XYLARIALES FUNGI: A COMPREHENSIVE REVIEW OF THEIR DIVERSITY AND ECOLOGICAL SIGNIFICANCE

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Abstract

The Xylariales fungal order is a diverse and ecologically significant group within the Ascomycota division. Primarily recognized as saprophytes, these fungi decompose and facilitate nutrient recycling. While being typically saprobic, certain Xylariales fungi exist as endophytes and can even transition to pathogens in response to environmental stresses under rare circumstances. The Xylariales order has been traditionally classified based on their distinct morphological characteristics. Still, due to recent advancements in molecular phylogeny, it has undergone extensive taxonomic revisions, leading to a more precise understanding of their classification. Among fungi, the Xylariales species are particularly prolific in producing bioactive secondary metabolites, which hold much economic importance. Renowned for its rich biodiversity, Sri Lanka harbours a potentially vast and unexplored array of Xylariales fungi. However, the full scope of the Xylariales fungal diversity and ecological significance within the country remains largely unknown. Molecular classification is crucial for accurately identifying and characterizing Xylariales fungi in Sri Lanka, enabling a deeper understanding of their ecological roles and potential applications. Further research is essential to unlock the untapped potential of these fungi in biotechnology, medicine, agriculture, and other fields.

Keywords: Ascomycota, Hypoxylaceae, molecular characterization, secondary metabolites, Xylariales, Xylariaceae.

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Introduction

Xylariales is a diverse order of fungi within the Ascomycota division, known for its ecological and economic importance (Stadler et al., 2013; Wendt et al., 2018; Konta et al., 2020). This order was first introduced under the class Sordariomycetes within the Ascomycota phylum in 1932 by Swedish mycologist Nannfeldt (Ma et al., 2022). Primarily inhabiting tropical regions, these fungi are mostly saprobic or endophytic and even pathogenic in certain instances (Rogers, 2000).

Xylariales fungi display unique and diverse morphological characteristics, including carbonaceous structures called stromata that facilitate the growth of their reproductive components. These stromata can exhibit variations in size, shape, and color (Konta et al., 2020). In most Xylariales fungi, the ascomata, which contain the asci that produce sexual spores, are usually enclosed within the stromata. The shape of the asci varies depending on the species, but they are generally cylindrical or elongated. Additionally, the asci have a prominent apical ring, which is often amyloid and contains eight spores (Konta et al., 2020). These ascospores in Xylariales fungi may have one or multiple germ slits, and the presence and arrangement of these slits are vital in species identification (Daranagama et al., 2018). In addition, there is a significant diversity in the morphology of asexual morphs of Xylariales fungi, which also plays a crucial role in identifying species (Wendt et al., 2018).

Traditionally classified based on morphology, the Xylariales order has undergone significant taxonomic revisions due to advancements in molecular phylogeny in recent years, resulting in a more accurate classification (Daranagama et al., 2018; Wendt et al., 2018; Konta et al., 2020). According to Helaly et al. (2018), the fungi belonging to Xylariales are among the fungal kingdom's most prolific producers of bioactive secondary metabolites. As a result, these fungi possess potential applications in medicine and agriculture. However, while extensively studied in regions like Thailand, India, and China, the diversity and ecological roles of Xylariales in Sri Lanka remain largely unexplored (Jayathunga et al., 2022). Comprehensive studies combining morphological and molecular approaches are necessary to address this knowledge gap and fully understand the potential of this fungal group in the country.

Methodology

Xylariales fungi were collected from two Sri Lankan Forest reserves, Kanneliya forest in the Galle district and Pilikutthuwa forest in the Gampaha district, to investigate their diversity and ecological roles. Morphological and molecular techniques were employed for a species-level identification, and species distribution patterns were analyzed. A comprehensive literature review was also conducted, focusing on original research articles published in reputable scientific journals and databases, including the Mycosphere Journal of Fungal Biology, Google Scholar, and PubMed. Subject-specific keywords and phrases, such as, 'Xylariales,' 'Xylariaceae,' 'Hypoxylaceae,' 'secondary metabolites of Xylariales,' 'Xylariales taxonomy,' and 'multi-gene approaches' were employed to find the relevant literature. Extracted data on taxonomic approaches, species diversity, distribution, ecological roles, and secondary metabolism of Xylariales fungi were analyzed to identify patterns, trends, and knowledge gaps with the findings of this study. This review aims to provide a comprehensive overview of Xylariales fungi in in both global and Sri Lankan contexts, and to highlight the importance of further fungal research in Sri Lanka.

Results and Discussion

Taxonomic classification of Xylariales species

Xylariales fungi belong to the Xylariomycetidae subclass of Sordariomycetes, which have undergone frequent revisions in recent years (Maharachchikumbura et al., 2016; Daranagama et al., 2018; Wendt et al., 2018; Konta et al., 2020; Hyde et al., 2020). The latest taxonomic classification of the

Sordariomycetes class, which includes 46 orders, 172 families, and 7 subclasses, was published by Wijayawardene et al. in 2022. According to Hyde et al. (2020), the Xylariomycetidae subclass is further classified into three orders: Xylariales, Amphisphaeriales, and Delonicicolales.

Initially, Xylariomycetidae was classified solely as the Xylariales order in a simpler classification (Maharachchikumbura et al., 2016). However, subsequent research utilizing phylogenetic data by Samarakoon et al. (2016) included the Amphispheriales order alongside Xylariales. Hyde et al. (2020) acknowledged 15 families within the Xylariales order. However, a more recent taxonomic classification by Wijayawardene et al. (2022) recognizes 20 families within the Xylariales order, including Anungitiomycetaceae, Barrmaeliaceae, Cainiaceae, Clypeosphaeriaceae, Coniocessiaceae, Diatrypaceae, Fasciatisporaceae, Graphostromataceae, Hansfordiaceae, Hypoxylaceae, Induratiaceae, Lopadostomataceae, Microdochiaceae, Polystigmataceae, Nothodactylariaceae, Requienellaceae, Vamsapriyaceae, Xyladictyochaetaceae, Xylariaceae, and Zygosporiaceae. Among these families, Xylariaceae, Hypoxylaceae, Graphostromataceae, and Lopadostomataceae are recognized as the four distinct families in the Xylariales order (Daranagama et al., 2018; Wendt et al., 2018). Hyde et al. (2020) currently accepts 160 genera within the Xylariales order.

Library user education is a vital service provided by libraries to help users develop the necessary skills and knowledge to access, evaluate, and use information effectively. Library guided tours are an effective way to introduce new users to the library and its resources, and by offering tips on how to use them effectively. This study aimed to assess users' proficiency in using library services after the library tour and gauge their overall satisfaction with the tour. The research employed both qualitative and quantitative mixed methodologies. The study population was two thousand nine hundred sixty-five students (2965) participating in a library tour, and they were the research population.

History of classification of Xylariales species

Barr (1983) initially classified Sordariomycetes based on morphological characteristics in the 1980s. Subsequently, Eriksson & Winka (1997) introduced three subclasses: Hypocreomycetidae, Sordariomycetidae, and Xylariomycetidae. However, Sordariomycetes underwent further revision, incorporating a broader morphological and molecular data range. This revision resulted in the addition of three more subclasses - Diaporthomycetidae, Lulworthiomycetidae, and Meliolomycetidae - thereby increasing the total number of subclasses to six (Maharachchikumbura et al., 2016).

Initially, Maharachchikumbura et al. (2016) proposed 22 families as constituents of the Xylariales order. Subsequent research employing molecular and phylogenetic data has refined the classification within Xylariales. This revised classification comprises 20 families and recognizes the uncertain positioning of certain families within the order (Samarakoon et al., 2016; Wijayawardene et al., 2018; Hyde et al., 2020; Wijayawardene et al., 2022).

Table 1
Taxonomic revision of families within the order Xylariales, as accepted by various researchers throughout the years

Order	Maharachchikumbura et al. (2016)	Hyde et al. (2020)	Wijayawardene et al. (2022)
Xylariales	Amphisphaeriaceae Apiosporaceae Bartaliniaceae	Barrmaeliaceae Cainiaceae Clypeosphaeriaceae	Anungitiomycetaceae Barrmaeliaceae Cainiaceae

	Beltraniaceae Cainiaceae Clypeosphaeriaceae Coniocessiaceae Diatrypaceae Hyponectriaceae Iodosphaeriaceae Lopadostomaceae Melogrammataceae Microdochiaceae Myelospermataceae Pestalotiopsidaceae Phlogicylindriaceae Pseudomassariaceae Requienellaceae Robillardaceae Sporocadaceae Vialaeaceae Xylariaceae	Coniocessiaceae, Diatrypaceae, Graphostromataceae Hansfordiaceae Hypoxylaceae Induratiaceae Lopadostomataceae Microdochiaceae Polystigmataceae Requienellaceae Xylariaceae Zygosporiaceae	Clypeosphaeriaceae Coniocessiaceae Diatrypaceae Fasciatisporaceae Graphostromataceae Hansfordiaceae Hypoxylaceae Induratiaceae Lopadostomataceae Microdochiaceae Polystigmataceae Nothodactylariaceae Requienellaceae Vamsapriyaceae Xyladictyochaetaceae Xylariaceae Zygosporiaceae

Among the families of Xylariales, Xylariaceae and Hypoxylaceae are two of the most prominent families in the order. Initially, Xylariaceae consisted of two subfamilies - Xylaroideae and Hypoxyloideae, which comprised 87 genera (Maharachchikumbura et al., 2016). However, Wendt et al. (2018) separated Hypoxyloideae into its family, Hypoxylaceae, based on morphology, phylogeny, and secondary metabolite analyses. Daranagama et al. (2018) provided an updated account of the genera within Xylariaceae and Hypoxylaceae. Hyde et al. (2020) recognize 32 genera within Xylariaceae and 19 genera within Hypoxylaceae. However, with the recently updated taxonomic classification, Wijayawardene et al. (2022) accepted 38 genera within Xylariaceae and 18 genera within Hypoxylaceae.

Table 2
Accepted genera of Xylariaceae and Hypoxylaceae by Wijayawardene et al. (2022).

Order	Xylariaceae	Hypoxylaceae
Xylariales	*Abieticola, Amphirosellinia, Anthostomella, Anthostomelloides, Ascotricha, Astrocystis, Atrozythia, Brunneiperidium, Catenuliconidia, Collodiscula, Coniolariella, Diabolocovidia, Engleromyces, Entalbostroma, Entoleuca, Euepixylon, Halorosellinia, Helicogermslita, Hypocopra, Hypocreodendron , Kretzschmaria, Kretzschmariella, Leprieuria, Linosporopsis, Linteromyces, Lunatiannulus, Nemania, Neoxylaria,*	*Annulohypoxylon, Chlorostroma, Daldinia, Durotheca, Entonaema, Hypomontagnella, Hypoxylon, Jackrogersella, Natonodosa, Phylacia, Pyrenomyxa, Pyrenopolyporus, Rhopalostroma, Rostrohypoxylon, Ruwenzoria, Thamnomyces, Theissenia, Thuemenella, Induratiaceae*

	Podosordaria, Poronia, Rosellinia, Sarcoxylon, Squamotubera, Stilbohypoxylon, Vamsapriya, Virgaria , Wawelia, Xylaria, Zygosporiaceae	

In the past, Xylariales were classified solely based on their morphological traits, such as the shape of their stroma, ascospores, germination slits, stromatal pigments, and asexual morphs (Daranagama et al., 2018). However, this approach had several drawbacks. Inaccurate classification resulted due to the variety and convergence of morphological characteristics among different lineages. Additionally, these methods faced difficulties in resolving complex evolutionary connections, particularly when morphological similarities did not accurately reflect genetic relatedness (Daranagama et al., 2018; Wendt et al., 2018). As a result, researchers had to turn their attention onto molecular data for a more accurate classification.

Evolution of Xylariales species

Rogers (2000) suggests that there has been a long-standing association between Xylariales fungi and angiosperms, dating back to the early diversification of flowering plants in the Cretaceous period. This idea is supported by fossil records, which indicate a period of rapid diversification for Xylariales that coincided with the rapid radiation of angiosperms. According to Rogers (2000), there is a strong correlation between the geographic distribution of fungal species, their speciation, and their associations with specific host plants. Furthermore, he proposes that the expansion of angiosperms during the Cretaceous period likely created new ecological niches for Xylariales, enabling them to colonize further and diversify. Certain Xylariales fungi, such as *Xylaria magnoliae* and *X. persicaria*, have even developed specific adaptations to host plants and their fruits or seeds, suggesting that their lengthy evolutionary history may have facilitated co-evolution (Rogers, 2000).

According to Chen et al. (2023), interpreting evolutionary relationships within the Sordariomycetes is challenging due to incomplete phylogenetic data and the use of a limited number of genetic loci in phylogenetic analyses. However, it is necessary to make taxonomic revisions and accurately interpret evolutionary relationships because paraphyletic and polyphyletic taxa at different levels hinder the accuracy of current classifications (Chen et al., 2023). Scientists used molecular data from gene loci, such as SSU, LSU, and RPB2 loci, to trace the evolutionary relationships within the Xylariales order (Chen et al., 2023). The subclass Xylariomycetidae, to which the Xylariales order belongs, is estimated to have diverged from its closest ancestor roughly 250 million years ago (mya). Further, molecular clock investigations showed that the Amphisphaeriales and Xylariales orders diverged approximately 181 mya (Chen et al., 2023). Consistent with previous studies, the most recent common ancestor of Xylariales is thought to have existed approximately 153 million years ago (Hyde et al., 2020).

Overview of documented Xylariales species globally

Firstly, let's examine the Hypoxylaceae fungi. These fungi primarily inhabit various organic matter such as wood, leaves, and fruits, either as saprobes or endophytes. In some cases, they even form a symbiotic relationship with insects (Wibberg et al., 2021). The sexual structures of Hypoxylaceae, known as stromata, can take on different forms, including discoid, glomerate, hemispherical, or they may be absent in certain species. These stromata typically contain one to several ascomata, which are mostly black-brown and contain extractable stromal pigments (Wendt et al., 2018; Wibberg et al., 2021). There is considerable variation in the size and shape of these ascomata, ranging from globose-subglobose to elongated. The asci, which are sacs that contain spores within the ascomata, usually contain 4 to 8 spores each. They possess a single wall (unitunicate) and exhibit various shapes, from cylindrical to club-shaped (clavate), although globular shapes are rare. The attachment of the asci to the ascomata can be either via a stalk (pedicellate) or directly (apedicellate). Furthermore, the apical region of the asci may have apical rings or thickenings (Wendt et al., 2018; Hyde et al., 2020). The asexual structures, known as conidiophores, are typically hyaline or light brown, smooth in texture, and branched. They can either be mononematous (arising from a single filament) or, less commonly, synnematous (formed from multiple filaments). The conidiogenous cells have swollen apices where conidia are produced. These conidia are usually colorless and have an ellipsoidal shape (Wendt et al., 2018; Hyde et al., 2020). The type genus of Hypoxylaceae is *Hypoxylon* Bull (Hyde et al., 2020). The *Hypoxylon* genus consists of over 170 species worldwide, mainly found on decomposing wood as saprobes. They can also exist as endophytes and facultative parasites (Daranagama et al., 2018).

In a significant revision of fungal taxonomy, Wendt et al. (2018) resurrected and redefined the Hypoxylaceae family. They achieved this by conducting a multi-gene phylogenetic analysis alongside morphological data. This approach allowed for the reevaluation and reclassification of several genera within the Xylariales order. As a result, several genera were excluded from their former families and temporarily placed within Xylariales *incertaesedis*. In addition, Wendt et al. (2018) highlighted the distinct separation within the Xylariaceae, revealing the presence of several major clades. One specific clade grouped *Annulohypoxylon, Hypoxylon, Daldinia*, and related genera. These genera share characteristics such as stromatal pigments and a nodulisporium-like asexual morph (Wendt et al., 2018).

Wibberg et al. (2021) constructed the first robust phylogenomic tree for the Hypoxylaceae family using a set of amino acid sequences, rather than nucleotide sequences, of 4912 core genes from 13 Hypoxylaceae members. The members included *Annulohypoxylon truncatum, Daldinia concentrica, Entonaema liquescens, Hypoxylon fragiforme, H. lienhwacheense, H. pulicicidum, H. rickii, H. rubiginosum, Jackrogersella multiformis, Pyrenopolyporus hunteri, Xylaria hypoxylon, Hypomontagnella monticulosa, Hypomontagnella spongiphila*. Additionally, this study was the first to apply a Percentage of Conserved Proteins (POCP) analysis to evaluate evolutionary relationships at the protein level across a broader range of fungal species. Using this method, scientists discovered that the Hypoxylaceae family exhibits an impressive 70% average level of protein conservation. This shared genetic makeup suggests a common evolutionary history and highlights the close relationships between these fungi in the Hypoxylaceae family (Wibberg et al., 2021). Furthermore, Wibberg et al. (2021) proposed *Hypomontagnella spongiphila* as a new species. Its identification was previously hindered by morphological similarities to other *Hypomontagnella* species, sterile cultures, and limited genetic data. However, phylogenomic approaches, such as POCP analysis provided the necessary resolution to establish *H. spongiphila* as a distinct species. This further underscores the significance of multigene and POCP analysis in taxonomic research.

Xylariaceae fungi, like Hypoxylaceae fungi, exhibit various nutritional modes, including saprobic, pathogenic, or endophytic lifestyles. They can be found in wood, leaves, fruits, and sometimes associate with insects (Maharachchikumbura et al., 2016; Daranagama et al., 2018; Hyde et al., 2020). The stromata of Xylariaceae fungi can have different forms, such as erect, flattened, effuse-pulvinate, or may be entirely absent in some species. They can occur individually or in clusters and contain one to several ascomata with ostioles on their surface. It is important to note that most Xylariaceae fungi do not have extractable pigments (Maharachchikumbura et al., 2016; Daranagama et al., 2018; Hyde et al., 2020).

The ascomata vary in size and are typically globose or pear-shaped (pyriform). They have a single or multi-layered structure and usually contain four to eight spores. The shape of the asci can range from cylindrical to club-shaped (clavate), and they may or may not be pedicellate. The apical region of the asci is rounded and may exhibit a J+ reaction (turning blue or green with iodine), an apical ring, or apical thickenings (Maharachchikumbura et al., 2016; Daranagama et al., 2018; Hyde et al., 2020). The ascospores come in different shapes, with ellipsoidal, slightly rounded (subglobose), and kidney-shaped (reniform) being the most common. Their colors typically range from brown to black, although hyaline (colorless) ascospores are also occasionally observed. Most ascospores have a germ slit to facilitate germination, and their form can be straight, spiral, or sigmoidal. The type genus of Xylariaceae is *Xylaria Hill* ex Schrank (Maharachchikumbura et al., 2016; Daranagama et al., 2018; Hyde et al., 2020).

In 2022, a multi-gene analysis was conducted using the ITS, RPB2, and β-tubulin gene (Ma et al., 2022). This analysis led to the discovery of four new endophytic *Xylaria* species in Southwest China. These species, namely *Xylaria rogersii, X. schimicola, X. theaceicola,* and *X. wallichii*, were found to be associated with fallen fruits and seeds (Ma et al., 2022). The phylogenetic analysis of this study revealed that the four newly identified species grouped into two distinct lineages. Interestingly, these species were not confined to a single clade but formed separate clusters within three different clades of the phylogenetic tree. This suggests the occurrence of convergent evolution (Ma et al., 2022).

Molecular classification of Xylariales species

According to Suwannasai et al. (2023), the morphological characteristics of Xylariales species are crucial for their preliminary and initial identification. However, variations in these characteristics can lead to situations where fungi that appear morphologically similar belong to different genetic lineages or are cryptic species. As a result, the absence of molecular information may lead to the oversight of these cryptic taxa, resulting in incorrect taxonomic classifications. Furthermore, morphological classification can be subjective and open to different interpretations by various researchers (Suwannasai et al., 2023).

One of the earliest instances of using molecular data in the classification of Xylariales was through the analysis of DNA loci, specifically the internal transcribed spacer region (ITS) of the nuclear ribosomal DNA (rDNA) (Pelaez et al., 2008). The ITS region is located between the small subunit (SSU) and large subunit (LSU) rRNA genes. The ITS region is commonly used as a genetic marker for species identification, especially in the identification of fungi, due to its inherent sequence variability and ease of amplification (Liu et al., 1999). However, the limited sequence divergence within the ITS region restricts its use in more detailed taxonomic classifications, particularly when dealing with closely related species (Hsieh et al., 2010; Wendt et al., 2018). Consequently, researchers have turned to other DNA loci for a more precise classification.

The LSU gene (large subunit of the nuclear rDNA) is responsible for synthesizing ribosomal RNA. It has a slower evolutionary rate compared to the ITS region and provides phylogenetic resolution at deeper taxonomic levels (Wendt et al., 2018). The RPB2 gene (second largest subunit of RNA Polymerase II) is involved in transcribing messenger RNA. It is valuable for both barcoding and phylogenetic analyses as it evolves at a moderate pace and can reveal deeper fungal relationships compared to the ITS region (Suwannasai et al., 2023). The TUB2 (β-tubulin) gene codes for the Beta-tubulin protein. It exhibits a moderate evolutionary rate and complements other markers in multigene phylogenetic analyses, offering a broader understanding of fungal evolutionary relationships (Wendt et al., 2018).

Tang et al. (2009) first used the protein-coding gene loci, α-actin (ACT) and β-tubulin (TUB2), as well as the LSU and RPB2 loci, to conduct a multigene analysis of the evolutionary relationships of Xylariaceae. However, this research had shortcomings in tracing the phylogeny due to the use of unverified and different fungal specimens (Wendt et al., 2018). Subsequently, Daranagama et al. (2015) released more rDNA and RPB2 sequencing data, which addressed several of these shortcomings. As a result, a more comprehensive and accurate classification of the Xylariales order was achieved (Daranagama et al., 2018; Wendt et al., 2018; Konta et al., 2020).

Ecological importance of Xylariales species

Xylariales species as saprobes

Most of the fungi in the order Xylariales are saprobes. They can be found in wood, dung, litter, and soil, and they are often associated with insects (Hyde et al., 2020). The fact that they are saprophytic is important because it means they play a crucial role in ecosystems by breaking down complex organic matter into simpler forms that plants and other organisms can use (Suwannasai et al., 2023). These fungi produce extracellular enzymes that break down plant cell walls, aiding in decomposition and releasing important nutrients like carbon, nitrogen, and phosphorus into the soil. This nutrient cycle enhances soil fertility and supports plant growth by making these essential nutrients available for uptake (Stadler et al., 2013).

Xylariales species as endophytes

As endophytes, Xylariales fungi reside within the tissues of roots, stems, leaves, and other parts of both vascular and non-vascular plants. They play crucial ecological roles and are important to many plant species (Suwannasai et al., 2023). By enhancing the host's tolerance to biotic and abiotic stresses, endophytic Xylariales fungi can improve plant health. Additionally, they can promote plant growth by enhancing nutrient uptake, including nitrogen and phosphorus (Suwannasai et al., 2023). The identification of numerous unique secondary metabolites produced by these fungi has sparked great interest in their potential for new medication discovery (Helaly et al., 2018). According to Becker and Stadler (2021), recent discoveries of new metabolites have mainly originated from endophytic *Xylaria* isolates.

Xylariales species as pathogens

While Xylariales fungi are generally not considered aggressive pathogens, they can act as opportunistic, weakly pathogenic facultative parasites under certain conditions (Rogers, 2000). These fungi primarily cause diseases such as needle blights, root roots, and canker diseases, which ultimately impact the health and productivity of the host plant. Needle blights, for instance, are commonly associated with *Rosellinia* species. Root rot infections in various plants are often caused by *Dematophora* and *Kretzschmaria*, which belong to the Xylariaceae family and are among the most prevalent and economically damaging fungi (Sivanesan & Holliday, 1972). Canker diseases, on the other hand, are caused by Xylariales fungi, particularly members of the Graphostromataceae family within the *Biscogniauxia* and *Camillea genera* (Wendt et al., 2018).

Secondary metabolism of Xylariales species

The fungi in the Xylariales family are known for producing a wide range of secondary metabolites, which have exciting potential in medicine and biotechnology. Examples of these impressive secondary metabolites include antiparasitic nodulisporic acids and antimycotic sordarins (Helaly et al., 2018). The *Xylaria* genus in particular, is a prolific source of structurally diverse secondary metabolites with nearly 445 different compounds discovered to date, consisting of 133 terpenoids, 112 nitrogen-containing compounds, 76 lactones, 70 polyketides and 56 others (steroids, fatty acids and benzene derivatives)

(Chen et al., 2024). Of the 445 compounds characterized, 177 were discovered to exhibit a wide range of biological activities, ranging from cytotoxicity and antimicrobial properties to anti-inflammatory, enzyme inhibitory, and immunosuppressive activities (Chen et al., 2024).

Alongside traditional morphological and molecular phylogenetic methods, the chemical diversity of these metabolites has proven to be a valuable tool for studying the evolutionary relationships within the Xylariales order. By comparing secondary metabolite profiles, researchers can identify distinct metabolites at the species, genus, or family level, aiding in the reconstruction of evolutionary relationships (Helaly et al., 2018). The significant value of Xylariales' secondary metabolism lies in its enormous potential for drug discovery. These fungal metabolites demonstrate promising bioactivities and therapeutic potential, making them excellent subjects for further research and development. The extensive metabolic diversity seen in Xylariales fungi, such as *Daldinia eschscholtzii* and *Hypoxylon rickii*, emphasizes the need for ongoing exploration in this field (Helaly et al., 2018).

Xylariales in Sri Lanka

According to Wijayawardene et al. (2023), a mycological study conducted in 19th century Sri Lanka by British researchers yielded a significant collection of over 1,800 identified fungal taxa, including both ascomycetes and basidiomycetes. However, many of these taxa lack molecular data and a considerable number of them have been deemed invalid or illegitimate, necessitating modifications to the taxonomy. The taxonomic and phylogenetic research on Xylariales in Sri Lanka is currently limited. Nonetheless, there is substantial evidence supporting the existence of diverse Xylariales species in the country. Ediriweera et al. (2014) identified three *Xylaria* species in the Sigiriya wilderness based on their macromorphological and microscopic characteristics: *Xylaria polymorpha, Xylaria longipes,* and *Daldinia concentrica*. Similarly, Palapathwala et al. (2021) conducted a study and identified three *Hypoxylon* species in the Pilikuththuwa lowland wet zone forest: *Hypoxylon anthochroum, Hypoxylon flavoargillaceum,* and *Hypoxylon piceum*.

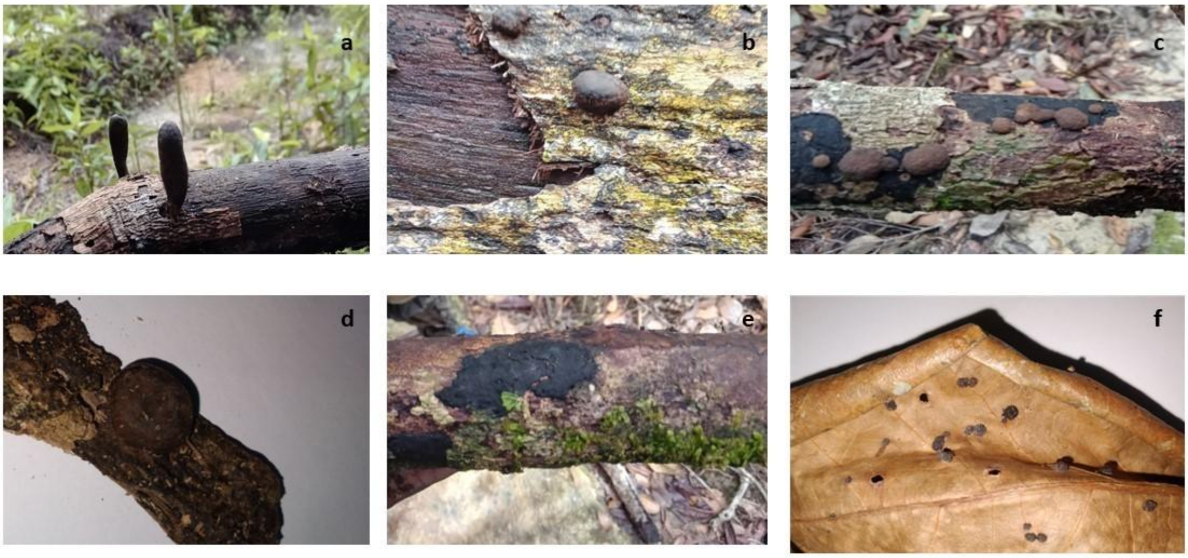

Figure 1
Diverse Xylariales species found in Sri Lanka: a: *Xylaria* sp. on decaying wood; b: *Daldinia* sp. on a log; c: *Hypoxylon* sp. on a decaying twig; d: *Daldinia* sp. e: *Biscogniauxia* sp. on a decaying trunk; f: *Annulohypoxylon* sp. on a fallen leaf

The immense potential of the secondary metabolites produced by Xylariales fungi in Sri Lanka has garnered attention from scientists over the years, which has resulted in a gradual rise of studies concerning these fungi. In one study, Fernando et al. (2016) examined the secondary metabolites and antioxidant capabilities of the endophytic white rot fungi, *Xylaria feejeensis*. These fungi were isolated from dry zone forest reserves in Dambulla and Mahiyanganaya areas of Sri Lanka. Another study conducted by Ratnaweera et al. (2014) identified certain endophytic *Xylaria* species on the *Anoectochilus setaceus*, which belongs to the Orchidae family. However, despite these findings, the full extent of the secondary metabolites produced by Xylariales fungi in Sri Lanka remains to be comprehensively explored.

Conclusion and recommendations

Xylariales fungi play crucial roles in ecosystem functioning, particularly in nutrient cycling, and their bioactive secondary metabolites holds promising applications in biotechnology. However, significant knowledge gaps persist regarding their diversity and distribution, especially in understudied regions such as Sri Lanka. To fully understand their ecological importance and unlock their potential benefits, further research employing multigene techniques is imperative. While previous studies in Sri Lanka have primarily relied on ITS1 and ITS4 regions for species identification, recent advancements demonstrate the power of multigene approaches in resolving taxonomic uncertainties and identifying novel species. Given the pivotal role of fungi in forest health and the unique biodiversity of Sri Lanka, comprehensive studies on fungal diversity, especially concerning Xylariales fungi are essential for both ecological conservation and the discovery of novel species with potential economic and medicinal values.

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