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One hundred new species of lichenized fungi: a signature of undiscovered global diversity

Phytotaxa 18: 1–127

The number of undescribed species of lichenized fungi has been estimated at roughly 10,000. Describing and cataloging these would take the existing number of taxonomists several decades; however, the support for taxonomy is in decline worldwide. In this paper we emphasize the dire need for taxonomic expertise in lichenology. We bring together 103 colleagues from institutions worldwide to describe a total of 100 new species of lichenized fungi, representing a wide taxonomic and geographic range. The newly described species are: *Acarospora flavisparsa*, *A. janae*, *Aderkomyces thailandicus*, *Amandinea maritima*, *Ampliotrema cocosense*, *Anomomorpha lecanorina*, *A. tuberculata*, *Aspicilia mansourii*, *Bacidina sorediata*, *Badimia multiseptata*, *B. vezdana*, *Biatora epirotica*, *Buellia sulphurica*, *Bunodophoron pinnatum*, *Byssoloma spinulosum*, *Calopadia cinereopruinosa*, *C. editae*, *Caloplaca brownlieae*, *C. decipioides*, *C. digitaurea*, *C. magnussoniana*, *C. mereschkowskiana*, *C. yorkensis*, *Calvitimela uniseptata*, *Chapsa microspora*, *C. psoromica*, *C. rubropulveracea*, *C. thalotrema*, *Chiodecton pustuliferum*, *Cladonia mongkolsukii*, *Clypeopyrenis porinoides*, *Coccocarpia delicatula*, *Coenogonium flammeum*, *Cresponea*

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ancistrosporelloides, *Crocynia microphyllina*, *Dictyonema hernandezii*, *D. hirsutum*, *Diorygma microsporum*, *D. sticticum*, *Echinoplaca pernambucensis*, *E. schizidiifera*, *Eremithallus marusae*, *Everniastrum constictovexans*, *Fellhanera borbonica*, *Fibrillithecis sprucei*, *Fissurina astroisidiata*, *F. nigrolabiata*, *F. subcomparimuralis*, *Graphis caribica*, *G. cerradensis*, *G. itatiaiensis*, *G. marusa*, *Gyalideopsis chicaque*, *Gyrotrema papillatum*, *Harpidium gavilaniae*, *Hypogymnia amplexa*, *Hypotrachyna guatemalensis*, *H. indica*, *H. lueckingii*, *H. paracitrella*, *H. paraphyscioides*, *H. parasinuosa*, *Icmadophila eucalypti*, *Krogia microphylla*, *Lecanora mugambii*, *L. printzenii*, *L. xanthoplumosella*, *Lecidea lygommella*, *Lecidella greenii*, *Lempholemma corticola*, *Lepraria sekikaica*, *Lobariella sipmanii*, *Megalospora austropacifica*, *M. galapagoensis*, *Menegazzia endocrocea*, *Myriotrema endoflavescens*, *Ocellularia albobullata*, *O. vizcayensis*, *Ochrolechia insularis*, *Opegrapha viridipruinosa*, *Pannaria phyllidiata*, *Parmelia asiatica*, *Pertusaria conspersa*, *Phlyctis psoromica*, *Placopsis imshaugii*, *Platismatia wheeleri*, *Porina huainamdungensis*, *Ramalina hircana*, *R. stoffersii*, *Relicina colombiana*, *Rhizocarpon diploschistidina*, *Sticta venosa*, *Sagenidiopsis isidiata*, *Tapellaria albomarginata*, *Thelotrema fijiense*, *Tricharia nigriuncinata*, *Usnea galapagona*, *U. pallidocarpa*, *Verrucaria rhizicola*, and *Xanthomendoza rosmarieae*. In addition, three new combinations are proposed: *Fibrillithecis dehiscens*, *Lobariella botryoides*, and *Lobariella pallida*.

CYMON J. COX, BERNARD GOFFINET, NORMAN J. WICKETT, SANDRA B. BOLES, A. JONATHAN SHAW

Moss diversity: A molecular phylogenetic analysis of genera

Phytotaxa 9: 175–195

In this study we present phylogenetic and molecular phylogenetic diversity analyses of moss taxa from a total of 655 genera of mosses. Three loci were sampled: chloroplast ribosomal small protein 4, the intronic region of the mitochondrial NADH dehydrogenase subunit 5, and partial sequences of the nuclear 26S ribosomal RNA. Maximum likelihood and Bayesian phylogenetic analyses were performed on individual loci and on multilocus data sets. A measure of phylogenetic diversity was calculated and contrasted among major lineages of mosses. We reveal many instances of incongruence among genomic partitions, but, overall, our analyses describe relationships largely congruent with previous studies of the major groups of mosses. Moreover, our greater sampling highlights the possible non-monophyly of many taxonomic families, particularly in the haplolepideous and pleurocarpous mosses. Comparisons of taxic and phylogenetic diversity among genera indicate that the Dicranidae (haplolepideous taxa) include about 15% of moss genera, but nearly 30% of the phylogenetic diversity. By contrast, the Hypnanae (hypnalian pleurocarps) contain about 45% of moss genera, but a lower percentage of phylogenetic diversity. Agreement between numbers of genera and phylogenetic diversity within other moss clades are remarkably consistent.

MAARTEN J. M. CHRISTENHUSZ, XIAN-CHUN ZHANG, HARALD SCHNEIDER

A linear sequence of extant families and genera of lycophytes and ferns

Phytotaxa 19: 7–54

Throughout the history of the classification of extant ferns (monilophytes) and lycophytes, familial and generic concepts have been in great flux. For the organisation of lycophytes and ferns in herbaria, books, checklists, indices and spore banks and on the internet, this poses a problem, and a standardized linear sequence of these plants is therefore in great need. We provide here a linear classification to the extant lycophytes and ferns based on current phylogenetic knowledge; this provides a standardized guide for organisation of fern collections into a more natural sequence. Two new families, Diplaziopsidaceae and Rhachidosoraceae, are here introduced.

SILVIA PRESSEL, MARTIN I. BIDARTONDO, ROBERTO LIGRONE, JEFFREY G. DUCKETT

Fungal symbioses in bryophytes: New insights in the Twenty First Century

Phytotaxa 9: 238–253

Fungal symbioses are one of the key attributes of land plants. The twenty first century has witnessed the increasing use of molecular data complemented by cytological studies in understanding the nature of bryophyte-fungal associations and unravelling the early evolution of fungal symbioses at the foot of the land plant tree. Isolation and resynthesis experiments have shed considerable light on host ranges and very recently have produced an incisive insight into functional relationships. Fungi with distinctive cytology embracing short-lived intracellular fungal lumps, intercellular hyphae and thick-walled spores in *Treubia* and *Haplomitrium* are currently being identified as belonging to a more ancient group of fungi than the glomeromycetes, previously assumed to be the most primitive fungi forming symbioses with land plants. Glomeromycetes, like those in lower tracheophytes, are widespread in complex and simple thalloid liverworts. Limited molecular identification of these as belonging to the derived clade *Glomus* Group A has led to the suggestion of host swapping from tracheophytes. Ascomycetes, all identified to date as *Rhizoscyphus ericae* and having an extremely wide host range extending into the Ericales, occur in the rhizoids of a range of leafy liverwort families that are sister to the Schistochilaceae, where the fungus induces rhizoid branching and septation. Dating of the Schistochilaceae suggests that these liverwort rhizoid associations predated ericoid mycorrhizas. A more restricted distribution of basidiomycetes, all identified as members of the genus *Sebacina*, is interpreted as a secondary acquisition in leafy liverworts following the loss of ascomycetes. Unlike the latter and ectomycorrhizal basidiomycetes in tracheophytes, these are host specific. Whereas there is no evidence

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of host digestion for either the ascomycetes or basidiomycetes in leafy liverworts, basidiomycetes in the Aneuraceae display regular colonization and digestion cycles. Considerable molecular diversity in the aneuracean fungi, mainly in the genus *Tulasnella* with occasional sebacinoids, mirrors the same in the host liverworts. Nesting of the only mycoheterotrophic liverwort *Cryptothallus* within *Aneura* is congruent with the phylogeny of the endophytes. Glomeromycete fungi have been identified in *Phaeoceros* and *Anthoceros* whereas *Dendroceros*, *Megaceros* and *Nothoceros* lack endophytes but the distribution of fungi across hornworts has yet to be explored. In contrast to liverworts and hornworts, there is no evidence of mycorrhiza-like associations in mosses. Claims that the fossil *Prototaxites* was a fossil fungus-associated liverwort are discounted.

MICHAEL STECH, DIETMAR QUANDT

20,000 species and five key markers: The status of molecular bryophyte Phylogenetics

Phytotaxa 9: 196–228

A number of reviews have accompanied and monitored the progress of molecular phylogenetic research on bryophytes, focusing on the publication record itself, bryophyte phylogeny and systematics in the molecular era, as well as the evolution and phylogenetic utility of markers from different genomes. However, none of the recent reviews include a detailed characterization of all molecular markers used in bryophyte phylogenetics. Here we provide an overview of the history and current state of marker utilization, including coding and non-coding sequence markers from all three genomes as well as fingerprinting approaches. The molecular architecture and evolutionary peculiarities, as well as practical aspects such as amplification and sequencing strategies, are outlined for the DNA sequence markers, with a focus on the most commonly employed regions. Their phylogenetic utility and potential for solving some of the remaining, pressing questions in bryophyte phylogeny, as well as their suitability for molecular species identification by DNA barcoding, are discussed.