
Fungal Biodiversity and Taxonomy in Coniferous Forest Ecosystems: A Survey

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Abstract

This survey paper explores the crucial roles of fungi, particularly within the Mytiliniaceae family and Sistotrema genus, in coniferous forest ecosystems. Highlighting their contributions to nutrient cycling, soil health, and ecological interactions, the paper underscores the significance of fungal biodiversity in maintaining forest ecosystem functions. The integration of advanced methodologies, including DNA barcoding and phylogenetic analyses, has enhanced the understanding of fungal taxonomy, enabling precise classifications and uncovering evolutionary relationships. Fungi's ecological functions, such as symbiotic associations with trees and organic matter decomposition, are pivotal for forest health and resilience, supporting essential ecosystem services. Despite these advancements, challenges in fungal taxonomy and identification remain, necessitating the refinement of methodologies and the development of integrative approaches that encompass molecular, morphological, and ecological data. The ongoing discovery of new fungal species and documentation of their ecological roles highlight the need for continued research and collaboration. Future research directions include addressing taxonomic ambiguities, expanding genomic sampling, and examining environmental impacts on fungal communities, which are vital for advancing the understanding of fungal diversity and informing ecosystem management and conservation strategies.

1 Introduction

1.1 Significance of Mytiliniaceae and Sistotrema

The Mytiliniaceae family and Sistotrema genus play crucial ecological roles in coniferous forest ecosystems, significantly contributing to fungal biodiversity and ecological balance. These fungi are essential for nutrient cycling, soil health, and overall forest ecosystem functions, akin to the critical importance of accurately identifying Basidiomycota species for comprehending fungal diversity [1]. Specifically, Mytiliniaceae facilitates organic matter decomposition, nutrient release, and soil fertility enhancement, vital for forest health. Additionally, the diverse morphological and ecological traits of Sistotrema underpin its pivotal role in symbiotic relationships, such as ectomycorrhizal associations that bolster coniferous tree growth and resilience [2]. Proper classification and understanding of these taxa are imperative for advancing fungal taxonomy and integrating recent phylogenetic insights. Furthermore, the discovery of new and rare corticioid fungi, particularly in regions like Ukraine and India, emphasizes the ecological significance of these fungi and the necessity for ongoing research to address knowledge gaps and deepen our understanding of fungal biodiversity in coniferous forests.

1.2 Importance of Studying Fungi in Coniferous Forests

Studying fungi in coniferous forest ecosystems is essential for a thorough understanding of biodiversity and ecosystem functioning. The Mytiliniaceae family and corticioid fungi are integral to decomposition processes and nutrient cycling, which are crucial for soil health and forest sustainability. Their contributions underscore the need for detailed studies [3]. The limited knowledge of

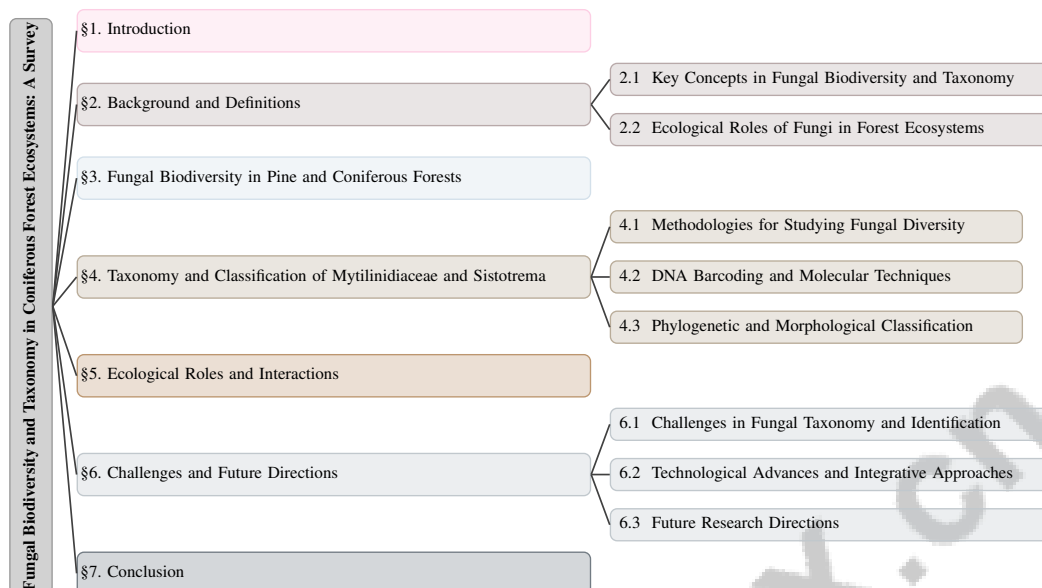


Figure 1: chapter structure

fungal biodiversity, especially in under-researched areas like the Southern Hemisphere, highlights the importance of targeted research to bridge these gaps [4]. Investigating fungal species is vital not only for understanding their ecological roles but also for discovering new and unrecorded species that can provide insights into ecosystem dynamics and species interactions. Additionally, the implications of fungal biodiversity on soil health and the effects of land-use changes on fungal communities further accentuate the significance of fungi in both managed and natural ecosystems [5]. Understanding speciation within genera such as *Hydnum* enhances recognition of species diversity and habitat structure, contributing to broader ecological and conservation objectives [6]. Collectively, these factors highlight the critical need for ongoing research and documentation of fungi in coniferous forests to elucidate their ecological importance and inform conservation strategies.

1.3 Structure of the Survey

This survey is systematically organized to provide a thorough exploration of fungal biodiversity and taxonomy within coniferous forest ecosystems. The introductory section highlights the significance of the Mytiliniaceae family and *Sistotrema* genus, clarifying their ecological roles and the necessity of studying fungi in these environments. The subsequent background and definitions section presents key concepts related to fungal biodiversity, taxonomy, and forest ecosystems, alongside a discussion on the ecological roles of fungi. The survey further examines fungal biodiversity in pine and coniferous forests, exploring species diversity, influencing factors, and the role of fungi in nutrient cycling and soil health. Following this, sections focus on the taxonomy and classification of the Mytiliniaceae family and *Sistotrema* genus, detailing methodologies, DNA barcoding, molecular techniques, and approaches to phylogenetic and morphological classification. The ecological roles and interactions section investigates fungi's interactions with other organisms, specifically the roles of endophytic and corticioid fungi. The survey concludes by addressing challenges and future directions, discussing current limitations in fungal taxonomy, the impact of technological advances, and suggesting areas for future research. The conclusion synthesizes key findings and emphasizes the importance of understanding fungal biodiversity and taxonomy for conservation and ecosystem management. The following sections are organized as shown in Figure 1.

2 Background and Definitions

2.1 Key Concepts in Fungal Biodiversity and Taxonomy

Fungal biodiversity and taxonomy are pivotal for classifying fungi within forest ecosystems. Basidiomycota species identification is complex due to variability in the ITS region, complicating

DNA barcoding [1]. This necessitates integrating molecular and morphological data, as seen in the Gloniaceae family [7]. High-throughput sequencing (HTS) has expanded our understanding of fungal communities but introduces biases that must be managed [8]. Bayesian nonparametric modeling assists in estimating species richness through accumulation curves, capturing distinct fungal entities [9]. The speciation of *Hydnum*, influenced by ecological and morphological traits, exemplifies the intricate biodiversity and taxonomy relationships [6]. Studies of ectomycorrhizal fungi in southern South America emphasize geographic context in biodiversity [4]. The underexplored corticioid fungi in Ukraine highlight the need for comprehensive biodiversity concept definitions [2]. Current models' limitations in accommodating an unbounded number of species in joint species distribution analysis call for more inclusive approaches to account for rare and newly discovered species [10]. These concepts collectively provide a framework for understanding fungi's ecological roles and evolutionary relationships within forest ecosystems [11].

2.2 Ecological Roles of Fungi in Forest Ecosystems

Fungi are crucial in forest ecosystems, influencing biodiversity and conservation strategies through their interactions and impacts on ecosystem health [3]. The interplay of marine and terrestrial influences results in diverse fungal communities, adding complexity to ecological frameworks [12]. Fungi, including corticioid species like *Kavinia alboviridis* and *Sistotrema porulosum*, are vital for nutrient cycling and organic matter decomposition, breaking down dead wood from various trees.

HTS technologies reveal vast fungal diversity but face challenges in accurately depicting ecological roles due to inherent biases [8]. Fungal biodiversity is essential for soil health, though complex interactions present research challenges [5]. Microbial interactions during early pine litter decomposition highlight fungi's role in ecosystem dynamics [13].

Associating environmental DNA sequences with known species is challenging, especially with potential species extinction due to habitat loss and climate change, underscoring fungi's ecological importance [4]. Difficulty in discovering novel species, modeled by Bayesian methods, reflects the challenges in capturing fungal biodiversity [9].

Additionally, insufficient studies on endophytic fungi in medicinal crops limit understanding of their ecological roles, revealing research gaps [14]. Fixed species lists in biodiversity studies often overlook rare species, crucial for a complete understanding [10]. Subjective taxonomic interpretations and incomplete knowledge of fungal diversity complicate ecological role understanding [15]. Limited genomic data for some taxa leads to ambiguities in phylogenetic placements, hindering support for evolutionary hypotheses and complicating ecological assessments [11]. These factors underscore fungi's indispensable roles in forest ecosystems and the need for ongoing research to fully comprehend their contributions to ecosystem health and resilience.

3 Fungal Biodiversity in Pine and Coniferous Forests

3.1 Diversity of Fungal Species

The diversity of fungal species in coniferous forests embodies the intricate ecological interactions and evolutionary dynamics of these ecosystems. Fungi are pivotal in maintaining forest biodiversity and contribute significantly to species richness [3]. Transitional habitats, such as lakes, have been identified as biodiversity hotspots, hosting a wide array of fungal taxa [12]. Advanced methodologies, including Bayesian nonparametric modeling, have refined species richness estimation, providing insights into fungal diversity that surpass traditional techniques like the Dirichlet and Pitman-Yor processes, as evidenced by Finnish data [9].

Discoveries in Ukraine, such as *Kavinia alboviridis* and rare species like *Sistotrema porulosum* and *Lobulicium occultum*, highlight efforts to document fungal diversity [16]. Research in India further illustrates this richness with the identification of new corticioid fungi species [17]. These findings underscore the necessity for ongoing exploration in these ecosystems [2]. An examination of 222 *Hydnum* specimens from various locations provides a comprehensive view of species diversity, reflecting the complex ecological and evolutionary dynamics sustaining this diversity [6]. These studies collectively highlight the extensive fungal biodiversity in coniferous forests and the need for continued research to fully understand their ecological roles.

3.2 Factors Influencing Fungal Diversity

Fungal diversity in coniferous forests is shaped by environmental conditions and forest management practices. A primary challenge in studying these communities is obtaining high-quality DNA from coniferous litter, crucial for microbial community analysis [13]. Climate, soil composition, and moisture levels critically influence fungal diversity by affecting nutrient availability and habitat suitability, thus determining community composition and dynamics.

Forest management practices, such as logging and reforestation, alter habitat structures and resource availability. The introduction of non-native species and shifts in forest composition can disrupt fungal community structures, potentially reducing diversity and ecosystem stability. Habitat fragmentation may isolate fungal populations, restricting gene flow and reducing genetic diversity, ultimately undermining the resilience of these organisms involved in nutrient cycling and symbiotic relationships with plants [8, 4, 3].

Interactions between fungi and other organisms, such as trees and soil microbes, are crucial for shaping fungal diversity, influencing nutrient cycling, ecosystem health, and symbiotic partnerships. Over 80% of plant species form beneficial associations with fungi, playing a vital role in terrestrial ecosystem colonization and maintenance [4, 5]. Disturbances that disrupt these interactions, such as soil compaction and pollution, can adversely affect fungal diversity and ecosystem health.

Understanding the factors influencing fungal diversity in coniferous forests requires a holistic approach considering environmental conditions and human activities. This understanding is critical for developing effective conservation strategies and management practices that enhance the preservation of fungal species and the ecological functions they fulfill. By leveraging advanced techniques like DNA barcoding and high-throughput sequencing, we can better document and interpret fungal diversity, improving conservation outcomes in forested habitats [8, 5, 4, 3].

3.3 Role in Nutrient Cycling and Soil Health

Fungi are essential for nutrient cycling and maintaining soil health in coniferous forest ecosystems, serving as primary decomposers of organic matter and facilitators of nutrient availability. The decomposition process involves dynamic shifts in microbial communities, with specialized fungal species emerging at various stages to break down complex organic compounds, underscoring the sequential nature of decomposition and nutrient release [13].

As illustrated in Figure 2, the multifaceted roles of fungi in soil ecosystems encompass their contributions to nutrient cycling, soil health, and ecosystem resilience. Key functions highlighted in the figure include decomposition processes, disease suppression, and symbiotic relationships, all vital for maintaining biodiversity and promoting sustainable agricultural practices.

Species such as *Kavinia albobiridis*, thriving on dead wood from both deciduous and coniferous trees, exemplify fungi's role in nutrient cycling through white rot, which degrades lignin and cellulose, recycling essential nutrients, and contributing to soil organic matter formation, thus enhancing soil structure and fertility [2].

Current research highlights fungi's multifaceted roles beyond decomposition, including disease suppression and soil structure formation, which are vital for ecosystem resilience and sustainable agricultural practices. By improving soil aggregation and porosity, fungi enhance water retention and root penetration, promoting plant growth and ecosystem productivity [5].

Interactions between fungi and other soil organisms further amplify their impact on nutrient cycling and soil health. Mycorrhizal associations facilitate nutrient exchange between fungi and host plants, enhancing nutrient uptake and promoting plant health. These symbiotic relationships among fungi, plants, and other organisms are critical for maintaining the stability and sustainability of forest ecosystems, especially as they face increasing pressures from changing environmental conditions. Such interactions support not only nutrient cycling and soil health but also overall biodiversity, essential for the resilience of forest habitats in the face of ecological challenges [13, 4, 5, 3, 10].

Fungi are crucial components of soil microbiota, influencing ecological processes through their diverse functions, including facilitating organic matter decomposition and forming symbiotic relationships with over 80% of plant species. Given that a significant number of fungal species remain undescribed and ongoing land-use shifts impact their diversity, continued research is essential to elucidate their

ecological roles, informing effective ecosystem management and conservation strategies in the context of climate change and habitat degradation [13, 3, 4, 5].

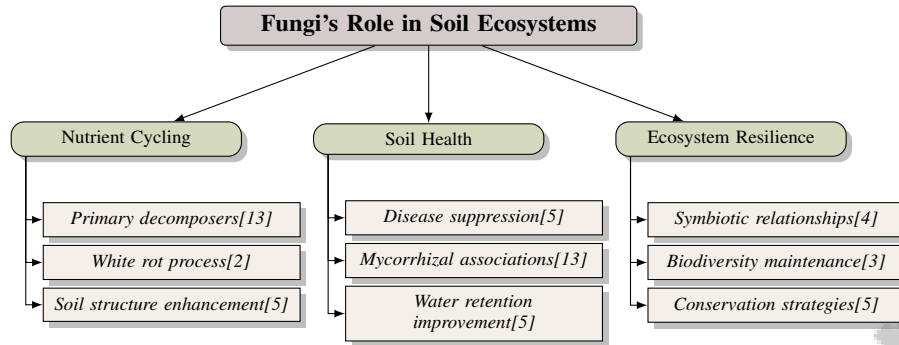


Figure 2: This figure illustrates the multifaceted roles of fungi in soil ecosystems, highlighting their contributions to nutrient cycling, soil health, and ecosystem resilience. Key functions include decomposition processes, disease suppression, and symbiotic relationships, all vital for maintaining biodiversity and promoting sustainable agricultural practices.

4 Taxonomy and Classification of Mytilinidiaceae and Sistotrema

The classification and relationships within the Mytilinidiaceae family and *Sistotrema* genus are best understood through an integrated approach, combining phylogenetic and morphological analyses. This dual perspective clarifies species boundaries and evolutionary dynamics, offering insights into fungal taxonomy and ecology. Table 1 offers a comparative overview of the primary methodologies used in fungal diversity research, detailing their core techniques and limitations. The following subsection delves into methodologies for studying fungal diversity, emphasizing the integration of both traditional and modern techniques.

4.1 Methodologies for Studying Fungal Diversity

Fungal diversity research in coniferous forests employs a blend of traditional and modern methodologies to achieve a comprehensive understanding of fungal taxonomy. A polyphasic approach, incorporating morphological, biochemical, and molecular methods, is increasingly preferred for its effectiveness in identifying and classifying fungi [18]. This strategy is crucial for understanding evolutionary relationships, as demonstrated by studies utilizing morphological characterization alongside multigene phylogenetic analysis [7].

DNA barcoding, integrated with traditional field inventories, exemplifies the synergy between modern sequence-based classifications and specimen-based approaches, enhancing our grasp of fungal diversity [4]. However, sole reliance on DNA sequences for taxonomy raises concerns about altering nomenclatural types, potentially leading to confusion [19]. Current nomenclature rules, which disallow formal descriptions based solely on sequence data, highlight the necessity for a balanced approach incorporating both molecular and morphological data [20].

High-throughput sequencing (HTS) technologies have transformed fungal community studies, offering detailed diversity insights despite biases in extraction, amplification, and sequencing [8]. Hierarchical classification systems incorporating phylogenetic data and divergence times enhance understanding of fungal relationships and ecological analyses [21]. Pure culture techniques have been pivotal in refining fungal taxonomy, as seen in *Hydnum* speciation studies [6].

Innovative models like TRACE, using latent Gaussian constructions, adapt to new discoveries by modeling binary species occurrences without pre-specified identities, enriching fungal diversity dynamics understanding [10]. The categorization of corticioid fungi based on ecological roles and morphological traits underscores their significance in ecosystem dynamics and taxonomy.

As depicted in Figure 3, this figure illustrates the diverse methodologies employed in studying fungal diversity, highlighting the polyphasic approach, DNA barcoding, and high-throughput sequencing as key strategies. Each method integrates various techniques to enhance the understanding of

fungal taxonomy and ecology. These methodologies collectively provide a comprehensive toolkit for studying fungal diversity, emphasizing the importance of integrating multiple approaches to capture the complexity of fungal taxonomy and ecology. The figures illustrate key tools in this field: a dendrogram representing hierarchical clustering and genetic similarities among fungal groups, and a bar and pie chart depicting bacterial OTU distribution in a sampled region, offering insights into OTU abundance and diversity. These methodologies underscore the intricate relationships and classifications within the fungal kingdom, laying a foundation for further exploration and understanding of fungal diversity [20, 4].

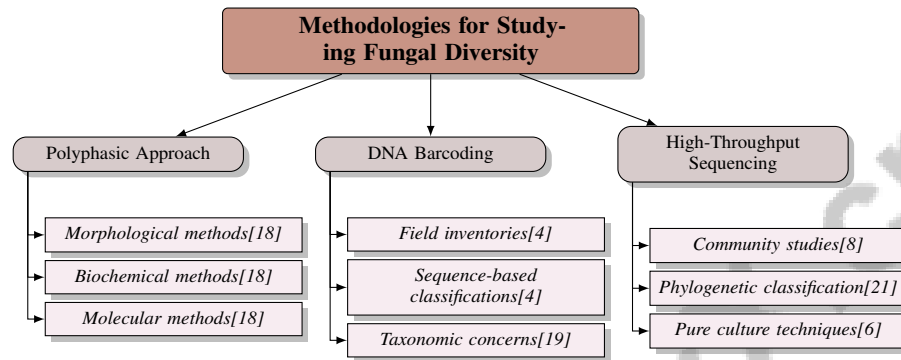


Figure 3: This figure illustrates the diverse methodologies employed in studying fungal diversity, highlighting the polyphasic approach, DNA barcoding, and high-throughput sequencing as key strategies. Each method integrates various techniques to enhance the understanding of fungal taxonomy and ecology.

4.2 DNA Barcoding and Molecular Techniques

Advancements in DNA barcoding and molecular techniques have significantly improved fungal species classification and identification, particularly within Basidiomycota. The complete internal transcribed spacer (ITS) region, including ITS1 and ITS2 sub-regions, serves as effective genomic markers for species identification, highlighting DNA barcoding's utility in fungal taxonomy [1]. However, reliance on DNA sequences as taxonomic types sparks debate, as it may undermine traditional classification stability [19]. Proposals to improve molecular identification-based nomenclature aim to enhance consistency and reliability [20].

Integrating molecular data into hierarchical classification systems has facilitated dated phylogeny construction, yielding clearer insights into evolutionary relationships and aiding consensus classification development. This approach categorizes research by integrating genotypic data from DNA sequencing, phenotypic traits, chemotaxonomic markers, and phylogenetic analysis, establishing a comprehensive framework for fungal classification that enhances species identification and synonym verification while addressing traditional morphological method limitations [18, 4].

High-throughput sequencing (HTS) technologies have revolutionized fungal diversity studies, despite inherent biases in extraction, amplification, and sequencing processes. Comparative analyses of various HTS methods highlight their strengths and weaknesses, emphasizing the need for careful sequencing platform selection to effectively capture fungal diversity [8]. Molecular phylogenetic analyses have demonstrated genera monophyly, such as in *Hydnum*, facilitating new species identification and showcasing DNA barcoding and molecular technique advancements [6].

Simulation studies assessing modeling frameworks' performance in predicting new species discovery contribute to understanding species distribution and occurrence probabilities [10]. Collectively, these advancements underscore DNA barcoding and molecular techniques' critical role in enhancing fungal classification, addressing knowledge gaps, and overcoming field challenges [22].

4.3 Phylogenetic and Morphological Classification

Fungal classification within coniferous forest ecosystems, particularly in the *Mytiliniaceae* family and *Sistotrema* genus, relies on phylogenetic and morphological approaches to accurately delineate

species boundaries and understand evolutionary relationships. Integrating morphological characteristics with molecular data is essential for a comprehensive understanding of species diversity and classification [14]. This approach involves isolation, morphological observation, and molecular identification stages, utilizing morphological traits and genetic sequencing for accurate species delineation.

Despite molecular technique advancements, reliance solely on DNA sequences for species recognition remains contentious. Physical specimens are argued to underpin species recognition protocols, as DNA sequences may not fully capture fungal community taxonomic diversity [19]. This perspective highlights the importance of combining morphological and molecular data for a robust classification framework.

Genomic markers like the complete ITS region are critical for Basidiomycota taxonomy and classification, emphasizing careful marker selection for accurate species identification [1]. However, sequence-based nomenclature for unculturable taxa reflects a shift towards integrating molecular data into traditional classification systems while recognizing current methodology limitations [20].

Phylogenetic and morphological classification of coniferous forest fungi requires a balanced approach leveraging both methodologies' strengths. This integrative strategy enhances understanding of fungal diversity and evolutionary relationships by combining field inventories with DNA-barcoding techniques, effectively addressing molecular data reliance limitations, such as the inability to connect many environmental sequences to known fungal species, ensuring a comprehensive and accurate classification system. This approach reveals fungi's vast, largely uncharted diversity—estimated at up to 3.8 million species—and facilitates deeper insights into their ecological roles and interactions within ecosystems [4, 8].

Feature	Methodologies for Studying Fungal Diversity	DNA Barcoding and Molecular Techniques	Phylogenetic and Morphological Classification
Primary Focus	Fungal Taxonomy	Species Classification	Species Boundaries
Core Technique	Polyphasic Approach	Dna Barcoding	Integrative Strategy
Key Limitation	Dna Sequence Reliance	Classification Stability	Molecular Reliance

Table 1: This table presents a comparative analysis of methodologies employed in studying fungal diversity, focusing on the primary features of fungal taxonomy, species classification, and species boundaries. It highlights the core techniques and key limitations associated with each methodology, providing insights into the strengths and challenges of integrating polyphasic approaches, DNA barcoding, and phylogenetic strategies.

5 Ecological Roles and Interactions

5.1 Fungal Interactions with Other Organisms

Fungi within coniferous forests are pivotal for ecological balance, primarily through symbiotic relationships like mycorrhizal associations, exemplified by the genus *Hydnum*, which enhance nutrient exchange and plant vitality, thereby supporting forest resilience [6]. Beyond symbiosis, fungi are essential for decomposing organic matter, a critical process for nutrient cycling and soil health that supports plant growth and microbial diversity [13, 4, 5]. These interactions form complex networks among soil microorganisms, adapting to environmental changes and enhancing soil resilience.

Research into fungal biodiversity underscores the need to understand these interactions for improved soil management in both agricultural and natural settings. Despite their importance, significant gaps remain in understanding certain fungi's ecological roles, particularly in under-explored regions like Ukraine [16]. Addressing these gaps is crucial for comprehending fungi's full contributions to forest ecosystems.

Exploring fungal interactions deepens our understanding of their ecological roles, especially in coniferous forests, and emphasizes fungi's potential as biodiversity surrogates in conservation. With many fungal species undescribed and their ecological functions emerging, continued research is vital for effective conservation and management strategies, ensuring forest ecosystem sustainability amid environmental changes [8, 5, 4, 3].

5.2 Endophytic and Corticioid Fungi

Endophytic and corticioid fungi are crucial to forest ecosystems, enhancing ecological balance and biodiversity. Endophytic fungi, residing in plant tissues without harm, improve plant health by boosting tolerance to environmental stress, nutrient uptake, and pathogen resistance, thus supporting forest stability and productivity [13, 4, 3, 5, 8]. Their presence across various plant species highlights their ecological significance and potential for sustainable forestry and agriculture.

Corticioid fungi, with their crust-like fruiting bodies, are key decomposers, breaking down lignocellulosic materials and contributing to nutrient cycling and soil health. Species like *Kavinia albobiridis* and *Sistotrema porulosum* exemplify their role in decomposing deadwood from both deciduous and coniferous trees, releasing nutrients back into the ecosystem. Discovering new corticioid species in regions such as Ukraine underscores the need for continued documentation to fully understand their ecological roles [16].

Interactions between endophytic and corticioid fungi and other forest organisms are crucial for nutrient cycling, plant health, and biodiversity. Endophytic fungi influence plant community dynamics, while corticioid fungi form networks with other decomposers and soil organisms, regulating nutrient cycling and ecosystem function [4, 14, 17, 5, 3]. Studying these fungi is essential for understanding their diverse ecological functions, which enhance biodiversity and ecosystem resilience [5, 4, 3]. Continued research and documentation are vital to uncover their full ecological contributions, informing conservation and management strategies for preserving forest biodiversity and health.

In recent years, the field of fungal taxonomy has faced numerous challenges that hinder its advancement. These challenges are not only methodological but also ecological and taxonomic in nature. To elucidate these complexities, Figure 4 illustrates the hierarchical structure of challenges, technological advances, and future research directions in fungal taxonomy and identification. This figure effectively highlights key issues such as methodological constraints, taxonomic ambiguities, and ecological challenges. Moreover, it emphasizes the pivotal role of high-throughput sequencing, integrative approaches, and innovative modeling frameworks in propelling the field forward. As depicted, future research directions aim to refine methodologies, enhance our understanding of ecological interactions, and improve taxonomic accuracy, thereby addressing the pressing issues currently faced in the discipline.

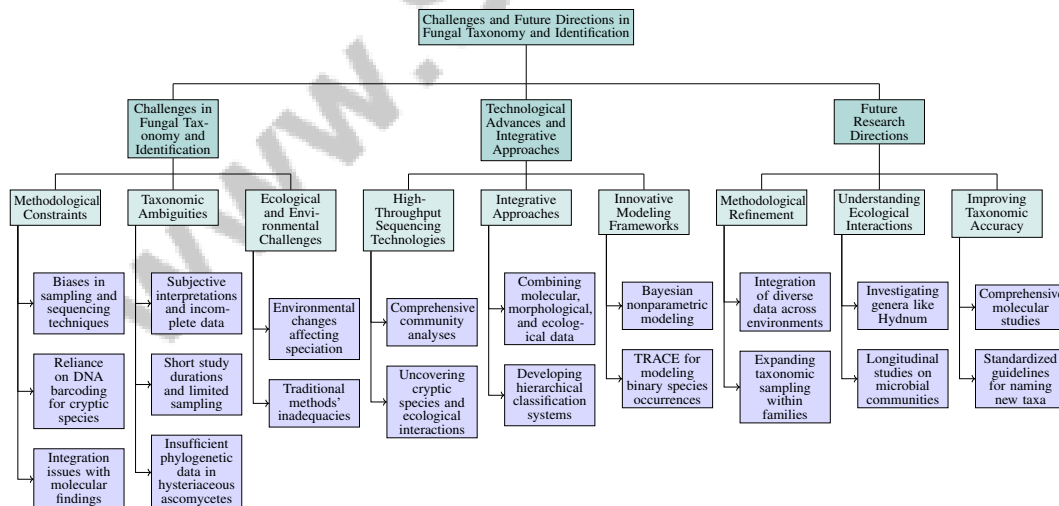


Figure 4: This figure illustrates the hierarchical structure of challenges, technological advances, and future research directions in fungal taxonomy and identification. It highlights methodological constraints, taxonomic ambiguities, and ecological challenges as primary issues, while emphasizing the role of high-throughput sequencing, integrative approaches, and innovative modeling frameworks in advancing the field. Future research directions focus on refining methodologies, understanding ecological interactions, and improving taxonomic accuracy.

6 Challenges and Future Directions

6.1 Challenges in Fungal Taxonomy and Identification

Fungal taxonomy and identification are impeded by methodological constraints and ambiguities within taxonomic classifications. Challenges arise from biases in sampling, sequencing techniques, and reference database availability, which obscure true diversity and ecological understanding [8]. The reliance on DNA barcoding is particularly problematic for cryptic species—those morphologically similar yet genetically distinct—complicating traditional identification methods [5]. Morphological diversity, especially among corticioid fungi, necessitates molecular phylogenetic approaches to validate traditional identifications [17]. However, integrating molecular findings into established taxonomies is often obstructed by subjective interpretations and incomplete data, leading to unresolved relationships within certain taxa. Short study durations and limited sampling may fail to capture microbial succession complexity, complicating efforts to understand fungal diversity and ecological roles [13]. Hierarchical structures used in correlation methods pose computational challenges, particularly with large datasets, limiting scalability [10]. Taxonomic ambiguity within hysteriaceae ascomycetes, due to insufficient phylogenetic data, exemplifies broader challenges in fungal taxonomy [7]. Ecological interactions and environmental changes affecting speciation, as seen in genera like *Hydnum*, underscore the need for further exploration [6]. Approximately 90% of fungal species remain undescribed, highlighting traditional methods' inadequacies, often relying solely on morphological traits that can mislead due to convergent evolution. Molecular approaches, such as DNA barcoding and high-throughput sequencing, provide powerful tools for uncovering hidden diversity but also present challenges in accurately associating environmental sequences with known taxa. A comprehensive, integrative approach to fungal identification is essential for enhancing our understanding of their ecological roles and improving conservation efforts [20, 4, 8, 22, 3].

6.2 Technological Advances and Integrative Approaches

Recent technological advancements have transformed fungal biodiversity and taxonomy studies, providing novel insights and expanding research scope. High-throughput sequencing (HTS) technologies enable comprehensive community analyses, despite biases in extraction, amplification, and sequencing processes [8]. These technologies facilitate exploration of fungal diversity at unprecedented scales, uncovering cryptic species and complex ecological interactions previously inaccessible. Integrative approaches combining molecular, morphological, and ecological data are crucial for addressing traditional methodologies' limitations and enhancing classification accuracy. DNA barcoding, particularly using the complete internal transcribed spacer (ITS) region, has proven effective for identifying Basidiomycota species [1]. However, reliance on DNA sequences has sparked debate regarding taxonomic classifications' stability and reliability [19]. Proposals to improve nomenclature based solely on molecular identification aim to enhance consistency in fungal taxonomy [20]. Developing hierarchical classification systems incorporating phylogenetic data and divergence times offers clearer insights into fungal relationships and facilitates ecological analyses [21]. This approach integrates genotypic, phenotypic, chemotaxonomic, and phylogenetic information, providing a comprehensive classification framework [18]. Bayesian nonparametric modeling estimates species richness, capturing the sequential recording of distinct fungal entities and offering a nuanced understanding of diversity dynamics [9]. Innovative modeling frameworks like TRACE utilize latent Gaussian constructions to model binary species occurrences without pre-specifying identities, adapting to new discoveries and enhancing understanding of diversity dynamics [10]. These integrative approaches and technological innovations collectively underscore the potential for new methodologies to overcome existing challenges in fungal studies, providing a more comprehensive understanding of biodiversity and taxonomy.

6.3 Future Research Directions

Future research in fungal biodiversity and taxonomy should refine methodologies to address current limitations, emphasizing the integration of molecular, morphological, and ecological data across diverse environments. Expanding taxonomic sampling within families like Gloniaceae is crucial for refining classifications and understanding phylogenetic relationships, enhancing our comprehension of fungal diversity [7]. Investigating ecological interactions of genera like *Hydnum* with various host species, alongside the impact of environmental changes on their speciation, will yield insights into

adaptive mechanisms and evolutionary trajectories in forest ecosystems [6]. Longitudinal studies are essential for capturing the full dynamics of microbial communities in litter decomposition, focusing on different microbial groups' functional roles in nutrient cycling. Comprehensive methodologies for assessing fungal functions in soil ecosystems are critical, especially considering climate change's effects on biodiversity. Fungi play vital roles in carbon and nutrient cycling, and their interactions with plants are essential for ecosystem stability and health. Current research emphasizes shifting from merely cataloging species to understanding their functional roles and interactions within soil ecosystems, particularly given that over 80% of plant species engage in symbiotic relationships with fungi, yet only about 10% of fungal species have been described. Advanced techniques like DNA barcoding and next-generation sequencing can enhance our understanding of these complex relationships and support soil health conservation amidst environmental changes [4, 5]. These studies should promote practices that enhance fungal diversity in agricultural settings, thereby supporting ecosystem resilience and productivity. Refining predictive models, including exploring alternative approaches for correlation structures, is critical for improving computational efficiency and facilitating routine application in ecological studies. Addressing taxonomic ambiguities through comprehensive molecular studies, including DNA barcoding and phylogenetic analyses, while establishing clear and standardized guidelines for naming new taxa, will improve accuracy and reliability in species identification. This dual approach will facilitate effective communication and documentation of fungal diversity, particularly for lineages currently represented only by sequence data. By integrating molecular and phenotypic data, researchers can achieve a more consistent framework for understanding biodiversity, crucial given that an estimated 90% of fungal species remain undescribed [20, 22, 4]. Increasing genomic sampling across diverse fungal taxa is essential for resolving contentious phylogenetic relationships and expanding our understanding of evolution and diversity. Collaborative research efforts will enhance our comprehensive understanding of fungal diversity, estimated to include up to 3.8 million species, and elucidate their critical roles in ecosystem dynamics, such as nutrient cycling and symbiotic relationships with over 80% of plant species. This underscores the necessity for ongoing investigation and interdisciplinary partnerships in mycology and conservation biology [8, 5, 4, 3].

7 Conclusion

The survey underscores the pivotal roles played by fungi, particularly within the Mytiliniaceae family and Sistotrema genus, in coniferous forest ecosystems. The application of advanced methodologies, such as DNA barcoding and phylogenetic analysis, has significantly expanded our knowledge regarding fungal diversity and their crucial contributions to nutrient cycling, soil vitality, and ecological interactions, thereby advancing our comprehension of fungal taxonomy and evolutionary dynamics. The ecological functions of fungi, including their symbiotic partnerships with trees and their role in organic matter decomposition, are fundamental to maintaining the health and resilience of forest ecosystems. These interactions are vital for promoting biodiversity and supporting essential ecosystem services, which are critical for effective conservation and management of forested areas. Despite these advancements, challenges in fungal taxonomy and species identification persist, necessitating the development of refined methodologies and integrative approaches that incorporate molecular, morphological, and ecological data. The ongoing discovery of new fungal species and their ecological roles highlights the importance of continued research and collaboration in the fields of fungal biodiversity and taxonomy. Future research efforts should focus on resolving taxonomic ambiguities, expanding genomic sampling, and evaluating the effects of environmental changes on fungal communities. Such initiatives are essential for enhancing our understanding of fungal diversity and informing strategies for ecosystem management and conservation.

References

- [1] Fernanda Badotti, Francislon Silva de Oliveira, Cleverson Fernando Garcia, Aline Bruna Martins Vaz, Paula Luize Camargos Fonseca, Laila Alves Nahum, Guilherme Oliveira, and Aristóteles Góes-Neto. Effectiveness of its and sub-regions as dna barcode markers for the identification of basidiomycota (fungi). *BMC microbiology*, 17:1–12, 2017.
- [2] . . . , (74, № 3):293–297, 2017.
- [3] Panu Halme, Jan Holec, and Jacob Heilmann-Clausen. The history and future of fungi as biodiversity surrogates in forests. *Fungal Ecology*, 27:193–201, 2017.
- [4] Camille Truong, Alija B Mujic, Rosanne Healy, Francisco Kuhar, Giuliana Furci, Daniela Torres, Tuula Niskanen, Pablo A Sandoval-Leiva, Natalia Fernández, Julio M Escobar, et al. How to know the fungi: combining field inventories and dna-barcoding to document fungal diversity. *New Phytologist*, 214(3):913–919, 2017.
- [5] Magdalena Fraç, Silja E Hannula, Marta Bełka, and Małgorzata Jędryczka. Fungal biodiversity and their role in soil health. *Frontiers in microbiology*, 9:707, 2018.
- [6] and . *Hydnum* .
- [7] Subashini C Jayasiri, Kevin D Hyde, EB Gareth Jones, Hiran A Ariyawansae, Ali H Bahkali, Abdallah M Elgorban, and Ji-Chuan Kang. A new hysteriform dothideomycete (gloniaceae, pleosporomycetidae incertae sedis), *purpurepithecium murisporum* gen. et sp. nov. on pine cone scales. *Cryptogamie, Mycologie*, 38(2):241–251, 2017.
- [8] R Henrik Nilsson, Sten Anslan, Mohammad Bahram, Christian Wurzbacher, Petr Baldrian, and Leho Tedersoo. Mycobiome diversity: high-throughput sequencing and identification of fungi. *Nature Reviews Microbiology*, 17(2):95–109, 2019.
- [9] Alessandro Zito, Tommaso Rigon, Otso Ovaskainen, and David Dunson. Bayesian nonparametric modelling of sequential discoveries, 2020.
- [10] Federica Stolf and David B. Dunson. Infinite joint species distribution models, 2024.
- [11] Timothy Y James, Jason E Stajich, Chris Todd Hittinger, and Antonis Rokas. Toward a fully resolved fungal tree of life. *Annual Review of Microbiology*, 74(1):291–313, 2020.
- [12] Olga A Grum-Grzhimaylo, Alfons JM Debets, and Elena N Bilanenko. Mosaic structure of the fungal community in the kisko-sladoe lake that is detaching from the white sea. *Polar Biology*, 41(10):2075–2089, 2018.
- [13] Marcin Gołębiewski, Agata Tarasek, Marcin Sikora, Edyta Deja-Sikora, Andrzej Tretyn, and Maria Niklińska. Rapid microbial community changes during initial stages of pine litter decomposition. *Microbial Ecology*, 77:56–75, 2019.
- [14] Hyeok Park, Chung Ryul Jung, and Ahn-Heum Eom. Three novel endophytic fungal species isolated from roots of medicinal crops in korea. *The Korean Journal of Mycology*, 47(2):113–120, 2019.
- [15] Nalin N Wijayawardene, Armin Mešić, Ana Pošta, Zdenko Tkalčec, and M Thines. Outline of fungi and fungus-like taxa–2021. 2022.
- [16] MV Shevchenko. New and rare for ukraine records of corticioid fungi. *Ukrainian Botanical Journal*, 74(3):293–297, 2017.
- [17] Avneet Pal Singh, Gurpaul Singh Dhingra, et al. Six new reports of corticioid fungi from india. *Journal of Threatened Taxa*, 16(12):26272–26282, 2024.
- [18] Jayoung Kim. Fungal identification based on the polyphasic approach: a clinical practice guideline. *Annals of Clinical Microbiology*, 27(4), 2024.

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- [19] Juan Carlos Zamora, Måns Svensson, Roland Kirschner, Ibai Olariaga, Svengunnar Ryman, Luis Alberto Parra, József Geml, Anna Rosling, Slavomír Adamčík, Teuvo Ahti, et al. Considerations and consequences of allowing dna sequence data as types of fungal taxa. *IMA fungus*, 9:167–175, 2018.
- [20] Robert Lücking, M Catherine Aime, Barbara Robbertse, Andrew N Miller, Takayuki Aoki, Hiran A Ariyawansa, Gianluigi Cardinali, Pedro W Crous, Irina S Druzhinina, David M Geiser, et al. Fungal taxonomy and sequence-based nomenclature. *Nature microbiology*, 6(5):540–548, 2021.
- [21] Leho Tedersoo, Santiago Sánchez-Ramírez, Urmas Kõljalg, Mohammad Bahram, Markus Döring, Dmitry Schigel, Tom May, Martin Ryberg, and Kessy Abarenkov. High-level classification of the fungi and a tool for evolutionary ecological analyses. *Fungal diversity*, 90:135–159, 2018.
- [22] Robert Lücking, M Catherine Aime, Barbara Robbertse, Andrew N Miller, Hiran A Ariyawansa, Takayuki Aoki, Gianluigi Cardinali, Pedro W Crous, Irina S Druzhinina, David M Geiser, et al. Unambiguous identification of fungi: where do we stand and how accurate and precise is fungal dna barcoding? *IMA fungus*, 11(1):14, 2020.

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