     | 176 WSP    | GQ853039 | GQ844840 | GU324762   | Hsieh et al. 2010                |
| *Podosordaria multi*        | 167 WSP    | GQ853038 | GQ844839 | GU324761   | Hsieh et al. 2010                |
| *Poronia pileiformis*       | 88113001 WSP | GQ853037 | GQ502720 | GU324760   | Hsieh et al. 2010                |
| *Poronia punctata*          | CBS 656.78 | -     | KX271281 | KT281904   | Senanayake et al. 2015           |
| *Rosellinia aquila*         | MUCL 51703 | KY624285 | KX271253 | KY610392   | Wendt et al. 2018                |
| *Rosellinia buxi*           | 99 JDR     | GQ844780 | GQ470228 | GU300070   | Hsieh et al. 2010                |
| *Rosellinia corticium*      | MUCL 51693 | KY624229 | KX271254 | KY610393   | Wendt et al. 2018                |
| *Rosellinia merrillii*      | 89112601 (HAST) | GQ844781 | GQ470229 | GU300071   | Hsieh et al. 2010                |
| *Poronia punctata*          | CBS 349.36 | -     | KY624310 | MH855818   | Wendt et al. 2018, Vu et al. 2019|
| *Sarcoxylon compunctum*     | CBS 359.61 | -     | KY624230 | KT281903   | Senanayake et al. 2015           |
| *Stilbohypoxylon ‘elaeticola’ elaedis* | MFLUCC 15-0295a | MT502416 | MT502420 | MT496745   | This study                       |
| *Stilbohypoxylon elaedis*   | MFLUCC 15-0295b | MT502417 | MT502421 | MT496746   | This study                       |
| *Stilbohypoxylon elaedicola*| Y.M.J. 173 | GQ844826 | EF025616 | EF026148   | Ju et al. 2007, Hsieh et al. 2010|
| *Stilbohypoxylon elaedicola*| 94082615 (HAST) | GQ844827 | GQ495933 | GU322440   | Hsieh et al. 2010                |
| *Stilbohypoxylon quisquiliarum* | Y.M.J. 172 | GQ853020 | EF025605 | EF026119   | Ju et al. 2007, Hsieh et al. 2010|
| *Stilbohypoxylon quisquiliarum* | 89091608 (HAST) | GQ853021 | EF025606 | EF026120   | Ju et al. 2007, Hsieh et al. 2010|
| *Stilbohypoxylon quisquiliarum* | PR39 | -     | -     | -          | Peláez et al. 2008                |
| *Xylaria acuminatilongissima* | 623 (HAST) | GQ853028 | GQ502711 | EU178738   | Ju & Hsieh 2007, Hsieh et al. 2010|
| *Xylaria adscendens*        | 865 JDR    | GQ844818 | GQ487709 | GU322432   | Hsieh et al. 2010                |
| *Xylaria aesthetiopa*        | YMJ 1136   | MH785222 | MH785221 | MH790445   | Fournier et al. 2018b            |
| *Xylaria apoda*             | 90080804 (HAST) | GQ844823 | GQ495930 | GU322437   | Hsieh et al. 2010                |
| *Xylaria arbuscula*         | CBS 126415 | KY624287 | KX271257 | MH864101   | Wendt et al. 2018, Vu et al. 2019|
| *Xylaria atrosphaerica*      | 91111214 (HAST) | GQ843842 | GQ495953 | GU322459   | Hsieh et al. 2010                |
| *Xylaria badia*             | 95070101 (HAST) | GQ844833 | GQ495939 | GU322446   | Hsieh et al. 2010                |
| *Xylaria bambusicola*       | 162 JDR    | GQ844801 | GQ478223 | GU300088   | Hsieh et al. 2010                |
| *Xylaria berteri*           | 90112623 (HAST) | GQ843862 | GQ502711 | EU178738   | Hsieh et al. 2010, 2005          |
| *Xylaria bruneovinosa*       | 720 (HAST) | GQ853023 | GQ502706 | EU179862   | Ju & Hsieh 2007, Hsieh et al. 2010|
| *Xylaria castarea*          | 600 PDD    | GQ853018 | GQ502703 | GU324751   | Hsieh et al. 2010                |
| *Xylaria cf. castarea*       | 91092303 (HAST) | GQ853019 | GQ502704 | GU324752   | Hsieh et al. 2010                |
| *Xylaria cf. glebulousa*     | 431 (HAST, JF) | GQ843845 | GQ495956 | GU322462   | Hsieh et al. 2010                |
| *Xylaria cf. heliscus*       | 88113010 (HAST) | GQ843855 | GQ502691 | GU324742   | Hsieh et al. 2010                |
| *Xylaria crozonensis*        | 398 (HAST, JF) | GQ843861 | GQ502697 | GU324748   | Hsieh et al. 2010                |
| *Xylaria cubensis*           | 159 GENT   | GQ853017 | GQ502702 | -          | Hsieh et al. 2010                |
| Species               | Isolate No. | RPB2     | TUB2     | ITS       | References         |
|----------------------|-------------|----------|----------|-----------|--------------------|
| *Xylaria culleniae*  | 189 JDR     | GQ844829 | GQ495935 | GU322442  | Hsieh et al. 2010 |
| *Xylaria curta*      | 494 (HAST, JF) | GQ844831 | GQ495937 | GU322444  | Hsieh et al. 2010 |
| *Xylaria digitata*   | 919 (HAST)  | GQ848338 | GQ495949 | GU322456  | Hsieh et al. 2010 |
| *Xylaria discolor*   | Y.M.J. 1280 | JQ087411 | JQ087414 | JQ087405  | Ju et al. 2012    |
| *Xylaria enterogenae*| 785 (HAST, JF) | GQ848349 | GQ502685 | GU324736  | Hsieh et al. 2010 |
| *Xylaria fifejeensis*| 91122401 (HAST) | GQ848338 | GQ495944 | GU322451  | Hsieh et al. 2010 |
| *Xylaria frustulosa* | 92092010 (HAST) | GQ844838 | GQ495944 | GU322451  | Hsieh et al. 2010 |
| *Xylaria globosa*    | 775 (HAST, JF) | GQ848348 | GQ502684 | GU324735  | Hsieh et al. 2010 |
| *Xylaria grammica*   | 479 (HAST)  | GQ844837 | GQ495944 | GU322451  | Hsieh et al. 2010 |
| *Xylaria haemorrhoidalis* | 89041207 (HAST) | GQ848347 | GQ502683 | GU324736  | Hsieh et al. 2010 |
| *Xylaria hypoxylon*  | CBS 122620  | KY624231 | KX271279 | KY610407  | Wendt et al. 2018 |
| *Xylaria ianthinovelutina* | 553 (HAST, JF) | GQ844828 | GQ495934 | GU322441  | Hsieh et al. 2010 |
| *Xylaria intracolorata* | 90080402 (HAST) | GQ848354 | GQ502690 | GU324741  | Hsieh et al. 2010 |
| *Xylaria karyophthora* | DRH059      | KY64216  | -        | KY64220   | Husbands et al. 2018 |
| *Xylaria laevis*     | 419 (HAST, JF) | GQ848359 | GQ502695 | GU324746  | Hsieh et al. 2010 |
| *Xylaria luteostromata* | 508 (HAST, JF) | GQ848352 | GQ502688 | GU324739  | Hsieh et al. 2010 |
| *Xylaria multiplex*  | 580 (HAST, JF) | GQ844814 | GQ487705 | GU300097  | Hsieh et al. 2010 |
| *Xylaria ophiopoda*  | 93082805 (HAST) | GQ848344 | GQ495955 | GU322461  | Hsieh et al. 2010 |
| *Xylaria oxyacantha* | 859 JDR     | GQ844820 | GQ495927 | GU322434  | Hsieh et al. 2010 |
| *Xylaria phyllocharis* | 604 PDD   | GQ844822 | GQ495929 | GU322436  | Hsieh et al. 2010 |
| *Xylaria polymorpha* | 1012 JDR    | GQ848343 | GQ495954 | GU322460  | Hsieh et al. 2010 |
| *Xylaria reevesiae*  | HMH-2010g   | GQ844821 | GQ495928 | GU322435  | Hsieh et al. 2010 |
| *Xylaria regalis*    | 92072001 (HAST) | GQ848357 | GQ502693 | GU324744  | Hsieh et al. 2010 |
| *Xylaria schweinitzii* | 92092023 (HAST) | GQ848346 | GQ495957 | GU322463  | Hsieh et al. 2010 |
| *Xylaria scruposa*   | 497 (HAST, JF) | GQ848341 | GQ495952 | GU322458  | Hsieh et al. 2010 |
| *Xylaria spinulosia* | GZUCC13016 | KM236098 | KM236099 | -         | Li et al. 2015b    |
| *Xylaria telfairii*  | 421 (HAST, JF) | GQ848350 | GQ502686 | GU324737  | Hsieh et al. 2010 |
| *Xylaria vivantii*   | HMH-2010h   | GQ844824 | GQ495931 | GU322438  | Hsieh et al. 2010 |

*Newly generated strains are in bold.
Results

Phylogeny

The combined dataset (ITS, RPB2 and TUB2) comprised 93 taxa from selected species of Xylariaceae with 2,701 characters including gaps (ITS: 1–493, RPB2: 494–1,647, TUB2: 1,648–2,701). The RAxML analysis resulted in the best scoring likelihood tree selected with a final ML optimization likelihood value of −51211.148170, which is represented in Fig. 2. The final likelihood tree was evaluated and optimized under GAMMA model parameters: with 1,431 distinct alignment patterns and 10.27% of undetermined characters or gaps. Bayesian posterior probabilities from MCMC were evaluated with a final average standard deviation of split frequencies less than 0.01.

ITS-RPB2-TUB2 phylogeny shows that our strain MFLUCC 15-0292 clusters with “*Xylaria juruensis*” (92042501HAST), basal to *Stilbohypoxylon* clade II with high statistical support (100% ML, 1.00 BYPP). The strains MFLUCC 15-0295a and MFLUCC 15-0295b formed a clade with *Stilbohypoxylon* clade II as a sister to *S. elaedicola* with high statistical support (95% ML, 0.99 BYPP). *Stilbohypoxylon quisquiliarum* (*Stilbohypoxylon* clade I) formed a separate clade and clustered with *Xylaria “PO”* clade II (58% ML, 0.95 BYPP, Fig. 2).

*Xylaria* is polyphyletic in Xylariaceae, which is in agreement with previous studies (Daranagama et al. 2018, Wendt et al. 2018). In this study, *Xylaria* can be separated into seven “PO” clades, two “HY” clades and a single “TE” clade. Delimitation of the *Xylaria* clades are mostly restricted to their morphological characteristics and habitats. *Xylaria “HY”* clades are represented by *X. hypoxylon* (*sensu stricto*, “HY” clade II) and taxa in these clades have pointed or sterile stromal apices. The *Xylaria “PO”* clades are represented by *X. polymorpha* where most taxa in these clades have blunt or fertile stromatal apices. The *Xylaria “TE”* clade is represented by taxa associated with termite nests.

Taxonomy

**Neoxylaria** Konta & K.D. Hyde, gen. nov.

Index Fungorum number: IF556650; Facesoffungi number: FoF06239

Etymology – In reference to the morphological resemblance to *Xylaria*

*Saprobic* on palms (Arecaceae). Sexual morph: *Stromata* erect, coriaceous, solitary, cylindrical, simple to branched from the base, arising separately or in small bundles, stipe (stem) with brown hairy-tomentose, fertile part, bearing exposed outlines, apex sterile with globose perithecia, free perithecia scattered along with a filiform stroma, arranged in zigzag or in rows, visible as black, thick, surface finely cracked, sterile apex attenuated conical. *Perithecia* immersed in stromatic tissues, globose, ostiolate with periphyses. *Peridium* thick-walled, composed of several layers, outwardly, comprising dark brown cells of *textura angularis* and inwardly, thick-walled, comprising hyaline to pale brown cells of *textura prismatica*. *Ostiole* hyaline, papillate, with a central periphyses ostiolar canal and brown to black surrounding disc appear on the surface. *Paraphyses* hyaline, filamentous, cylindrical, septate, unbranched. *Ascii* 6–8-spored, uniseriate, cylindrical, long pedicellate, apically rounded, with a J+, apical ring, inverted hat-shaped. *Ascospores* uniseriate, hyaline to pale brown when immature, dark brown at maturity, smooth-walled, unicellular, a lot of small guttules when immature, two large guttules at maturity, smooth-walled, with a straight germ slit throughout ascospore-length. Asexual morph: Undetermined.

Type species – *Neoxylaria arengae* Konta & K.D. Hyde

Notes – Species of *Xylaria* cluster in ten subclades in the phylogenetic tree (Fig. 2) indicating that the genus is polyphyletic representing three major clades as *Xylaria “HY”*, “PO” and “TE”. The type species, *X. hypoxylon* clusters in *Xylaria “HY”* clade II which can be regarded as *Xylaria sensu stricto*. However, it is hard to justify the other clades (*Xylaria sensu lato*) as new genera without examining old types of these species or obtaining well-defined and identified fresh collections with molecular data.
Figure 2 – RAxML tree based on analysis of a combined dataset of ITS-RPB2-TUB2 sequence dataset from selected species of Xylariaceae. Bootstrap support values for maximum likelihood (ML) greater than 50%, and Bayesian posterior probabilities (BYPP) greater than 0.90 are given at the nodes. Ex-type strains are in bold. Newly generated taxa are in red. The tree is rooted to...
The sexual morph of *Xylaria hypoxylon* comprises a stroma that is grey to dull black, cylindrical to narrowly fusiform to fan-shaped, with a long persistent white peeling outer layer and ostiolar papillae. The perithecia are immersed, brown to black, with a low conical papilla at center, asci are cylindrical with J+, apical ring, and ascospores are brown ellipsoid-inequilateral with a sinuous germ slit and cellular appendage (Peršoh et al. 2009, Daranagama et al. 2018). The new species collected in this study is clearly different from members of *Xylaria sensu stricto* based on host preferences and perithecia bulging from the long, but relatively small stromata.

Based on the morpho-molecular differences, we introduce a new genus *Neoxylaria* to accommodate *Neoxylaria arengae*. *Xylaria culleniae*, *X. ianthinovelutina*, *X. aethiopica* and *X. vivantii* (*Xylaria “PO” clade V) also clustered with *Neoxylaria* and these species form conspicuously exposed perithecial contours under a narrowly striped outer layer, which is similar to *Neoxylaria*. Even though the morphological similarities exist, these species do not form a monophyletic clade. Therefore, we do not treat them under *Neoxylaria*. Further morpho-molecular studies are essential to clarify their generic boundaries.

*Neoxylaria arengae* Konta & K.D. Hyde, sp. nov. Fig. 3

Index Fungorum number: IF556651; Facesoffungi number: FoF03395

Etymology – Refers to the name of the host genus, *Arenga*

Holotype – MFLU 15-0267

*Saprobic on dead petiole of Arenga pinnata* (Arecaceae). Sexual morph: *Stromata* (1.6–)4–27(–30) × 0.5–1 mm (x̅ = 13 × 0.7 mm, n = 30), erect, coriaceous, solitary, cylindrical, simple to branched from the base, unbranched when immature, branching from the base at maturity with 3(–5) branches, arising separately or in small bundles, stipes (stem) (1.7–)2.1–4.6(–7.1) × 0.4–1 mm (x̅ = 3.2 × 0.7 mm, n = 20, up to 12 mm), cylindrical, longitudinally, black, with a hairy-tomentose broadened base, smooth to downy to hairy-tomentose above; tomentum black to dark brown, fertile part (1.7–)2.5–18(–25) mm (x̅ = 9 mm, n = 20), bearing 29 to 35(–45) exposed perithecia, apex sterile, rarely find finely longitudinally furrowed delimiting narrow stripes, roughened with prominent ostiolar papillae, perithecia scattered along the stroma, arranged in a zigzag or in straight rows, without circumferential wrinkles isolating groups of perithecia, perithecial contours most often conspicuous, visible as black single or small fusiform ascoma, surface, outer crust, thick, coriaceous, cracked, interior solid, brown with white tissue surrounding perithecal layer, sterile apex attenuated conical, up to 1–2(–3) mm. *Perithecia* 400–620 × 260–570 μm (x̅ = 493 × 464 μm, n = 10), pale brown, immersed in stromatic tissues, globose to subglobose, ostiolate, papillate, slightly conspicuous, with periphyses. *Peridium* 80–130 μm wide (x̅ = 100 μm, n = 20), thick-walled, composed of several layers, outwardly, thick-walled, comprising dark brown cells of *textura angularis* and inwardly, thick-walled, comprising hyaline to pale brown cells of *textura prismatic*ica. *Ostiole* 150–215 × 150–285 μm (x̅ = 180 × 210 μm, n = 5), raised-discoid, brown to black surrounding disc appear on the surface; hyaline, papillate, with a central periphyses. *Paraphyses* 3–5(–7) μm wide (x̅ = 4 μm, n = 10), filamentous, cylindrical, septate, unbranched. *Asci* 74–160(–180) × 5–12 μm (x̅ = 115 × 7 μm, n = 20), 6–8-spored, unitunicate, cylindrical, long pedicellate, apically rounded, with a J+, apical ring, inverted hat-shaped. *Ascospores* 10–18(–22) × 3.5–6(–7.5) μm (x̅ = 15 × 5 μm, n = 20), uniseriate, hyaline to pale brown when immature, dark brown at maturity, broad fusoid, unicellular, a lot of small guttules when immature, two large
guttules at maturity, smooth-walled, with a straight, full length germ slit. Asexual morph: Undetermined. *Appressoria* 4–9 × 3–10 µm (x̄ = 6 × 6 µm, n = 20), solitary, hyaline, mostly globose, irregular in shape, thick-walled.

Culture characteristics – Ascospores germinated on MEA within 24 hours and germ tube was produced from germ slit. Mycelium immersed in the medium, septate, branched, and smooth-walled hyphae. Colonies on MEA, medium dense, irregular in shape, flowered-like, surface slightly rough with curled margin, radiating outward colony, flat, slightly raised at the centre, hairy, fluffy, initially white, becoming white at the margin, greyish white near the centre, with black and white curled, radiated near the centre; reverse zonate, yellow and white, curled with black radiating outward colony; not produced pigmentation on medium.

Material examined – THAILAND, Phang-nga Province, on dead petiole of *Arenga pinnata* (Wurmb) Merr. (Arecaceae), 5 December 2014, S. Konta, PHR03d (MFLU 15-0267, holotype; KUN-HKAS 100698, isotype), ex-type living culture, MFLUCC 15-0292.

Notes – *Neoxylaria arengae* resembles *N.* (syn. *Xylaria*) *juruensis*, but it has shorter stromata (fertile part) (1.6–)4–27(–30) mm vs 15–40 mm), forms branches at the base, smaller perithecia (0.4–0.6 diam. mm vs 0.7–0.9 diam. mm), slightly larger in asci (74–160 × 5–12 µm vs 100–120 × 4–6 µm) and ascospores overlapping in size (10–18(–22) × 3.5–6(–7.5) µm vs 12–17 × 4–5 µm). However, *N. arengae* was found on a dead part of *Arenga pinnata*, while *N. juruensis* was reported from a rotten palm frond and on *Arenga engleri* (Arecaceae) (Hennings 1904, Hsieh et al. 2010, Becerril-Navarrete et al. 2018).

*Xylaria queenslandica* is similar to *Neoxylaria* and is transferred in this paper. *Neoxylaria arengae* is similar to *X. tucumanensis* in the appearance of the stromata, but our new species has larger stromata (4–27 × 0.5–1 vs 12–15 × 0.5–0.6 mm), shorter stipes (2.1–4.6 × 0.4–1 vs 6–7 × 0.2–0.3 mm), forming 3 (–5) branches at base, while *X. tucumanensis* form simple (unbranched), and larger numbers of perithecia (bearing 29–35 vs 9–17 perithecia per stroma) (Hladki & Romero 2010). *Neoxylaria arengae* also shares similar stomatal characters with *X. diminuta*, *X. enteroleuca*, *X. filiformioidea*, *X. himalayensis*, *X. mellissi*, and *X. subgracillima*, but differs in having branches at the base, of longer stromata (fertile part), and more perithecia per stromata than other species (Cooke 1883, Hennings 1904, Martin 1970, Narula et al. 1985, Hladki & Romero 2010, Huang et al. 2014). We also cross checked with *X. diminuta*, *X. enteroleuca*, *X. filiformioidea*, *X. himalayensis*, *X. mellissi* and *X. subgracillima*, but only *X. enteroleuca* has DNA sequence data, thus, we included *X. enteroleuca* in the phylogenetic tree (not shown) and found that it did not form a branch close to *Stilbohypoxyon* or *Neoxylaria*.

*Neoxylaria juruensis* (Henn.) Konta & K.D. Hyde, comb. nov.

Index Fungorum number: IF556652; Facesoffungi number: FoF06240
≡ *Xylaria juruensis* Henn., Hedwigia 43(4): 262 (1904)

Notes – *Xylaria juruensis* was introduced by Hennings (1904) from decayed palm material collected in Brazil. It similar to *Neoxylaria arengae* in having erect stromata, with prominent perithecia and a sterile apex. There is no sequence data for the type of *Xylaria juruensis*, but there is for a putatively named collection (92042501 HAST) from Taiwan (Hsieh et al. 2010). In the phylogenetic tree, the strain from Taiwan clustered together with *N. arengae* with strong support (100% ML, 1.00 BYPP, Fig. 2) and maybe the same genus, but is unlikely to be *Xylaria juruensis* sensu stricto, because of its location.

*Neoxylaria queenslandica* (Joanne E. Taylor, K.D. Hyde & E.B.G. Jones) Konta & K.D. Hyde, comb. nov.

Index Fungorum number: IF557765; Facesoffungi number: FoF08464
≡ *Xylaria queenslandica* Joanne E. Taylor, K.D. Hyde & E.B.G. Jones, in Taylor & Hyde, Fungal Diversity Res. Ser. 12: 236 (2003)

Notes – *Xylaria queenslandica* was also collected from a palm (*Archontophoenix alexandrae*) in Australia and is very similar to *Neoxylaria arengae* (Taylor & Hyde 2003). *Xylaria*
*queenslandica* differs from *N. arengae* in its average ascospore size (13 × 4.7 vs 10–18(–22) × 3.5–6(–7.5) µm) and mid red brown versus dark brown mature ascospores (Taylor & Hyde 2003).

**Figure 3** – *Neoxylaria arengae* (MFLU 15-0267, holotype). a–b Stromata on host substrate. c, e Perithecia and sterile apex strongly conical. d Stem with brown hair (Pubescent). f Section of a stroma. g Periphyses. h Peridium. i Paraphyses. j–l Asci. m–p Ascospores. q Ascospore with germ slit. r J+, apical ring in Melzer’s reagent. s Germinated ascospore. t Germinated ascospore with appressoria-like structures. u–z Appressoria-like structures. aa, ab Colony on MEA. Scale Bars: a = 5 mm, b, d, e = 0.5 mm, c = 2 mm, f, g = 0.1 mm, h, i, t = 20 µm, j–l = 50 µm, m–s = 10 µm, u–z = 5 µm.
**Stilbohypoxylon** Henn., Hedwigia 41: 16 (1902)

Index Fungorum number: IF5264; Facesoffungi number: FoF06306

*Saprobic* on various hosts in tropical and subtropical regions. Sexual morph: *Stromata* superficial, carbonaceous perithecia, solitary to gregarious, lining in row or in groups, dark brown to black, smooth or rugulose or with cracks or warts or minute furrows, with or without conical to acicular synnematal remnants borne on mature stromata. *Ascomata* globose to pulvinate, ampulliform or mambiiform, black carbonaceous, brittle, fragile, ostiolate, papillate, encircled with vaguely flattened area. *Synnemata* borne laterally on mature stromata or directly on wood, acicular to conical to somewhat cylindrical, light-brown or black, carbonaceous, brittle, fragile, sometimes covered by green-grey conidiophores at the base, or covered by yellow, greenish-yellow, or ochraceous scales, powdery or hyphae-like at early state. *Paraphyses* hyaline, filamentosus, cylindrical, septate, unbranched, longer than asci. *Asci* 8-spored, unitunicate, cylindrical, pedicellate, apically rounded, with a J+, inverted hat-shaped, apical ring. *Ascospores* uniseriate, hyaline to pale brown when immature, dark brown at maturity, ellipsoidal to broad-fusoid, unicellular, with two large guttules, smooth-walled, with a straight germ slit over the whole spore length, surrounded by a thin mucilaginous sheath, with a pad of denser mucilage at each apex.

Asexual morph: Hyphomycetous, geniculosporium-like. *Synnemata* green, scattered, acicular to conical, cylindrical, branched or unbranched. *Conidiophores* dense, dark brown palisades dichotomously branched several times from the bases. *Conidiogenous cells* terminal, cylindrical, hyaline, smooth, bearing lateral and terminal denticulate conidial secession scars. *Conidia* produced holoblastically in sympodial sequence, hyaline to pale yellow, yellowish to pale olivaceous, smooth, obovate, with a truncate base (adapted from Rogers & Ju 1997, Daranagama et al. 2018).

Type species – *Stilbohypoxylon moelleri* Henn.

Notes – *Stilbohypoxylon* contains 11 species, viz. *S. elaeidicola*, *S. hypoxylinum*, *S. ignobile*, *S. immundum*, *S. macrosporum*, *S. minus*, *S. moelleri* (type), *S. novae-zelandiae*, *S. quisquiliarum*, *S. samuelsii* and *S. theissenii* (Hyde et al. 2020, Index Fungorum 2020). All taxa are characterized by superficial, globose (sphaerical) stromata, with a smooth or delicately wrinkled surface that is usually overlain with yellow, greenish yellow or ochraceous scales at an early stage, unitunicate asci, unicellular ascospores with a straight germ slit, with or without mucilaginous sheath and a pad of denser mucilage at each end (Rogers & Ju 1997, Fröhlich & Hyde 2000, Hladki & Romero 2003, Petrini 2004, Daranagama et al. 2018).

According to Hsieh et al. (2010), Li et al. (2017), Daranagama et al. (2018) and Wendt et al. (2018), *Stilbohypoxylon* species clusters with *Xylaria* species in two subclades and it was mentioned that *Stilbohypoxylon* is polyphyletic. Currently, only *S. elaeidicola* and *S. quisquiliarum* have sequence data, while the generic type of *Stilbohypoxylon* (*S. moelleri*) has not yet been sequenced. Therefore, the phylogenetic affinity of *Stilbohypoxylon* is uncertain.

A lot of clumping has previously occurred in defining *Stilbohypoxylon* species (Fröhlich & Hyde 2000). Rogers & Ju (1997) revisited the genus and designated an epitype for the type species, *S. moelleri*, which was collected from a palm, *Euterpe* sp., in South America. We therefore follow Rogers & Ju (1997) and place the recent collections from palms in *Stilbohypoxylon sensu stricto*. *Stilbohypoxylon quisquiliarum* was collected in French Guiana on “wood” (Montagne 1840) and described in Miller (1961). Rogers & Ju (1997) have described the asexual morph of *S. quisquiliarum* and illustrated the ascospores with a spiral germ slit from an isotype specimen, which differentiates it from *Stilbohypoxylon sensu stricto*. *Stilbohypoxylon quisquiliarum* does not group with the clade comprising *S. elaeidis* and *S. elaeidicola* (*Stilbohypoxylon* clade II, Fig. 2). Therefore, we leave *S. quisquiliarum* as *Stilbohypoxylon sensu lato* (*Stilbohypoxylon* clade I, Fig. 2) until it is epitypified and described as a new genus. Unfortunately, the epitype specimen of *S. moelleri* has not yet been sequenced. Therefore, the congeneric status of the representative species (*S. elaeidis* and *S. elaeidicola*) with *S. moelleri* and the phylogenetic status of *Stilbohypoxylon sensu stricto* still need to be proven, however they all occur on decaying palm material.

The type species of *Stilbohypoxylon*, *S. moelleri* was detailed in Rogers & Ju (1997) and its lectotype was observed by Daranagama et al. (2018). *Stilbohypoxylon moelleri* is characterized by
sphaerical, gregarious, black, carbonaceous, fragile stromata, bearing 1–3-conical to acicular synnemata, cylindrical asci with apical ring bluing in Melzer’s reagent, brown to dark brown ascospores and a geniculosporium-like asexual morph (Rogers & Ju 1997, Daranagama et al. 2018). A comparison of S. moelleri and S. elaeidis shows that S. elaeidis has solitary stroma with a smooth surface and lack of synnemata on stromata surface.

Stilbohypoxylon elaeidis Konta & K.D. Hyde, sp. nov.

Index Fungorum number: IF558007; Facesoffungi number: FoF05123

Etymology – Refers to the name of the host genus, Elaeis

Holotype – MFLU 15-0270

Saprobic on dead petiole of Elaeis guineensis (Arecaceae). Sexual morph: Stromata superficial, visible as a black conical, or globose on the top view of host surface, solitary, or in groups, bearing conical to acicular synnematal remnants on mature stromata, carbonaceous, brittle, fragile, curved to straight. Ascomata 440–730 × 360–660 μm (x̅ = 565 × 530 μm, n = 25), black, carbonaceous, brittle, conical to mammiform, 1 per stroma, glabrous, covered with remnants of host tissue, disappearing at maturity, with indistinct ostiolate. Synnemata 250–470 μm (x̅ = 340 μm, n = 10), solitary, covered with yellow hyphae-like when immature, spine-like, wide at the base narrow towards the apex, black. Peridium 65–120(–130) μm wide (x̅ = 90 μm, n = 25), thick-walled, composed of several layers, outwardly comprising dark brown to black cells 2–4 μm, of textura angularis. Paraphyses 2.3–3.7 μm wide (x̅ = 3 μm, n = 20), filamentous, cylindrical, septate, unbranched, longer than asc. Asci 113–136 × 7–12 μm (x̅ = 125 × 9 μm, n = 20), 6–8-spored, unitunicate, cylindrical, long pedicellate, apically rounded, with a J+, inverted, hat-shaped apical ring, 2–5 × 2–3 μm (x̅ = 5 × 2 μm, n = 10). Ascospores 13–21 × 5–8 μm (x̅ = 17 × 6 μm, n = 30), uniseriate, hyaline to pale brown when immature, dark brown at maturity, equilateral ellipsoidal to broadly fusoid, unicellular, with two large guttules, smooth-walled, with a straight germ slit over the whole spore length, surrounded by thin mucilaginous sheath, with a pad of denser mucilage at each apex. Asexual morph: Undetermined.

Culture characteristics – Ascospores germinated on MEA within 24 hours and germ tube produced from germ slit. Mycelium immersed in media, mycelium at the center appears as grey to dark-green, mycelium towards margin appears white, hyphae, septate, branched, and smooth. Colonies on MEA, medium dense, irregular in shape, flowered-like, surface slightly rough with curled and undulate edge, radiating outward colony, flat, slightly raised at the centre, felty to cotonny, white at the margin, grey to dark grey near the centre, with black curled radiating towards the centre; reverse yellowish, curled with black radiating towards the centre; not produced pigmentation on medium.

Material examined – THAILAND, Krabi Province, on a dead petiole of Elaeis guineensis Jacq. (Arecaceae), 3 December 2014, S. Konta, KBF01a (MFLU 15-0270, holotype), ex-type living cultures, MFLUCC 15-0295a, MFLUCC 15-0295b. Addition sequence data – LSU: MT496755, SSU: MT495460, TEF: MT495461 (MFLUCC 15-0295a); LSU: MT496756, SSU: MT495461 (MFLUCC 15-0295b).

Notes – Stilbohypoxylon elaeidis is closely related to S. elaeidicola and both species are from palms. They form a well-separated branch with high statistical support in the combined ITS-RPB2-TUB2 phylogenetic analysis (Fig. 2). A comparison of ITS, RPB2 and TUB2 sequence data including gaps shows that S. elaeidis differs from S. elaeidicola (strains Y.M.J. 173 and 94082615 HAST) in 6 bp and 4 bp (1% and 0.68% of nucleotide base) for ITS; 7 bp and 3 bp (0.6% and 0.26% of nucleotide base) for RPB2; 53 bp and 42 bp (3.35% and 2.6% of nucleotide base) for TUB2. Furthermore, phylogenetic analysis showed that S. elaeidis clusters with S. elaeidicola strain JF-GUY-12-031 with good bootstrap support (97% ML, 1.00 BYPP, Fig. 2). However, this strain has no morphological description and only ITS sequence is available in GenBank database. Therefore, we rename this strain as S. elaeidis. Morphological comparison of Stilbohypoxylon species are detailed in Table 3.
**Figure 4** – *Stilbohypoxylon elaeidis* (MFLU 15-0270, holotype). a Immature and mature stromata on the host substrate from above. b Immature stromata covered with remnants of host material. c Close up of mature stromata. d Synnematal remnants. e Close up of synnematal remnants. f Peridium. g Section of stromata showing the perithecia. h Synnematal remnants covered by yellow hyphae-like. i–k Immature asci. l–m Mature asci. n, o Immature ascospores. p, q Mature ascospores. r Ascospore with germ slit. s J+, apical ring in Melzer’s reagent. t Paraphyses. u Germinated ascospore. v Colony on MEA from above and below. Scale Bars: a, b = 1000 μm, c, d, g, h = 500 μm, e = 200 μm, f, n–t = 10 μm, i–m = 50 μm, u = 20 μm.
### Table 3: Morphological comparison of species of *Stilbohypoxylon*.

| Taxa                      | Stromata (µm) | Synnemata (µm) | Peridium (µm) | Asci (µm) | Apical ring (µm) | Ascospores (µm) | References                        |
|---------------------------|---------------|----------------|---------------|-----------|-----------------|----------------|-----------------------------------|
| *Stilbohypoxylon elaeidicola* | (550–)813 ± 110(–1125) diam. × (400–)605 ± 80(–825) high, rough, rugose surface, sometimes with cracks, dull or shiny, sometimes covered by host material, sometimes 2–3 fused together | Up to 550 high | 50–75        | 11–16 × 105–130 | Upper 2–3 × 2–4 high | (6–)7 ± 0.5(–8.5) diam. × (13–)16 ± 1.5(–22) high, straight germ slit, slimy cap at each end and on the flat side | Hennings 1895, Petrini 2004 |
| *S. elaeidis*             | 367–664 diam. × 440–730 high (x̄ = 527 × 565), globose, smooth, with cracks of the host on the surface, solitary, 1 ascoma per stroma, surrounded by synnematal remnants on host substrate | 253–470 high, covered by yellow hypheae-like at early stage | 65–120(–130), composed of *textura angularis* | 7–12 × 113–136 | 2×3–2×5 high | 5–8 diam. × 13–21 high (x̄ = 6 × 17, n = 30) straight germ slit, thin mucilaginous sheath, with a pad mucilage at each apex | This study |
| *S. hypoxylinum*          | 375–450 wide × 450–700 high, globose to ampulliform, dull, powdery covered on stromata, solitary, synnemata | -             | 25           | -          |       |                  | Petrini 2004 |
| *S. ignobile*             | 625–800 wide × 750–925 high, cupulate with an elongate broad base, with cracks and warts on the surface, singly or 2–4 fused together, crowded, touching each other | -             | 25–50        | -          | -     | 4.5–5 diam. × 9–10.5 high (n = 3), straight germ slit | Petrini 2004 |
| *S. immundum*            | 625–920 ± 190(–1250) diam. × (625–930 ± 175(–1300) high, globose, subglobose, obovate to cupulate, surface warty, cylindrical synnemata, crowded, with perithecia closely adherent | -             | Up to 125    | -          | Upper 4–7, lower 3.5–6 × 6–11 high | (8.5–)11 ± 1.5(–14) diam. × (27–)32 ± 3(–39) high, straight, rarely oblique germ slit | Petrini 2004 |
| *S. macrosporum*          | 600–900 diam., globose or semi-globose, smooth, solitary or slightly fuseante, gregarious, with 1–2 synnemata on mature stromata, verrucose to rugulose | 400–500 high | -            | 9–12 × 200–260 | 6.5 × 8–10.5 high | 12–13 diam. × 30–40 high, spiral germ slit | Hladki & Romero 2003, Daranagama et al. 2018 |
Table 3 Continued.

| Taxa                  | Stromata (µm) | Synnemata (µm) | Peridium (µm) | Ascii (µm) | Apical ring (µm) | Ascospores (µm) | References                      |
|-----------------------|---------------|----------------|---------------|------------|-----------------|-----------------|---------------------------------|
| S. minus              | 400–600 diam., perithecoid, globose, rarely fusionate, gregarious, with 1 small synnema on immature stromata, shining, furfuraceous | 100–200 high | -             | 13–14.5 × 165–185 | 6.5–7.8 × 5–6.5 | 12–13 × 23.5–26(–27.5), straight germ slit | Hladki & Romero 2003 |
| S. moelleri (type species) | 600–1000 diam., rough, overlain with yellow to greenish yellow scales at early stage, texture brittle | 200–800 high | -             | 8–10 × 60–220 | 2.5–3.5 × 3–5 | 6–8 × 14.5–17, straight germ slit, enclosed by a thin hyaline sheath | Rogers & Ju 1997, Daranagama et al. 2018 |
| S. novae-zelandiae    | (400–)553 ± 82(–775) diam. × (350–)485 ± 70(–700) high, globose to subglobose, cupulate, rugose, with small cracks, solitary or densely crowded | -             | ≥ 25          | -          | Upper 2.4–3.8, lower 1.9–2.8 × (1.9–)2.3 ± 0.4(–3.3) | (5.8–)6.7(–8.2) × (9.6–)15.3 (–18.2) often with one cellular appendage, surrounded by a slimy sheath, sigmoid or straight germ slit | Petrini 2003 |
| S. quisquiliarum      | (600–)1020 ± 265(–1500) diam. × (575–)955 (–1600) high, globose to subglobose, ovoid, covered by yellow scales when young, later turning brown, surface warty, powdery, cracks, crowded, solitary to 9 fused together with 1 synnemata on immature stromata | -             | Up to 75      | -          | Upper 5–8, lower 4–7 × 6–10 | (10–)13(–16) × (23–)28(–34), sigmoid to spiral germ slit | Rogers & Ju 1997, Esteban et al. 2013, Daranagama et al. 2018 |
| S. samuelsii          | 700–1200 diam., spherical, gregarious, conical to acicular synnematal remnant, rugulose, sometimes overlain with ochraceous scales, texture hard | 200–400 high | -             | 12–15.5 × 235–285(–315) | 5.5–7 × 8–13 | 8.5–11(–13) × (27–)30–36(–40), straight germ slit | Rogers & Ju 1997, Petrini 2004 |
| S. theissenii         | 750–1000 diam. × 750–1000 high, globose, subglobose, with a dull, rugose surface covered with fine cracks, conical synnemata | -             | 25–50         | -          | Upper 4–5.5, lower 3–5 × 6–7 | (7–)8.5 (–11) × (22–)27(–33), large subglobose cellular appendage, straight to oblique germ slit | Petrini 2004 |
Stilbohypoxylon elaeidicola (Henn.) L.E. Petrini [as ‘elaeicola’], Sydowia 56(1): 55 (2004).

Index Fungorum number: IF631505; Facesoffungi number: FoF08465
≡ Rosellinia elaeidicola Henn. [as ‘elaeicola’], Bot. Jb. 22: 77 (1895)

Notes – In our phylogenetic analysis based on DNA sequencedata from ITS region (data not shown) and combined sequence data of ITS, RPB2 and TUB2, Stilbohypoxylon elaeidicola clustered with S. elaeidis with high statistical support (Fig. 2). A comparison of S. elaeidicola with S. elaeidis shows they are different; S. elaeidis has solitary stromata (440–730 × 360–660 μm) with a smooth surface and forms synnemata remnants on the host, and covered the stroma when mature. Stilbohypoxylon elaeidicola has larger stromata (550–1,125 × 400–825 μm high), single or fused in clusters of 2–3, with rough to rugose walls, and with synnemata on the substrate or the stroma; while in S. elaeidicola asci and ascospores overlap in size with those of S. elaeidis (asci 105–130 × 11–16 μm vs 113–136 × 7–12 μm; ascospores 13–17 × 7–9 μm vs 13–21 × 5–8 μm) (Hennings 1895, Petrini 2004).

Discussion

There have been several taxonomic revisions of the larger Xylariaceae (sensu Daranagama et al. 2016) using traditional morphological concepts (e.g. Jaklitsch & Voglmayr 2012, Daranagama et al. 2015, Wendt et al. 2018, Lambert et al. 2019). In this paper, we introduce Neoxylaria which has a discrete morphology and is also phylogenetically distinct from Xylaria sensu stricto. Xylaria-like taxa have generally been lumped in a single genus pending an upcoming monograph (Stadler et al. pers. comm) and species/genera resolution has not advanced for numerous years. It is clear from the phylogenies generated in different studies (Hsieh et al. 2009, U’Ren et al. 2016, Daranagama et al. 2018, Wendt et al. 2018), that Xylaria is not monophyletic and should be split into several distinct genera. Xylaria hypoxylon, the type species is well-resolved and morphologically and phylogenetically characterized (Peršoh et al. 2009). Hsieh et al. (2010) and U’Ren et al. (2016) showed that there are three major Xylaria clades: Xylaria species associated with termite nests “TE clade” (including X. nigripes), X. hypoxylon (Xylaria sensu stricto) and closely related species “HY clade” and X. polymorpha and closely related species “PO clade”. Several other xylaria-like species also cluster in different clades such as Entoleuca, Euepixylon, Kretzmaria, Nemania, Podosordaria, Poronia and Rosellinia. However, theoretically the HY clade (Xylaria “HY” clade II, Fig. 2) is the only acceptable cluster for strictly naming Xylaria species and other clades should represent other genera. Therefore, it is timely that xylaria-like taxa are resolved using both morphology and phylogeny.

This is not unique for Xylaria, but also similar for some other stromatic xylarialean taxa. Wendt et al. (2018) emphasized that ascal and ascospore characters have been the main discriminative criteria in traditional taxonomy and are artificial. Following a polyphasic taxonomic approach, Wendt et al. (2018) and Lambert et al. (2019) introduced several genera in Hypoxylaceae which were earlier placed in Hypoxylon. A similar approach should resolve the taxonomic confusion surrounding xylaria-like species. It is also not necessary to wait for a monograph as most of the old specimens cannot be sequenced and therefore, we can use fresh specimens to describe any new genera. Whether any old taxa are identical will be speculative, based on morphology and any combinations will be subjective (Dayarathne et al. 2016). Even though our new collection has superficial stromata similar to other Xylaria (sensu stricto) species, it is morphologically distinct in the palm host and perithecia which bulge from the stroma (as compared to immersed under a smooth stroma) and also phylogenetically distinct. The novel xylariaceous genus, Neoxylaria is therefore introduced in this paper and will help to stabilize the classification of Xylariaceae. Phylogenetic analysis using three combined genes gave fair resolution for this order (Fig. 2).

Anthostomella-like species were also all clumped mostly under a single genus because they have immersed ascomata with or without a clypeus or a poorly or well-developed stroma, asci with a J+ or J- apical ring, dark unicellular ascospores (sometimes aiospores) with or without a germ-slitr. Asci and ascospores were minute to large. Anthostomella-like taxa have now been shown to cluster in several different genera which are scattered in trees. Some authors used a single unique
character to separate anthostomella-like taxa into distinct genera, such as *Helicogermslita* (Hawksworth & Lodha 1983), which had spiral germ-slits but their introduction was subjective. One species that Duong et al. (2004) found was also anthostomella-like but introduced as a new genus *Emarcea* and eventually was shown to be sister to *Induratia* in a new family in Xylariales (Samarakoon et al. 2020). There are likely to be many other xylariaceous genera introduced in the future, just like as in *Anthostomella*.

We also introduced *Stilbohypoxylon elaeidis* as a new species confirmed by its phylogenetic placement. *Stilbohypoxylon* is polyphyletic and in this paper, we have defined *Stilbohypoxylon sensu stricto* and shows that *S. quisquiliarum* is distantly related and requires its own genus. Recent studies on tropical or poorly studied fungal genera have revealed an amazing diversity and numerous new species and this is likely to continue (Hyde et al. 2017, 2020). Thus, this study will help to resolve the naming and placement of the novel tropical taxa discoveries. Interestingly, *Stilbohypoxylon sensu stricto* (*S. elaeidis* and *S. elaeidicola*) occurred on the same host family, Areccaceae, with *Neoxylaria*, and they also share similar cultured characteristics. Both genera have cultured characteristics different from *Xylaria sensu stricto*, suggesting that both *Stilbohypoxylon* and *Neoxylaria* are likely ancient and related (but not the same genera) (Fig. 3 aa, ab, Fig. 4v).

Konta et al. (2016) reported appressoria formation in saprobic *Oxydothis* species. *Xylaria* species are mostly saprobes or endophytes and only a few species are pathogens (Miller & Nielsen 1957, Kodsueb et al. 2008, Okane et al. 2008, Karun & Sridhar 2015, Srihanant et al. 2015, Li et al. 2017, Adnan et al. 2018b, Chen et al. 2018, Debnath et al. 2018, Husbands & Aime 2018). *Xylaria* species can also form appressoria when they germinate (Daranagama, pers obs). In the case of *Neoxylaria arengae*, we observed appressoria-like structures produced at the tips of germinating hyphae on media (Fig. 3t–z). Thus, it is interesting that *Neoxylaria*, *Oxydothis* and *Xylaria* species collected from palms produce appressoria which indicate they may have different life modes.

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**References**

Adnan M, Alshammari E, Ashraf SA, Patel K et al. 2018a – Physiological and molecular characterization of biosurfactant producing endophytic fungi *Xylaria regalis* from the cones
of *Thuja plicata* as a potent plant growth promoter with its potential application. BioMed Research International 2018, 1–11.

Adnan M, Patel M, Reddy MN, Alshammari E. 2018b – Formulation, evaluation and bioactive potential of *Xylaria primorskensis* terpenoid nanoparticles from its major compound xylaranic acid. Scientific Reports 8, 1–12.

Becerril-Navarrete AM, Gómez-Reyes VM, Palestina Villa EN, Medel-Ortiz R. 2018 – Nuevos registros de *Xylaria* (Xylariaceae) para el estado de Michoacán, México. Scientia fungorum 48, 61–75.

Cedeño-Sanchez M, Wendt L, Stadler M, Mejia LC. 2020 – Three new species of *Hypoxylon* and new records of Xylariales from Panama. Mycologia 11, 1457–1476.

Chen R, Tang JW, Li XR, Liu M et al. 2018 – Secondary metabolites from the endophytic fungus *Xylaria* sp. hg1009. Natural Products and Bioprospecting 8, 121–129.

Cooke MC. 1883 – On *Xylaria* and its allies. Grevillea 11, 81–94.

Daranagama DA, Camporesi E, Tian Q, Liu X et al. 2015 – *Anthostomella* is polyphyletic comprising several genera in Xylariaceae. Fungal Diversity 73, 203–238.

Daranagama DA, Hyde KD, Sir EB, Thambugala KM et al. 2018 – Towards a natural classification and backbone tree for Graphostromataceae, Hypoxylaceae, Lopadostomataceae and Xylariaceae. Fungal Diversity 88, 1–165.

Daranagama D, Jones E, Liu X, To-Anun C et al. 2016 – Mycosphere Essays 13-Do xylariaceous macrofungi make up most of the Xylariomycetidae?. Mycosphere 7, 582–601.

Dayarathne MC, Boonmee S, Braun U, Crous PW et al. 2016 – Taxonomic utility of old names in current fungal classification and nomenclature: Conflicts, confusion & clarifications. Mycosphere 7, 1622–1648.

Debnath S, Majumdar K, Das P, Saha AK. 2018 – New distribution record of five species of *Xylaria* from Tripura, Northeast India. Research & Reviews: A Journal of Life Sciences 8, 1–10.

Duong LM, Lumyong S, Hyde KD, Jeewon R. 2004 – *Emarcea castanopsidicola* gen. et sp. nov. from Thailand, a new xylariaceous taxon based on morphology and DNA sequences. Studies in Mycology 50, 253–260.

Elias LM, Fortkamp D, Sartori SB, Ferreira MC et al. 2018 – The potential of compounds isolated from *Xylaria* spp. as antifungal agents against anthracnose. Brazilian Journal of Microbiology 49, 840–847.

Esteban B, Perera TC, Romero AI, Hladki AI. 2013 – *Stilbohypoxylon quisquiliarum* (Ascomycota, Xylariaceae), nuevacita para la Argentina. Darwiniana 1, 289–294.

Fournier J, Ju YM, Hsieh HM, Lindemann U. 2018a – *Xylaria aethiopica* sp. nov. – a new pod-inhabiting species of *Xylaria* (Xylariaceae) from Ethiopia. Ascomycete.org 10, 209–215.

Fournier J, Lechat C, Courtecuisse R. 2018b – The genus *Xylaria sensu lato* (Xylariaceae) in Guadeloupe and Martinique (French West Indies) I. Taxa with penzigioid stromata. Ascomycete.org 10, 131–176.

Frohlich J, Hyde KD. 2000 – Palm microfungi. Fungal Diversity Research Series. 3, 1–393.

Fröhlich J, Hyde KD. 2000 – Palm microfungi. Fungal Diversity Research Series. 3, 1–393.

Greville RK. 1824 – Flora Edinensis: Or A Description of Plants Growing Near Edinburgh with a Concise Introduction to the Natural Orders of the Class Cryptogamia: Blackwood.

Hawksworth DL, Lodha BC. 1983 – *Helicogermisita*, a new stromatic xylariaceous genus with a spiral germ slit from India. Transactions of the British Mycological Society 81, 91–96.

Hennings P. 1895 – Fungi camerunenses I. Botanische Jahrbücher für Systematik Pflanzengeschichte und Pflanzengeographie 22, 72–111.

Hennings P. 1902 – Fungi blumenaviensis I, a cl. Alfr. Moller lecti. Hedwigia 41, 1–33.

Hennings P. 1904 – Fungi amazonici II, a cl. Ernesto Ule collecti. Hedwigia 43, 262–263.

Hladki AI, Romero AI. 2003 – Two new species of *Stilbohypoxylon* and the taxonomic positions of *Hypoxylon cyclopicum*, *H. chionostomum* and *Anthostoma chionostoma*. Sydowia 55, 65–76.
Hladki AI, Romero AI. 2010 – A preliminary account of *Xylaria* in the Tucuman Province, Argentina, with a key to the known species from the Northern Provinces. Fungal Diversity 42, 79–96.

Hongsanan S, Maharachchikumbura SSN, Hyde KD, Samarakoon MC et al. 2017 – An updated phylogeny of Sordariomycetes based on phylogenetic and molecular clock evidence. Fungal Diversity 84, 25–41.

Hsieh HM, Ju YM, Rogers JD. 2005 – Molecular phylogeny of *Hypoxylon* and closely related genera. Mycologia 97, 844–865.

Hsieh HM, Lin CR, Fang MJ, Rogers JD et al. 2010 – Phylogenetic status of *Xylaria* subgenus *Pseudoxyliaria* among taxa of the subfamily Xylarioidae (Xylariaceae) and phylogeny of the taxa involved in the subfamily. Molecular Phylogenetics and Evolution 54, 957–969.

Huang G, Guo L, Liu N. 2014 – Two new species of *Xylaria* and *X. diminuta* new to China. Mycotaxon 129, 149–152.

Huelsenbeck JP, Ronquist F. 2001 – MRBAYES: Bayesian inference of phylogenetic trees. Bioinformatics 17, 754–755.

Husbands D, Aime M. 2018 – Emerging forest diseases: a case study of greenheart (*Chlorocardium* spp., Lauraceae) and the newly described fungus, *Xylaria karyophthora*. Forests 9, 365.

Husbands DR, Urbina H, Lewis SM, Aime MC. 2018 – *Xylaria karyophthora*: a new seed-inhabiting fungus of Green heart from Guyana. Mycologia 110, 434–447.

Hyde KD, Maharachchikumbura SSN, Hongsanan S, Samarakoon MC et al. 2017 – The ranking of fungi: a tribute to David L. Hawksworth on his 70th birthday. Fungal Diversity 84, 1–23.

Hyde KD, Norphanphoun C, Maharachchikumbura SSN, Bhat DJ et al. 2020 – Refined families of Sordariomycetes. Mycosphere 11, 305–1059.

Index Fungorum. 2020 – http://www.indexfungorum.org/names/Names.asp. (Accessed January 2020).

Jaklitsch WM, Gardiennet A, Voglmayr H. 2016 – Resolution of morphology-based taxonomic delusions: *Acrocordiella*, *Basiseptospora*, *Blogiascospora*, *Clypeosphaeria*, *Hymenopleella*, *Lepteutypa*, *Pseudapiospora*, *Requienella*, *Seiridium* and *Strickeria*. Persoonia: Molecular Phylogeny and Evolution of Fungi 37, 82–105.

Jaklitsch WM, Voglmayr H. 2012 – Phylogenetic relationships of five genera of Xylariales and *Rosasphaeria* gen. nov. (Hypocreales). Fungal Diversity 52, 75–98.

Jayasiri SC, Hyde KD, Ariyawansa HA, Bhat DJ et al. 2015 – The Faces of Fungi database: fungal names linked with morphology, phylogeny and human impacts. Fungal Diversity 74, 3–18.

Johnston PR, Rogers JD, Park D, Martin NA. 2016 – *Entalbostroma erumpens* gen. et sp. nov. (Xylariaceae) from Phormium in New Zealand. Mycotaxon 131, 765–771.

Ju YM, Hsieh HM. 2007 – *Xylaria* species associated with nests of *Odontotermes formosanus* in Taiwan. Mycologia 99, 936–957.

Ju YM, Hsieh HM, Ho MC, Szu DH, Fang MJ. 2007 – *Theissenia rogersii* sp. nov. and phylogenetic position of *Theissenia*. Mycologia 99, 612–621.

Ju YM, Hsieh HM, Rogers JD, Fournier J et al. 2012 – New and interesting penzigioid *Xylaria* species with small, soft stromata. Mycologia 104, 766–776.

Ju YM, Rogers JD, Hsieh HM. 2018 – *Xylaria* species associated with fallen fruits and seeds. Mycologia 110, 726–749.

Karun N, Sridhar K. 2015 – *Xylaria* complex in the south western India. Plant Pathology & Quarantine 5, 83–96.

Katoh K, Rozewicki J, Yamada KD. 2017 – Mafft online service: multiple sequence alignment, interactive sequence choice and visualization. Brief Bioinform.

Kodsueb R, McKenzie E, Lumyong S, Hyde K. 2008 – Diversity of saprobic fungi on Magnoliaceae. Fungal Diversity 30, 37–53.

Konta S, Hongsanan S, Tibpromma S, Thongbai B et al. 2016 – An advance in the endophyte story: Oxydothidaceae fam. nov. with six new species of *Oxydothis*. Mycosphere 7, 1425–1446.
Konta S, Maharachchikumbura SSN, Senanayake IC, McKenzie EHC et al. 2020 – A new genus *Allodiatrype*, five new species and a new host record of diatrypaceous fungi from palms (Arecaceae). Mycosphere 11, 239–268.

Koyani R, Patel H, Vasava A, Rajput K. 2016 – Xylariaceae: overview and addition to fungal diversity of Gujarat state. Studies in Fungi 1, 69–79.

Kumar S, Stecher G, Tamura K. 2016 – MEGA7: molecular evolutionary genetics analysis version 7.0 for bigger datasets. Molecular Biology and Evolution 33, 1870–1874.

Lambert C, Wendt L, Hladki AI, Stadler M, Sir EB. 2019 – *Hypomontagnella* (Hypoxylaceae): a new genus segregated from *Hypoxylon* by a polyphasic taxonomic approach. Mycological Progress 18, 187–201.

Lee JS, Ko KS, Jung HS. 2000 – Phylogenetic analysis of *Xylaria* based on nuclear ribosomal ITS1-5.8 S-ITS2 sequences. FEMS Microbiology Letters 187, 89–93.

Li Q, Liu L, Zhang X, Shen X, Kang J. 2017 – *Xylaria spinulosa* sp. nov. and *X. strosphaerica* from China. Mycosphere 8, 1070–1079.

Li QR, Kang JC, Hyde KD. 2015a – Two new species of the genus *Collodiscula* (Xylariaceae) from China. Mycological progress 14, 52.

Li Q, Wen TC, Kang JC, Hyde KD. 2015b – A new species of *Collodiscula* (Xylariaceae) from China. Mycotaxon 205, 187–196.

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.

Maharachchikumbura SSN, Hyde KD, Jones EBG, McKenzie EHC et al. 2016 – Families of Sordariomycetes. Fungal Diversity 79, 1–317.

Martin P. 1970 – Studies in the Xylariaceae: VIII. *Xylaria* and its allies. Journal of South African Botany 36, 73–137.

Miller JH. 1961 – A monograph of the world species of *Hypoxylon*. University of Georgia Press, Athens, 158 pp.

Miller JH, Nielsen L. 1957 – A new species of *Xylaria*. Mycologia 49, 112–114.

Montagne JPFC. 1840 – Séconde centurie de plantes cellulaires exotiques nouvelles, Décades VI, VII et VIII. Annales des Sciences Naturelles Botanique 14, 321–350.

Narula A, Rawla G, Kaushal S. 1985 – Two new species of *Xylaria* (Pyrenomycetes) from India. Willdenowia 409–411.

Nylander J. 2004 – MrModeltest v2. Program distributed by the author. Evolutionary Biology Centre, Uppsala University, Uppsala.

Okane I, Toyama K, Nakagiri A, Læssøe T et al. 2008 – Study of endophytic Xylariaceae in Thailand: diversity and taxonomy inferred from rDNA sequence analyses with saprobes forming fruit bodies in the field. Mycoscience 49, 359–372.

O’Donnell K, Cigelnik E. 1997 – Two divergent intragenomic rDNA ITS2 types within a monophyletic lineage of the fungus *Fusarium* are nonorthologous. Molecular Phylogenetics and Evolution 7, 103–116.

Peláez F, González V, Platas G, Sánchez Ballesteros J, Rubio V. 2008 – Molecular phylogenetic studies within the Xylariaceae based on ribosomal DNA sequences. Fungal Diversity 31, 111–134.

Peršoh D, Melcher M, Graf K, Fournier J et al. 2009 – Molecular and morphological evidence for the delimitation of *Xylaria hypoxylon*. Mycologia 101, 256–268.

Petrini LE. 2003 – *Rosellinia* and related genera in New Zealand. New Zealand Journal of Botany 41, 71–138.

Petrini LE. 2004 – A revision of the genus *Stilbobhypoxylon* (Xylariaceae). Sydowia 56, 51–71.

Pourmoghadam MJ, Khodaparast SA, Krisai-Greilhuber I, Voglmayr H, Stadler M. 2018 – Two new species and one new record of *Kretzschmaria* (Ascomycota, Xylariales) from Iran. Mycosphere 9, 1197–1208.

Rambaut A. 2006 – FigTree. Tree figure drawing tool version 1.4. 0. University of Edinburgh: Institute of Evolutionary Biology, (http://tree.bio.ed.ac.uk/software/figtree/).
Rogers JD, Ju YM. 1997 – The genus *Stilbohypoxylon*. Mycological Research 101, 135–138.
Rogers JD. 2000 – Thoughts and musings on tropical Xylariaceae. Mycological Research 104, 1412–1420.
Samarakoon M, Hyde KD, Promputtha I, Ariyawansa H, Hongsanan S. 2016 – Divergence and ranking of taxa across the kingdoms Animalia, Fungi and Plantae. Mycosphere 7, 1678–1689.
Samarakoon MC, Thongbai B, Hyde KD, Brünstrup M et al. 2020 – Elucidation of the life cycle of the endophytic genus *Muscodor* and its transfer to *Induratia* in Induratiaceae fam. nov., based on a polyphasic taxonomic approach. Fungal Diversity 101, 177–210.
Schrank FvP. 1789 – Baierische Flora. 1, 1–753.
Senanayake IC, Maharachchikumbura SSN, Hyde KD, Bhat DJ et al. 2015 – Towards unraveling relationships in Xylariomycetidae (Sordariomycetes). Fungal Diversity 73, 73–144.
Silvestro D, Michalak I. 2012 – raxmlGUI: a graphical front-end for RAxML. Organisms Diversity & Evolution 12, 335–337.
Srihanant N, Petcharat V, Vasilyeva LN. 2015 – *Xylaria thailandica* – a new species from southern Thailand. Mycotaxon 130, 227–231.
Stadler M, Hellwig V. 2005 – Chemotaxonomy of the Xylariaceae and remarkable bioactive compounds from Xylariales and their associated asexual stages. Research Signpost 41–93.
Stadler M, Kuhnert E, Persoh D, Fournier J. 2013 – The Xylariaceae as model example for a unified nomenclature following the “One Fungus-One Name” (1F1N) concept. Mycology 4, 5–21.
Stamatakis A. 2006 – RAxML-VI-HPC: maximum likelihood-based phylogenetic analyses with thousands of taxa and mixed models. Bioinformatics 22, 2688–2690.
Tang AM, Jeewon R, Hyde KD. 2007 – Phylogenetic relationships of *Nemania plumbea* sp. nov. and related taxa based on ribosomal ITS and RPB2 sequences. Mycological Research 111, 392–402.
Tang A, Jeewon R, Hyde KD. 2009 – A re-evaluation of the evolutionary relationships within the Xylariaceae based on ribosomal and protein-coding gene sequences. Fungal Diversity 34, 127–155.
Taylor JE, Hyde KD. 2003 – Microfungi of tropical and temperate palms. Fungal Diversity Research series 12, 121–459.
Tibpromma S, Hyde KD, Jeewon R, Maharachchikumbura SSN et al. 2017 – Fungal diversity notes 491–602: taxonomic and phylogenetic contributions to fungal taxa. Fungal Diversity 83, 1–261.
U’Ren JM, Miadlikowska J, Zimmerman NB, Lutzoni F et al. 2016 – Contributions of North American endophytes to the phylogeny, ecology, and taxonomy of Xylariaceae (Sordariomycetes, Ascomycota). Molecular Phylogenetics and Evolution 98, 210–232.
Voglmayr H, Friebes G, Gardiennet A, Jaklitsch WM. 2018 – *Barrmaelia* and *Entosordaria* in Barrmaeliaceae (fam. nov., Xylariales) and critical notes on *Anthostomella*-like genera based on multigene phylogenies. Mycological Progress 17, 155–177.
Vu D, Groenewald M, De Vries M, Gehrmann T et al. 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.
Wendt L, Sir EB, Kuhnert E, Heitkämper S et al. 2018 – Resurrection and emendation of the Hypoxylaceae, recognised from a multigene phylogeny of the Xylariales. Mycological Progress 17, 115–154.
White TJ, Bruns T, Lee SJWT, Taylor JW. 1990 – Amplification and direct sequencing of fungal ribosomal RNA genes for phylogenetics. PCR Protocols: A Guide to Methods and Applications 18, 315–322.
Wijayawardene NN, Hyde KD, Lumbsch HT, Liu JK et al. 2018 – Outline of ascomycota: 2017. Fungal Diversity 88, 167–263.
Wijayawardene NN, Hyde KD, Al-Ani LKT, Tedersoo L et al. 2020 – Outline of Fungi and fungus-like taxa. Mycosphere 11, 1060–1456.