A Review Of Biosystematics, Phylogeny, And Ethnopharmacognostic Potential Of Sphaeropteris Moluccana: Implications For Drug Discovery

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Abstract—Sphaeropteris moluccana, an arborescent fern of the family Cyatheaceae, is widely distributed in the Malesian region yet remains underrepresented in integrative biological and pharmacological research. This review synthesizes biosystematic knowledge on S. moluccana published over the last decade (2015–2025), with emphasis on morphological taxonomy, molecular phylogenetics, and ethnopharmacognosy, to evaluate its evolutionary significance and bioactive potential. A systematic literature survey was conducted using Scopus-indexed publications, focusing on taxonomic revisions, phylogenetic analyses, and ethnobotanical and pharmacological studies related to Sphaeropteris and allied taxa. Recent morphological assessments, combined with the adoption of the Pteridophyte Phylogeny Group I classification, have stabilized the taxonomic placement of Sphaeropteris within Cyatheaceae. Meanwhile, molecular phylogenetic studies have confirmed its monophyly and clarified evolutionary relationships at the genus and family levels. However, species-level molecular data for S. moluccana remain limited. Ethnopharmacognostic evidence suggests that tree ferns are traditionally used for wound healing and anti-inflammatory purposes, although direct pharmacological validation of S. moluccana is limited. By integrating systematics with ethnopharmacological insights, this review highlights critical knowledge gaps and proposes a biosystematics-driven framework to guide future drug discovery and conservation-oriented research on S. moluccana.

Keywords—Sphaeropteris moluccana; Cyatheaceae; biosystematics; molecular phylogeny; ethnopharmacognosy; drug discovery.

I. INTRODUCTION

Tree ferns (Cyatheaceae) represent one of the most ancient and morphologically distinctive lineages within extant pteridophytes, exhibiting high ecological importance in tropical and subtropical forest ecosystems. Members of this family play a crucial role in forest structure, nutrient cycling, microhabitat formation, and successional dynamics, particularly in montane and humid lowland forests. Among them, the genus *Sphaeropteris* is recognized as a well-supported monophyletic group based on both morphological and molecular evidence, distinguished from other cyatheoid ferns by the absence of marginate scales and specific soral and indusial characteristics (Korall & Pryer, 2014; PPG I, 2016).

Sphaeropteris moluccana (R.Br. ex Desv.) R.M.Tryon is a widespread arborescent fern distributed throughout Malesia, including Indonesia, Papua New Guinea, and surrounding regions. Despite its broad distribution and conspicuous growth form, *S. moluccana* remains understudied from an integrative biosystematic perspective. Existing taxonomic treatments largely rely on macromorphological characters, while comprehensive analyses integrating spore micromorphology, molecular phylogenetics, and applied ethnopharmacognostic knowledge are still fragmentary.

Biosystematics, as an integrative discipline combining classical taxonomy with modern analytical approaches, is essential for resolving species boundaries, evolutionary relationships, and intraspecific variation in morphologically conservative plant groups

such as tree ferns. In Cyatheaceae, morphological convergence and phenotypic plasticity—driven by environmental gradients such as altitude, humidity, and light availability—often obscure species delimitation when morphology is used in isolation. Consequently, complementary data sources such as spore micromorphology and molecular markers have become increasingly important in modern fern systematics.

Spore micromorphology, particularly when analyzed using scanning electron microscopy (SEM), provides stable taxonomic characters related to spore size, ornamentation, laesura type, and exospore–perispore architecture. Previous studies across Cyatheaceae and related fern families have demonstrated that spore ornamentation patterns can reflect phylogenetic relationships and serve as diagnostic features at both generic and species levels. However, detailed micromorphological descriptions of spores of *S. moluccana* remain notably scarce in recent literature.

Molecular phylogenetic studies have reshaped the understanding of evolutionary relationships within Cyatheaceae, revealing deep divergences among major lineages and supporting the segregation of traditional broad genera into more natural clades. Plastid markers such as *rbcL*, *atpB*, *rps4*, and *trnL–F*, as well as complete plastome data, have proven effective in resolving phylogenetic relationships among tree ferns. Nevertheless, species-level molecular data for *S. moluccana* are still underrepresented in publicly available datasets, limiting robust phylogeographic and population-level interpretations.

In addition to its systematic significance, *S. moluccana* holds potential relevance in ethnopharmacognosy. Ferns have historically received less attention than angiosperms in ethnomedicinal research, despite documented traditional uses of several tree fern species for food, wound healing, postpartum care, and general health maintenance in various tropical cultures. Ethnopharmacognostic investigations, which integrate traditional knowledge with phytochemical and pharmacological validation, are increasingly recognized as valuable for drug discovery and biodiversity-based innovation. However, no focused synthesis currently exists on the ethnopharmacognostic potential of *S. moluccana*, particularly within a biosystematic framework.

Therefore, this review aims to synthesize current knowledge on *Sphaeropteris moluccana* by integrating morphological, spore micromorphological, molecular, and ethnopharmacognostic perspectives based on literature published within the last decade. By adopting a biosystematic approach, this article seeks to highlight existing knowledge gaps, evaluate the taxonomic and applied significance of the species, and provide a conceptual foundation for future multidisciplinary research.

II. MATERIALS AND METHODS

This review employed a systematic–narrative approach to synthesize biosystematic knowledge on Sphaeropteris moluccana. Literature was retrieved primarily from the Scopus database using targeted keyword combinations related to morphology, spore micromorphology, molecular phylogenetics, and ethnopharmacognosy of Sphaeropteris and Cyatheaceae. Searches were limited to peer-reviewed English-language articles published between 2015 and 2025. Inclusion criteria comprised studies providing original data, taxonomic treatments, or comprehensive reviews relevant to biosystematics and traditional medicinal use, while non-peer-reviewed sources and articles lacking clear methodological frameworks were excluded. Taxonomic nomenclature and species validity were verified using Plants of the World Online and the Pteridophyte Phylogeny Group I classification. Data extracted included diagnostic morphological traits, spore characteristics, molecular markers and phylogenetic approaches, and documented ethnobotanical or pharmacological evidence. The information was synthesized qualitatively through thematic integration to cross-validate morphological, micromorphological, molecular, and ethnopharmacognostic evidence and to identify knowledge gaps.

III. PROGRESSION OF BIOSYSTEMATIC KNOWLEDGE OVER THE LAST DECADE (2015–2025)

A synthesis of Scopus-indexed literature published between 2015 and 2025 reveals that biosystematic knowledge of *Sphaeropteris moluccana* has advanced indirectly through broader studies on Cyatheaceae and tree ferns, rather than through species-specific integrative analyses. Morphological research during this period has focused primarily on re-evaluating diagnostic characters at the genus and family levels, including trunk architecture, scale morphology, frond dissection patterns, and soral arrangement, which have proven valuable for clarifying generic boundaries within Cyatheaceae (Lehnert, Korall, & Moran, 2018; Moran et al., 2020). These studies reaffirm the placement of *Sphaeropteris* as a morphologically coherent lineage, although they rarely address intraspecific variation within *S. moluccana*.

Micromorphological investigations, particularly those employing scanning electron microscopy (SEM) to examine spore ornamentation, have contributed to comparative systematics of tree ferns but remain limited in taxonomic resolution. Spore characters such as ornamentation type, perispore structure, and laesura configuration have shown utility at higher taxonomic ranks, yet their application to species delimitation within *Sphaeropteris* is still underexplored (Large & Braggins, 2019). The absence of targeted palynological studies on *S. moluccana* represents a significant gap in integrative biosystematics.

The most substantial progress over the last decade has occurred in molecular systematics. Plastid phylogenomics and multi-locus analyses have significantly improved phylogenetic resolution within Cyatheaceae, confirming the monophyly of *Sphaeropteris* and elucidating its evolutionary relationships with allied genera (Korall et al., 2017; Wang et al., 2019). However, molecular datasets are heavily biased toward representative taxa, and *S. moluccana* is frequently absent or represented by limited sequence data. This pattern reflects a broader trend in fern systematics, where advances in molecular phylogeny have outpaced species-level integrative and applied studies.

Ethnopharmacognostic knowledge related specifically to *S. moluccana* remains fragmentary. While ethnobotanical surveys in Southeast Asia and the Pacific report medicinal uses of tree ferns for wound treatment, inflammation, and antimicrobial purposes, these accounts are typically documented at the genus or family level without pharmacological validation (Hidayat et al., 2018; Zhang et al., 2021). Experimental studies on bioactive compounds in Cyatheaceae remain rare, highlighting a disconnect between traditional knowledge and modern pharmacological research.

Collectively, the literature trajectory from 2015 to 2025 indicates a shift toward molecular-driven classification frameworks, while morphological, micromorphological, and ethnopharmacological dimensions lag behind at the species level. This imbalance underscores the urgent need for integrative biosystematic studies combining morphology, spore micromorphology, molecular data, and ethnopharmacognosy to fully resolve the biological and applied significance of *Sphaeropteris moluccana*.

Table 1. Progress of Biosystematic Research on *Sphaeropteris moluccana* and Cyatheaceae (2015–2025)

Biosystematic Aspect	Key Authors (Year)	Study Focus	Major Findings	Research Progress
Morphology	Lehnert et al. (2018); Moran et al. (2020)	Comparative morphology of Cyatheaceae	Clarified generic boundaries and diagnostic traits	Moderate (genus/family level)
Spore micromorphology	Large & Braggins (2019)	SEM analysis of fern spores	Spore ornamentation useful for higher-level taxonomy	Low (no species-specific data)
Molecular systematics	Korall et al. (2017); Wang et al. (2019)	Plastid and multilocus phylogenetics	Confirmed monophyly of *Sphaeropteris*	High (limited species sampling)
Classification framework	PPG I (2016)	Global fern classification	Standardized Cyatheaceae taxonomy	High (baseline reference)
Ethnopharmacognosy	Hidayat et al. (2018); Zhang et al. (2021)	Traditional medicinal use of ferns	Reported medicinal use of tree ferns	Low (mostly descriptive)

IV. MOLECULAR PHYLOGENETICS AND EVOLUTIONARY INTERPRETATION

Over the last decade, molecular phylogenetic studies have fundamentally reshaped the systematic understanding of Cyatheaceae and provided a robust evolutionary framework for interpreting the placement of *Sphaeropteris moluccana*. Advances in plastid DNA sequencing and phylogenomics have consistently recovered *Sphaeropteris* as a well-supported monophyletic lineage within Cyatheaceae, resolving long-standing taxonomic ambiguities that arose from morphology-based classifications alone (Korall et al., 2017; Wang et al., 2019). Analyses employing multiple plastid loci (e.g., *rbcL*, *atpB*, *matK*, *trnL–F*) and complete plastome datasets have demonstrated that *Sphaeropteris* diverged early within tree ferns, with diversification patterns closely linked to Mesozoic–Cenozoic geological events and tropical forest expansion.

Phylogenomic evidence further suggests that evolutionary radiation within *Sphaeropteris* is associated with biogeographic processes in the Malesian and Pacific regions, supporting hypotheses of vicariance and long-distance dispersal mediated by spore dispersal capacity (Wang et al., 2019; Lehnert et al., 2018). However, despite these methodological advances, species-level resolution remains uneven. *Sphaeropteris moluccana* is frequently absent from molecular datasets or represented by limited sequence data, reflecting a broader sampling bias toward model or accessible taxa. As a result, evolutionary interpretations for *S. moluccana* are often inferred indirectly from closely related congeners rather than tested explicitly.

Molecular clock analyses and ancestral character reconstructions conducted at the family level indicate that arborescent habit and large frond architecture evolved early in Cyatheaceae and were subsequently conserved, lending molecular support to the taxonomic stability inferred from morphology (Korall et al., 2017). Nonetheless, incongruence between molecular phylogenies and certain morphological characters highlights the potential influence of homoplasy and phenotypic plasticity in tree ferns. This reinforces the view that molecular data provide a necessary, but not sufficient, basis for species delimitation. Integrative approaches combining dense taxon sampling, genomic-scale markers, and complementary morphological and micromorphological evidence are therefore essential to refine evolutionary hypotheses for *Sphaeropteris moluccana*.

Table 2. Progress of Molecular Phylogenetic Research on *Sphaeropteris* and Cyatheaceae (2015–2025)

Molecular Aspect	Key Authors (Year)	Data Type	Main Findings	Progress Level
Multilocus plastid phylogeny	Korall et al. (2017)	*rbcL*, *atpB*, plastid loci	Confirmed monophyly of *Sphaeropteris*	High
Phylogenomics	Wang et al. (2019)	Complete plastomes	Improved resolution of Cyatheaceae relationships	High
Evolutionary timing	Korall et al. (2017)	Molecular clock analyses	Early divergence of arborescent tree ferns	Moderate
Biogeographic inference	Wang et al. (2019)	Plastome + distribution data	Malesian–Pacific diversification patterns	Moderate
Species-level sampling (*S. moluccana*)	—	—	Limited or absent molecular data	Low (major gap)

V. ETHNOPHARMACOGNOSY AND BIOACTIVE POTENTIAL

Ethnopharmacognostic knowledge related to *Sphaeropteris moluccana* remains limited and largely indirect, reflecting a broader underrepresentation of tree ferns in pharmacological research despite their documented traditional use. Ethnobotanical surveys conducted in Southeast Asia and the Pacific region report that arborescent ferns belonging to Cyatheaceae are traditionally used for wound healing, anti-inflammatory treatments, fever reduction, and as general tonics, particularly utilizing young fronds, trunk pith, or decoctions of aerial parts (Hidayat et al., 2018; Zhang et al., 2021). However, these uses are frequently recorded at the genus or family level, and *S. moluccana* is seldom cited explicitly, underscoring a taxonomic resolution gap in ethnobotanical documentation.

From a pharmacognostic perspective, recent studies have demonstrated that several fern taxa possess bioactive secondary metabolites, including flavonoids, phenolic acids, terpenoids, and glycosides, which exhibit antioxidant, antimicrobial, and anti-inflammatory activities (Chen et al., 2018; Ma et al., 2020). Although direct phytochemical investigations of *Sphaeropteris moluccana* are scarce, comparative evidence from Cyatheaceae and related fern lineages suggests a high likelihood of conserved bioactive compound classes. This inference is supported by phylogenetic proximity and shared metabolic pathways observed among medicinal ferns, reinforcing the value of a biosystematic framework for guiding pharmacological exploration.

Despite growing interest in fern-derived natural products, experimental validation of traditional claims remains minimal. Most studies published between 2015 and 2025 focus on preliminary bioactivity screening or broad ethnobotanical inventories, with limited integration of taxonomic verification, compound isolation, or mechanism-of-action analysis (Ma et al., 2020; Zhang et al., 2021).

The absence of molecularly authenticated plant material further constrains reproducibility and translational potential. Consequently, while ethnopharmacological knowledge suggests promising medicinal relevance, the bioactive potential of *Sphaeropteris moluccana* remains largely hypothetical.

Integrating ethnopharmacognosy with biosystematics offers a strategic pathway to address these limitations. Molecular identification can ensure taxonomic accuracy, while phylogenetic inference may aid in predicting metabolite profiles and prioritizing taxa for drug discovery. Thus, *S. moluccana* represents a compelling yet underexplored candidate for integrative research linking traditional knowledge, systematics, and modern pharmacology.

Table 3. Progress of Ethnopharmacognostic and Bioactive Research Related to *Sphaeropteris* and Tree Ferns (2015–2025)

Research Aspect	Key Authors (Year)	Taxonomic Scope	Main Findings	Progress Level
Ethnobotanical surveys	Hidayat et al. (2018)	Ferns (Indonesia)	Medicinal use of tree ferns documented	Moderate
Asian ethnopharmacology	Zhang et al. (2021)	Ferns (Asia-wide)	Traditional medicinal applications summarized	Moderate
Phytochemical screening	Chen et al. (2018)	Fern lineages	Presence of flavonoids and phenolics	Low–Moderate
Bioactivity assays	Ma et al. (2020)	Medicinal ferns	Antioxidant and antimicrobial activity	Moderate
Species-specific studies (*S. moluccana*)	—	*Sphaeropteris moluccana*	No targeted pharmacological studies	Very low (major gap)

VI. INTEGRATIVE DISCUSSION: FROM BIOSYSTEMATICS TO DRUG DISCOVERY

The synthesis of morphological, micromorphological, molecular, and ethnopharmacognostic evidence highlights the critical role of biosystematics as a foundational framework for advancing drug discovery from underexplored fern lineages such as *Sphaeropteris moluccana*. Over the last decade, substantial progress in molecular phylogenetics has stabilized higher-level classification within Cyatheaceae, providing a robust evolutionary context in which biological traits, ecological adaptations, and secondary metabolite profiles can be interpreted (Korall et al., 2017; Wang et al., 2019). However, the translational potential of these advances remains largely unrealized due to limited species-level integration and applied research.

Morphological and micromorphological characters continue to provide indispensable taxonomic anchors, particularly for field identification and herbarium-based studies. Yet, the high degree of phenotypic plasticity observed in tree ferns restricts their utility for predicting bioactive potential when used in isolation (Moran et al., 2020). In contrast, molecular phylogenetics offers a more conservative and predictive framework by revealing evolutionary relationships that may reflect shared biosynthetic pathways. Phylogenetically informed approaches have proven effective in angiosperm drug discovery and are increasingly recognized as equally valuable for pteridophytes, where chemically rich but poorly studied clades persist (Chen et al., 2018; Ma et al., 2020).

Ethnopharmacognostic data, although fragmentary for *S. moluccana*, provide important heuristic signals for bioactivity, particularly when interpreted within a phylogenetic context. Traditional medicinal uses documented for Cyatheaceae and related fern lineages suggest conserved therapeutic functions, such as wound healing and anti-inflammatory activity, that may be underpinned by shared secondary metabolites (Hidayat et al., 2018; Zhang et al., 2021). However, the frequent absence of precise taxonomic identification in ethnobotanical studies severely limits reproducibility and pharmacological validation. Integrating molecular authentication into ethnopharmacological research is therefore essential to bridge traditional knowledge and modern drug discovery pipelines.

An integrative biosystematic strategy combining detailed morphological assessment, spore micromorphology, phylogenomic analysis, and ethnopharmacological evidence offers a powerful pathway to prioritize *Sphaeropteris moluccana* for bioprospecting.

Phylogenetic proximity can guide the selection of target taxa, while systematics ensures chemical data are biologically interpretable and evolutionarily meaningful. Such an approach reduces redundancy, enhances predictive accuracy, and aligns natural product discovery with evolutionary theory.

In this context, *Sphaeropteris moluccana* emerges not merely as a taxonomic entity but as a biologically coherent unit with untapped pharmacological potential. Future research should focus on generating species-level molecular data, conducting comparative metabolomic analyses across Cyatheaceae, and experimentally validating ethnopharmacological claims using authenticated material. By embedding drug discovery within a biosystematic framework, research on *S. moluccana* can transition from descriptive systematics to hypothesis-driven exploration, thereby contributing to both evolutionary biology and the discovery of novel bioactive compounds.

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