

MycoKeys, or why we need a new journal in mycology?

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The launch of MycoKeys coincided with several revolutionary changes to the International Code of Botanical Nomenclature (ICBN) (Knapp et al. 2011 and Hawksworth 2011, in this volume, Miller et al. 2011) that occurred during the Nomenclature Section of the XVIII International Botanical Congress (IBC2011) in Melbourne, Australia. The path to the present launch, however was paved years ago by the lively discussions on electronic publication and dissemination of biodiversity information in the Internet era (e.g., Knapp and Wright 2010, Penev et al. 2010a), as well as by the successful start of its sister journals, PhytoKeys and ZooKeys.

In short, there are several challenges in the publishing practices in mycology that both mycologists and publishers now face: (1) Allowance of electronic publication of nomenclatural acts and its successful application in practice; (2) Mandatory electronic registration for nomenclatural acts for fungi in electronic registers such as MycoBank (effective on and after 1st of January 2013); (3) Removal of Article 59 of the Vienna Code that allowed existence of more than one valid name for the different forms (asexual and sexual) of a fungus species; the elimination of Article 59 is often interpreted as the “one fungus - one name” rule; (4) Open access publishing of information and data as already established best practice in academic communication (Suber 2010); (5) Forthcoming Web 2.0 and Linked Open data (LOD) era allows permanent cross-linking and data exchange between the leading biodiversity data holders, such as the Global Biodiversity Information Facility (GBIF), Encyclopedia of Life (EOL), MycoBank, Index Fungorum, the Global Information System for Lichenized and Non-Lichenized Ascomycetes (LIAS), Genbank, Plazi the Wiki environment (Species-Id, Wikispecies) and many others (Penev et al. 2010a; see also Fig. 1); (6) Semantic

markup of published texts permit unprecedented increase of visibility, citations and re-use of the biodiversity information (Penev et al. 2010b).

There are also other exciting and novel advances in biodiversity science that change the field with a speed never seen before. Electronic media helps not only in fast and efficient publication and communication between researchers but becomes themselves tools and platforms for indexing, aggregating and retrieval of information, providing unique opportunities to accelerate biodiversity research and understanding. The research process itself is accelerated by methods to increase the speed and efficiency of sampling and discovery of new taxa, as well as with their identification through an array of new techniques such as DNA sequencing.

MycoKeys is launched to respond to the challenges described above through a transformative publishing model with innovative approaches to publication and dissemination. The journal will publish papers across all disciplines dealing with taxonomy, systematics, evolution, phylogeny, biogeography, taxon-based ecology, and conservation of the monophyletic kingdom Fungi. *MycoKeys* will publish taxonomic or ecological data on any taxon of any geological age from any part of the world with no limit to manuscript size. Special attention will be paid to works offering integrative and inter-disciplinary approaches that promote innovative ways of presenting the research information.

Mycokeys will consider publishing works on the following topics:

- Descriptions of new taxa, if they are accompanied with proper diagnoses and/or keys to distinguish them from close relatives or similar taxa, and if DNA sequence data are deposited in Genbank prior to publication. All new taxa need to be registered at Mycobank and Mycobank numbers indicated in the manuscript. New taxa should ideally be described in connection with a phylogenetic analysis or evidence that the barcode gene (ITS) is unique for the new taxon.
- Taxonomic revisions of extant (or “recent”) and fossil fungal groups
- Checklists and catalogues
- Phylogenetic and evolutionary analyses, if alignments are deposited in TreeBase (with accession number listed in the text).
- Papers in descriptive and/or historical biogeography
- Methodology papers, including description of new software, if released as an open source license and released as supplementary material to the article.
- Data mining and literature surveys
- Monographs, conspecti, atlases
- Primer notes
- Letters to the Editor and “Points of View” commentaries
- Collections of papers, Festschrift volumes, conference proceedings
- Data papers (manuscripts describing large datasets published through the GBIF, Barcode of Life, or other international data repositories)

Extensive overviews on a taxon in a country or larger region are welcome. Short mycological contributions may be considered if they are based on significant or unex-

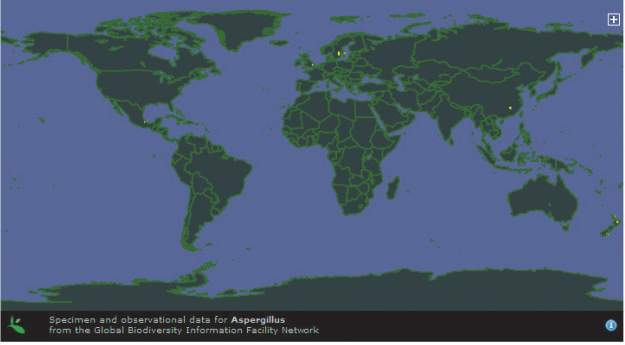
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Aspergillus

Global Biodiversity Information Facility



Specimen and observational data for *Aspergillus*
from the Global Biodiversity Information Facility Network

[Click here to go to the GBIF search results for this taxon](#)

Gene Sequences and PubMed links

Inherited blast name: Plants

Rank: genus

Lineage:
cellular organisms; Eukaryota; Opisthokonta; Fungi; Dikarya; Ascomycota; saccharomyceta;
Pezizomycotina; leotiomycota; Eurotiomycetes; Eurotiomycetidae; Eurotiales; Trichocomaceae;
mitosporic Trichocomaceae

Entrez records	Subtree links
Database name	7394
PubMed Central	137289
Nucleotide	126291
Protein	702
Taxonomy	468
PopSet	

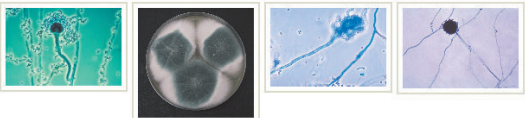
Related links found in database

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To get a complete list [click here](#).

Disclaimer: The NCBI taxonomy database is not an authoritative source for nomenclature or classification - please consult the relevant scientific literature for the most reliable information.

Images from Wikimedia



Biodiversity Heritage Library

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v.2 1877: 221, 222.

Actes de la Société linnéenne de Bordeaux.
t.48 (1895).

The actinomycetes.
3: 33, 208, 407, 423.

To get a complete list [click here](#).

General

- GBIF** Global Biodiversity Information Facility
- EOL** Encyclopedia of Life
- Catalogue of Life**
- ITIS** Integrated Taxonomic Information System
- World Register of Marine Species**
- Wikipedia
- Wikispecies
- IUCN
- BioLib BioLib

Taxonomy

- Index Fungorum**
- The Gymnosperm Database
- TreeBase**
- Chilobase**

Gene Sequences

- National Center for Biotechnology Information**
- Barcode of Life**

Images

- Morphobank**
- Wikimedia
- Yahoo! Yahoo

Literature

- Google Scholar**
- PubMed**
- Biodiversity Heritage Library**

Disclaimer

Some of the searched sites, particularly taxon-oriented databases, do not provide either "AND" or "Exact phrase" search functions, or Application Programming Interface (API). This may lead to the listing of various homonyms, e.g., the taxon profile of spruce (*Picea abies*) will also display the chloppod species *Lichobius oheus picea Matic*, 1957 in *Chilobase* and the fly *Tachia picea* Walker, 1853 in *Chilobase*.

Figure 1. Pensoft Taxon Profile (PTP) for the genus *Aspergillus* (Eurotiomycetes) obtained dynamically from external web resources. The profile is generated by clicking on any taxon name published in a MycoKeys paper, in this case in the paper by Raja et al. (2011). The links on the left bar, if in bold font, lead to various biodiversity platforms where information on this taxon is available; links in normal font indicate that there is no information on the taxon in the particular platform. The PTP tool is available also as standalone application at <http://www.ptp.pensoft.eu>

pected discoveries. Regular contributions may eventually be published in special issues devoted to a region/country.

In addition *MycKeys* will respond to the present-day cultural and technological shift in scholarly publishing and communication through:

- Mandatory open access to all journal articles, providing an unlimited and barrier-free distribution of published content
- Pre-publication recording of all new names in Mycobank as well as rapid post-publication registration in Index Fungorum and LIAS
- Inclusion of the Mycobank registration numbers in the original descriptions (protologues)
- All new taxa and other taxon descriptions and associated images are provided to the Encyclopedia of Life on the day of publication
- All taxon treatments are provided to the Plazi treatment repository
- All new taxa are exported to the Wiki environment (Species-Id) on the day of publication; the link to the Wiki version of a treatment is included in the protologue and citation of the original description is always explicitly shown in the Wiki version
- An established infrastructure for data publishing in cooperation with the GBIF, the Consortium for Barcode of Life, and Dryad Data Repository
- Data matrices and primary data files for interactive keys (e.g., Lucid, Intkey, MX, and others) can be published as supplementary files to facilitate use and reuse by future workers
- Immediate alert service on new publications through email, RSS, Twitter, Facebook, Mendeley, and other networks
- Immediate distribution and dissemination of your publication to scientific databases, indices and search engines (ISI Web of Knowledge, Google Scholar, CABI Abstracts, DOAJ, and others)
- Archiving of your publication, electronically and in print, in trusted (e-) archives and libraries, in the first case PubMedCentral
- Continuous development and implementation of cutting-edge publishing technologies: XML-based editorial work flow and mark up process, data publication and various semantic enhancements to published texts to ensure a pleasant and efficient reading process as well as a wide dissemination of separate parts of a logically 'atomised' article's content
- Automated cross-linking of any taxon mentioned in the *MycKeys* papers through the Pensoft Taxon Profile (Fig. 1) with major indexing and aggregation platforms such as the GBIF, EOL, MycoBank, Index Fungorum, the International Plant Name Index (IPNI), ZooBank, the National Center for Biodiversity Information (NCBI), Genbank, Barcode of Life, the Biodiversity Heritage Library (BHL), PubMed, PubMedCentral, and others
- Publication of identical content in four different formats to serve different target user groups: (1) full-colour, high-resolution print version; (2) PDF for reference to the printed version and easy archiving; (3) HTML for easy

reading, browsing and applying semantic enhancements to the text; and (4) XML to provide a machine-readable file for archiving and data mining

- Quick turnaround time; papers published within one to three weeks time after acceptance
- No restrictions and no charges for colour either in the online or in the printed version

On behalf of its authors, *MycoKeys* will place special effort on increasing public awareness of published scientific discoveries through an established system of press releases to science news distributors, mass media, blogs, social networks and others.

A new journal can only succeed when it is appreciated by an enthusiastic community of authors, reviewers, editors and readers. We are confident that the new opportunities offered by *MycoKeys* will be embraced and warmly welcomed by all mycologists to the great benefit of scientists, research funders and society in general.

Finally, we would like to thank all of the authors, editors and readers of *MycoKeys* for their support of the journal, as well as the translators of the paper of Knapp et al. (2011): Li-Bing Zhang (Chinese), Jefferson Prado, Regina Y. Hirai, and Cíntia Kameyama (Portuguese), Irina Belyaeva and Maria Vorontsova (Russian), and Carmen Ulloa Ulloa, Lourdes Rico Arce, and Renée H. Fortunato (Spanish). Special thanks are due to all teams that made possible the establishment of the innovative workflow of Pensoft's journals: Plazi, the Global Biodiversity Information Facility (GBIF), the Encyclopedia of Life (EOL), the Biodiversity Heritage Library (BHL), the National Library of Medicine of the U.S. (NLM), and the ViBRANT EU FP7 project.

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A new dawn for the naming of fungi: impacts of decisions made in Melbourne in July 2011 on the future publication and regulation of fungal names

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Abstract

A personal synopsis of the decisions made at the Nomenclature Section meeting of the International Botanical Congress in Melbourne in July 2011 is provided, with an emphasis on those which will affect the working practices of, or will otherwise be of interest to, mycologists. The topics covered include the re-naming of the *Code*, the acceptance of English as an alternative to Latin for validating diagnoses, conditions for permitting electronic publication of names, mandatory deposit of key nomenclatural information in a recognized repository for the valid publication of fungal names, the discontinuance of dual nomenclature for pleomorphic fungi, clarification of the typification of sanctioned names, and acceptability of names originally published under the zoological code. Collectively, these changes are the most fundamental to have been enacted at a single Congress since the 1950s, and herald the dawn of a new era in the practice of fungal nomenclature.

Key words

Amsterdam Declaration; Code of Nomenclature; electronic publication; MycoBank; nomenclature; pleomorphic fungi; registration; sanctioned names; taxonomy.

Introduction

The internationally agreed rules that regulate how fungi are named are examined and revised at each International Botanical Congress, the last published being those re-

sulting from the Vienna Congress in 2005 (McNeill et al. 2006). These Congresses are now held every six years, and the subsequent one in Melbourne in July 2011 was faced with a staggering 338 proposals made to modify the Vienna edition of the *International Code of Botanical Nomenclature* (McNeill and Turland 2011). This was the largest number to have confronted any Congress since that held in Paris in 1954. The issues that the Melbourne Congress had to address included topics as fundamental as the language required for the valid publication of names, the acceptability of electronic publication, and the unease amongst mycologists on how decisions were made.

It may seem weird to 21st century biological science students that fungi are embraced in a *Code* with just “botanical” in the title. However, the actual remit was all organisms traditionally studied in departments of botany in museums and universities, regardless of their current classification in the kingdoms of *Life* – even all bacteria were covered until the Montreal Congress of 1959. Some rules are, nevertheless, applicable only to particular systematic groups or categories, and since the Brussels Congress of 1910 there have been special regulations which only apply to the names of fungi. Foremost amongst these have been issues related to: (1) the date at which the nomenclature of fungi was deemed to commence; (2) the status of living cultures as name-bearing types; and (3) the separate naming of morphs in pleomorphic fungi. Any proposed changes in the rules relating to particular groups or categories (e.g. fossils) are discussed by a series of permanent committees, the members of which are elected at the end of each Congress and serve to the next. In the case of the fungi, the permanent committee is now called the Nomenclature Committee for Fungi (NCF). A valuable synopsis of how the current system operates is given by McNeill and Greuter (1986), while Nicolson (1991) provides an authoritative historical account of the development of the *Code*.

During recent decades, and especially in the 2000s, many mycologists had become increasingly dissatisfied with various aspects of the rules concerning the naming of fungi. This was reflected in sessions and debates at various national, regional, and international meetings, culminating in three Nomenclature Sessions held as a part of the IXth International Mycological Congress (IMC9) in Edinburgh in August 2010. During those sessions, various already published proposals for change were discussed, and in addition all delegates to the Congress were invited to complete a questionnaire to canvass their views on key issues and possible ways forward; a report of those Sessions and the results of the questionnaires are provided by Norvell et al. (2010).

The decisions taken at the Melbourne Congress were so fundamental, with respect to both “botanical” nomenclature as a whole, and especially with specific topics that concerned fungi, that these need to be widely promulgated. A formal report of those decisions is provided by McNeill et al. (2011), and more detailed information of those pertaining to fungi is presented by Norvell (2011). Those reports include the new approved wordings, though they may still undergo some fine-tuning by the Editorial Committee appointed by the Congress. The Editorial Committee is to meet in London in December 2011, and it is anticipated that the finalized *Melbourne Code* will be printed in mid-2012. However, changes effected at an International Botanical

Congress come into effect immediately they are approved by the Plenary Session of the Congress unless specifically limited by date. It is, therefore, essential that all mycologists involved in the naming of fungi are made aware of both the changes made that come into force before the *Code* is printed, and those that are to be anticipated from 1 January 2013.

The purpose of the present article is to alert mycologists as a whole to the fundamental changes made at the Melbourne Congress, a package which represents a paradigm shift in how fungi are now to be named, and to indicate the implications of those changes for working practices. It is not, however, to be considered authoritative, and the final version of the *Melbourne Code* should be consulted as soon as it becomes available.

Principle changes and their impacts

Name of the Code changed

Mycologists, tired of appearing subservient to botanists, and for mycology to be treated as a part of botany (Hawksworth 1997, Minter 2011) made proposals for the name of the *Code* to be changed to reflect their independence (Hawksworth et al. 2009). This view had been supported at IMC9 (Norvell et al. 2010), and the Melbourne Congress agreed that the new *Code* should be called the *International Code of Nomenclature for algae, fungi, and plants*. The lower case letters used for the words “algae”, “fungi”, and “plants” are employed to make clear these terms are being used in a colloquial sense, for instance the inclusion of cyanobacteria in algae, and chromistan fungal analogues, slime moulds, and lichens in “fungi”.

The Congress further agreed that editorial changes should be made throughout the text so that it referred to “organisms” governed by the *Code*, and no longer used “plants” where fungi were included in the concept.

Governance of fungal nomenclature to be considered

Proposals to transfer decision-making on issues concerning fungi from International Botanical to International Mycological Congresses (Hawksworth et al. 2009), and which had been strongly supported at IMC9 (Norvell et al. 2009) were not accepted. However, a Subcommittee on governance of the *Code* with respect to fungi was established under a Special Committee mandated with examining how the Nomenclature Section operated. That Committee (and Subcommittee) are to report to the next International Botanical Congress in 2017. In view of this move, mycologists will now have to consider whether to put on hold the question of the need for an independent *Code* for fungi (see below) pending that report. The matter needs to be placed on the agenda for Nomenclature Sessions to be convened during IMC10 in 2014.

English or Latin validating diagnoses permitted

The issue of whether to discontinue the requirement for validating diagnoses or descriptions in Latin has been raised at almost all International Botanical Congresses since this requirement was first introduced in 1935. The Melbourne Congress was presented with proposals from botanists to allow any language, as is the practice in zoology, and some alternative ones, including one by mycologists to require Latin or English for fungi (Norvell et al. 2010, Demoulin 2010). There was a precedent in that the alternative of Latin or English was already allowed for fossils in the Vienna Code. The Congress not only supported the mycological proposal, but also decided that it should apply not just to fungi but to *all* organisms treated under the *Code*. Further, so enthusiastic was the meeting, that it was agreed that this provision should operate from 1 January 2012, not 1 January 2013. Consequently, mycologists no longer need to struggle with coining a few sentences of pseudo-Latin when describing new fungi. However, in consequence, I personally see value in presenting both a diagnosis (i.e. a short statement of how the fungus differs from others) and a separate description (i.e. a detailed account of all the features of the fungus) when describing a new fungus. If a diagnosis were in Latin or English, the description could then continue to be in any language of the author's choice. A diagnosis has been required for the introduction of new scientific names in zoology since 1930 (International Commission on Zoological Nomenclature 1999: Art. 13), and the practice has much to commend it.

Electronic publication permitted (but with restrictions)

The issue of the acceptability of works published only electronically as a vehicle for the effective publication of scientific names has been the subject of a series of Special Committees established by successive International Botanical Congresses since that held in Tokyo in 1993, and is also an issue currently being actively debated by zoologists (Michel et al. 2009). With the increasing proliferation of new electronic journals, and established journals also increasingly being available in both electronic and hard-copy forms, the issue was becoming increasingly urgent. A Special Committee established by the Vienna Congress in 2005, considered the matter in depth (Chapman et al. 2010) and prepared detailed proposals for consideration by the Melbourne Congress (Special Committee on Electronic Publication 2010). The Melbourne Congress accepted many of these proposals, and the pertinent revised texts and guidelines as to best practice are given by Knapp et al. (2011). The key points agreed were that from 1 January 2012, works published in electronic form on the worldwide web in an unchangeable Portable Document Format (PDF) are to be treated as effectively published, *provided that* they have either an International Standard Serial Number (ISSN) or an International Standard Book Number (ISBN). However, non-final versions made available online in advance of a definitive version (e.g. accepted papers as yet unedited or proof-read) are not treated as effectively published. Where both electronic and hard-copy versions of a work

are made available, the date of effective publication of both is treated as being the same. Guidance as to how copies can be differentiated is included in Knapp et al. (2011).

It is important to appreciate that the new provisions do not mean that material placed on or available through websites and lacking ISSN or ISBN numbers constitutes effective publication. Authors considering submitting to an electronic journal, should therefore first check that it has an ISSN number. It is also recommended that electronic-only works containing new taxa are drawn to the attention of appropriate indexing centres, and mycologists should endeavour to do that until the requirement for the prior deposit of key nomenclatural information becomes mandatory on 1 January 2013.

Deposit of key nomenclatural information made mandatory for fungi

The concept of some form of obligatory registration of newly proposed scientific names for fungi goes back to the 1950s (Ainsworth and Ciferri 1955). Following the establishment of a Special Committee on Registration at the Berlin Congress in 1987, and a series of subsequent workshops, a provision to make this a requirement for all groups of organisms covered by the *Code* was accepted by the Tokyo Congress in 1993 – but then rejected at the St Louis Congress in 1999 despite successful trials (Greuter 2009). The development of the worldwide web, however, has made it possible to devise much-improved systems from those that were possible in the 1980s and early 1990s. Following informal discussions during the 2002 International Mycological Congress (IMC7) in Oslo, in 2004 the CBS-KNAW Fungal Biodiversity Centre in Utrecht established an online system for the deposit of key information on newly proposed names of fungi – MycoBank. This voluntary system proved popular with mycologists, and also with mycological journals, as a way of rapidly expediting information on nomenclatural novelties. Since 2007 Mycobank has operated under the auspices of the International Mycological Association (IMA) which now has long-term responsibility for its continuance.

Formal proposals to make the deposit of key nomenclatural information in a recognized online repository a mandatory requirement for valid publication of new scientific names in fungi at all taxonomic ranks (including new combinations and replacement names) were then developed (Hawksworth et al. 2010). Those proposals were overwhelmingly endorsed by the International Mycological Congress in Edinburgh later in the same year (Norvell et al. 2010). The Melbourne Congress approved the formal proposals with some “friendly” amendments, mainly based on suggestions for avoiding unnecessary inflation of names in the repositories (Morris et al. 2011). In addition a recommendation that information on choices made between competing names or homonyms, spelling or gender also be deposited (Gams 2010) was approved.

The new requirement comes into force on 1 January 2013, after which date scientific names of fungi which are published without a unique identifier by a recognized repository will not be considered as validly published; i.e. they will not exist for nomenclatural purposes and need not be considered when determining the correct name

for a taxon under the *Code*. While the requirement is only for information required by the rules of the *Code*, such as the diagnosis and information as to the nomenclatural type or a basionym, as appropriate, there is no objection to databases also including additional information and the prospects are enormously exciting (Lumbsch et al. 2011).

The responsibility of appointing online depositaries was given to the Nomenclature Committee for Fungi, which will need to advise mycologists as to which are approved. No single repository was specified in the proposals, thus leaving the possibilities open in the rapidly-moving electronic age. At present it is deposit in MycoBank which is now required by almost all mycological journals.

Mycologists should note that the prudent way to proceed is to make the online deposit of the required data, and obtain the numerical identifier, only *after* their work has been accepted for publication. This is to ensure that the information included agrees in every detail that which will appear in the publication which establishes the name. This will not affect the priority of the name as the effective date of publication will be that of the electronic or hard-copy publication and not the date information is deposited. The lodging of a name and associated details in a repository such as MycoBank will not in itself establish a name.

This exciting move means that, for the first time ever, mycologists will have immediate and free online access to the key nomenclatural and diagnostic information on newly proposed fungal names. It also means that it is the authors of new names which will now have the responsibility of ensuring that names they propose are incorporated into international indexing repositories.

Dual nomenclature of pleomorphic fungi discontinued

The concept of permitting separate names for anamorphs of fungi with a pleomorphic life-cycle has been an issue of debate since the phenomenon was recognized in the mid-19th century. This was even before the first international rules for “botanical” nomenclature were issued in 1867 (Weresub and Pirozynski 1979, Taylor 2011). Special provisions are to be found in the earliest *Codes*, which were then modified several times, and often substantially (Weresub and Pirozynski 1979). The rules became increasingly complex, and by the mid-1970s they were being interpreted in different ways by different mycologists – even ones working on the same genus. Following intensive discussions under the auspices of the International Mycological Association (IMA), drastic changes were made at the Sydney Congress in 1981 to clarify and simplify the procedures – and the now familiar terms anamorph, teleomorph, and holomorph entered general use. An unfortunate effect of the simplification was that many name changes had to be made as a consequence, including ones of some well-known and economically important species; at that date, the conservation of species names was not allowed under the *Code*.

Unforeseen in the 1970s, when the 1981 provisions were crafted, was the impact of molecular systematics. A decade later, it was starting to become obvious that fungi

with no known sexual stage could confidently be placed in genera which were typified by species in which the sexual stage was known (Reynolds and Taylor 1991), and the issue of the abandonment of the dual nomenclatural system was posited (Reynolds and Taylor 1992). This possibility was debated at subsequent International Mycological Congresses, and on other occasions (e.g. Seifert et al. 2000, Seifert 2003), and the need for change was increasingly recognized. Cannon and Kirk (2000) regarded deletion as inevitable in the long-term, and further calls for deleting the provision followed (e.g. Rossman and Samuels 2005). At the International Botanical Congress in Vienna in 2005, some minor modifications were made which allowed anamorph-typified names to be epitypified by material showing the sexual stage when it was discovered, and for that name or epithet to continue to be used where there was no previously sexually-typified name available.

More importantly, the Vienna Congress established a Special Committee to investigate the issue further, but unfortunately it was unable to reach a consensus (Redhead 2010). Matters were becoming increasingly desperate as mycologists using molecular phylogenetic approaches started to ignore the provisions, or interpret them in different ways (Rossman and Seifert 2010). The view that emerged from the International Mycological Congress in Edinburgh the same year, was that mycologists, as a whole, favoured gradual progress towards a single nomenclature (Norvell et al. 2010). In the meantime, various proposals were made to improve the situation, but the situation was becoming so complex that few mycologists were likely to take the time to understand them fully and implement them correctly. In order to progress the matter, an international symposium was held in Amsterdam in April 2011, under the auspices of the International Commission on the Taxonomy of Fungi (ICTF), to explore ways to obtain a solution. If a solution could not be reached at the Melbourne Congress, the prospect was for no substantive change to be made until after the 2017 International Botanical Congress. This situation would then have become intolerable as mycologists increasingly ignore the rules.

The Amsterdam symposium prepared a declaration of principles which, it was hoped, would be accommodated in any change made to Article 59 (Hawksworth et al. 2011). In effect these amounted to the ending of dual nomenclature, but with safeguards to minimize changes in familiar names. The “Amsterdam Declaration” prompted a critical response from some other mycologists who perceived difficulties in aspects of the declaration, and wished to continue allowing dual nomenclature (Gams et al. 2011). Both these documents were made available to delegates at the Melbourne Congress. In order to ensure some resolution of the issue, proposals for three possible options were developed by Redhead, in consultation with various mycologists, for presentation at the meeting. Following extensive discussions at the Congress, the option to discontinue the dual nomenclature system was approved, but with some safeguards to limit resultant instability (Norvell 2011, McNeill et al. 2011).

After 1 January 2013, one fungus can only have one name; the system of permitting separate names to be used for anamorphs then ends. This means that all legitimate names proposed for a species, regardless of what stage they are typified by, can serve

as the correct name for that species. All names now compete on an equal footing for priority regardless of the stage represented by the name-bearing type. In order not to render names that had been introduced in the past for separate morphs as illegitimate, it was agreed that these should not be treated as superfluous alternative names in the sense of the *Code*. It was further decided that anamorph-typified names should not be taken up to displace *widely used* teleomorph-typified names until the case has been considered by the General Committee established by the Congress¹. Recognizing that there were cases in some groups of fungi where there could be many names that might merit formal retention or rejection, a new provision was introduced. It was decided that lists of names can be submitted to the General Committee and, after due scrutiny, names accepted on those lists are to be treated as conserved over competing synonyms (and listed as Appendices to the *Code*). Lichen-forming fungi (but not lichenicolous fungi) were always excluded from the provisions permitting dual nomenclature; the new *Code* will include a paragraph to make it explicit that lichen-forming fungi are excluded from the newly accepted provisions.

Mycologists need now to work to implement this major change. In cases where a later teleomorph-typified name is not widely used, it can be anticipated that mycologists will now simply adopt the earlier anamorph-typified name. If others consider a decision inappropriate, a proposal for the conservation of the teleomorph-typified name over the earlier anamorph-typified name can be made to the Nomenclature Committee for Fungi (NCF). Although no detailed arrangements were made at the Congress, it is anticipated that, where specialist working groups on particular fungal genera or families exist, as is the case for subcommissions of the International Commission on the Taxonomy of Fungi (ICTF), draft lists of names for possible approval will be prepared by them. In my personal view, there could also be some advantage in endeavouring to have one list covering all potentially affected generic names, if mechanisms to achieve that could be put in place. In the early part of 2012, the NCF is to work closely with the ICTF and other groups where they exist (e.g. within the International Union of Microbiological Societies, IUMS) to develop processes for the preparation of lists on particular groups. Draft lists will need to be made available for comment by mycologists at large (e.g. through the IMA and ICTF web sites), and they will then require revising them in the light of comments received. Lists received by the NCF would, after due consideration by that Committee, then be forwarded to the General Committee for approval.

Where mycologists wish still to refer to anamorphs separately, the new provisions do not prohibit informal usages, such as “*acremonium*-state” or “*acremonium*-like”, ideally with a small initial letter and normal not italic type as suggested by Cannon and Kirk (2000). This form of typography makes clear that the designations are not scientific names governed by the *Code*.

¹ The General Committee is elected at each International Botanical Congress, and is responsible for receiving, considering, and approving reports from the various permanent nomenclature committees, such as the Nomenclature Committee for Fungi, for the period up to the next Congress..

Typification of sanctioned names clarified

The dates on which the nomenclature of fungi was deemed to start were changed from 1801 or 1821 to 1753 by the International Botanical Congress in Sydney in 1981. This change was made because the later-starting point system had come to be interpreted in different ways, and because of difficulties in ascertaining the first usages of already proposed names after the proscribed dates (Demoulin et al. 1981). In order to minimize the resultant name changes, the concept of “sanctioning” was introduced. Sanctioning permitted the continued use of names that had been adopted in the 1801 *Synopsis Methodica Fungorum* of Persoon, or the 1821–32 *Systema Mycologicum* of Fries over names that otherwise would have to be taken up under the normal rules of priority, homonymy, etc. However, the wording of the rule in the Sydney Code was somewhat ambiguous and, although modified slightly at the Berlin Congress in 1987, it could still be interpreted as meaning either that the typification of a sanctioned name should be made only on materials cited in the sanctioning work, or that it could be based on materials cited in the original pre-sanctioning place of publication.

Proposals to address this issue were published before the Melbourne Congress (Perry 2010, Redhead et al. 2010), but there were concerns over these. In consequence, a series of informal discussions was held in Melbourne, which involved the proposers and other concerned mycologists. Those meetings led to the formulation of a series of proposals which were adopted by the Congress (McNeill et al. 2011, Norvell 2011). The net effect of the changes made is that a name that has been sanctioned can now be lectotypified (not neotypified) by material from among the elements associated with either the original protologue of the name, the sanctioning treatment, or both. A further and welcome clarification is that in cases where in the sanctioning work elements associated with the original protologue did not include a subsequently designated type selected for the sanctioned name, the sanctioning author is considered to have introduced a later homonym that is to be retained because of its sanctioned status.

No particular date was mentioned in the adopted proposals, which means that they became operative when approved by the Melbourne Congress. They are also retroactive, and so safeguard many typifications made since the 1981 Congress which were based on material cited in the original protologue, or on material of the sanctioning author where that differed. The adoption of these clarifications is most welcome as it removes the need for many typifications made since 1981 to be revisited, something that could have had unfortunate implications for the stability of many sanctioned names.

Names of fungi first described as animals are validly published

The revelation that *Microsporidia*, a group traditionally studied by zoologists, belonged to kingdom *Fungi* posed a threat to numerous names in use in the phylum. This situation arose as, while those names had been correctly published and were available for use under the provisions of the International Code of Zoological Nomenclature, many

did not meet the requirements of the botanical *Code*. At the Vienna Congress in 2005, it was agreed that names within *Microsporidia*, and other organisms that had originally been published under the zoological code, were to be treated as validly published under the botanical *Code*. However, in accordance with the wishes of workers on these fungi, the Melbourne Congress accepted proposals made by Redhead et al. (2009) that these organisms should be excluded from governance by the botanical *Code* and continue to be covered by the zoological one, despite their phylogenetic position. It was further agreed that this principle should be adopted for other groups of organisms traditionally treated under other codes.

Explicitly indicate the physiological state of type cultures

A rule in the current *Code* allows cultures of algae and fungi to serve as name-bearing types, provided that they are “preserved in a metabolically inactive state”. In practice, the physiological state of cultures designated as types is often not stated by describing authors. In order make this explicit, it is now recommended that the phrase “permanently preserved in a metabolically inactive state”, or equivalent, be used when cultures are designated as types.

Names based on fossil parts loose special provisions

In recent years there have been extensive debates in the palaeobotanical community on how to revise the provisions relating to the naming of parts of fossil organisms treated under the *Code* – and which applied to fungi as well as plants. Competing sets of proposals were submitted to the Melbourne Congress. As in the case of ending the separate naming of anamorphs in pleomorphic fungi, the Congress decided to abandon the practice of separately naming parts of fossils. Consequently, names of fossils which prove to be parts of a single species will now compete with each other for priority, in the same way as occurs for names not based on fossils.

The Draft BioCode and MycoCode need to be revisited

Moves towards increased harmonization between the various codes of nomenclature were initiated in 1985. However, the prospect, in the long-term, of having a set of rules governing the future nomenclature of all organisms was developed in the early 1990s (Hawksworth 1995). This culminated in the publication of a *Draft BioCode* in 1996 which had been prepared by the IUBS²/IUMS International Committee on Bio-

² The International Union of Biological Sciences, in which the International Mycological Association represents general mycology.

nomenclature (ICB)³. Little progress was made in taking the initiative further as the mechanisms and resources to develop the prerequisite lists of names to be considered available were not forthcoming. The project was subsequently revived as a scientific programme of IUBS in 2009, and an updated *Draft BioCode* was prepared and released for further discussion in January 2011 (Greuter et al. 2011). That draft was the subject of a session and debate at Biosystematics 2011 (which incorporated the International Congress of Systematic and Evolutionary Biology) in Berlin in February 2011. This initiative was mentioned briefly in the final session of the Nomenclature Section meetings in Melbourne, but was not considered in any depth. A suggestion that the Section establish a Special Committee to liaise with those involved in the revision of the draft was not approved.

The possibility of having an independent code for mycology was raised and received considerable vocal support at the International Mycological Congress (IMC8) in Cairns in 2006. However, the option of renaming and revising the botanical *Code* was the one favoured at the subsequent Congress in Edinburgh in 2010 (Norvell et al. 2010). The issue was also raised at the Amsterdam symposium in April 2011 which was primarily convened to address the issue of dual nomenclature. At that symposium it was suggested that the *BioCode* model could provide a framework for the future regulation of the nomenclature of fungi (Hawksworth et al. 2011). Key to any movement in this direction, was seen as the extent to which the botanical *Code* would change to meet the needs of mycologists (Taylor 2011). In view of the major changes made at the Melbourne Congress, the issue of whether an independent MycoCode is really now required needs to be debated at the International Mycological Congress (IMC10) in Bangkok in 2014.

Discussion

I have participated in all International Botanical Congresses since that held in St Petersburg in 1975, and served on the Editorial Committee of the botanical *Code* since 1987. The progress made in adapting the rules to the needs of both user and practitioner mycologists over that period has been considerable. These have included, for example, the change in starting point, the conservation and rejection of species names, the designation of interpretive types (“epitypes”), and allowing living metabolically inactive cultures to be nomenclatural types. The powers of the permanent Nomenclature Committees have also been enhanced over the years, so that they can now recommend rejection of any name whose adoption is regarded as disadvantageous.

Even against this background of increasing adaptation, the raft of changes effected at the Melbourne Congress in 2011, has to be seen as the dawn of a new era for botani-

³ The IUBS/IUBS International Committee on Bionomenclature comprises representatives of the five internationally mandated organismal codes of nomenclature: botanical, cultivated plant, prokaryote, viral, and zoological; it was formally established in 1994.

cal and mycological nomenclature, truly bringing it into the modern age. The decisions made with respect to the name of the *Code*, its coverage, electronic publication, and the requirement for the deposition of key information in a recognized depository as a requirement for the publication of fungal names, place the *Melbourne Code* ahead of what zoologists are currently endeavouring to do.

There is still much to be achieved by mycologists, especially with respect to the implementation of the consequences of the end of dual nomenclature for pleomorphic fungi, although the regulatory mechanisms are now in place. A major issue that remains is how best to designate taxa only known from molecular studies of environmental samples, and to consider whether that requires any changes in the *Code* (Hawksworth et al. 2011, Hibbett et al. 2011, Taylor 2011).

Finally, I must stress that the views and interpretations presented in this overview are personal, and that mycologists should check the decisions and verify actual wordings agreed in Melbourne for themselves, especially in the official report of the Nomenclature Section meetings (McNeill et al. 2011), and then the edited published version of the *International Code of Nomenclature for algae, fungi, and plants* when it becomes available in mid-2012.

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Changes to publication requirements made at the XVIII International Botanical Congress in Melbourne – what does e-publication mean for you?

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Abstract

Changes to the *International Code of Botanical Nomenclature* are decided on every 6 years at Nomenclature Sections associated with International Botanical Congresses (IBC). The XVIII IBC was held in Melbourne, Australia; the Nomenclature Section met on 18–22 July 2011 and its decisions were accepted by the Congress at its plenary session on 30 July. Several important changes were made to the *Code* as a result of this meeting that will affect publication of new names. Two of these changes will come into effect on 1 January 2012, some months before the *Melbourne Code* is published. Electronic material published online in Portable Document Format (PDF) with an International Standard Serial Number (ISSN) or an International Standard Book Number (ISBN) will constitute effective publication, and the requirement for a Latin description or diagnosis for names of new taxa will be changed to a requirement for a description or diagnosis in either Latin or English. In addition, effective from 1 January 2013, new names of organisms treated as fungi must, in order to be validly published, include in the protologue (everything associated with a name at its valid publication) the citation of an identifier issued by a recognized repository (such as MycoBank). Draft text of the new articles dealing with electronic publication is provided and best practice is outlined.

To encourage dissemination of the changes made to the International Code of Nomenclature for algae, fungi, and plants, this article will be published in *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, *Plant Diversity and Resources*, *Systematic Botany* and *Taxon*.

Introduction

At the XVIII International Botanical Congress in Melbourne, Australia, in July 2011, two important changes were made to the *International Code of Botanical Nomenclature* (now the *International Code of Nomenclature for algae, fungi, and plants*) that will take effect from 1 January 2012. These changes will affect everyone who publishes names governed by this *Code*. As the *Melbourne Code* will not be published until approximately mid-2012, we felt it would be helpful to outline these changes, particularly those concerning effective publication in electronic media (in Articles 29, 30, and 31). For a concise report on all the changes to the *Code* accepted in Melbourne, see McNeill et al. (2011).

A draft wording of the revised Articles, Notes, and Recommendations on effective publication is provided to aid editors and publishers in establishing best practice for implementing this aspect of the *Code*. We also outline here what these changes do *not* mean, to guide those wishing to publish new names and typifications by electronic means. We urge readers to consult the report of the Special Committee on Electronic Publication accompanying the changes proposed before the Congress (Chapman et al. 2010), wherein the reasoning for the changes now accepted into the *Code* is set out.

Draft wording of revised Articles 29, 30, and 31 and Recommendations 29A, 30A, and 31A

Here we reproduce the wording of all of the relevant Articles, Notes, and Recommendations (omitting the Examples), with the changes highlighted in **bold**. The wording here is provisional, pending the meeting of the Editorial Committee in December 2011 to finalize the printed version of the *Melbourne Code*.

Article 29

29.1. Publication is effected, under this *Code*, by distribution of printed matter (through sale, exchange or gift) to the general public or at least to botanical institutions with libraries accessible to botanists generally. **Publication is also effected by electronic distribution of material in Portable Document Format (PDF; see also Art. 29.3 and Rec. 29A.1) in an online publication with an International Standard Serial Number (ISSN) or an International Standard Book Number (ISBN).** Publication is not effected by communication of new names at a public meeting, by the placing of names in collections or gardens open to the public, by the issue of microfilm made from manuscripts, typescripts or other unpublished material, or by distribution electronically **other than as described above**.

29.2. **For the purpose of this Article, “online” is defined as accessible electronically via the World Wide Web.**

29.3. Should Portable Document Format (PDF) be succeeded, a successor international standard format communicated by the General Committee (see Div. III) is acceptable.

29.4. The content of a particular electronic publication must not be altered after it is first issued. Any such alterations are not themselves effectively published. Corrections or revisions must be issued separately to be effectively published.

Recommendation 29A

[Existing Recommendation replaced by the following:]

29A.1. Publication electronically in Portable Document Format (PDF) should comply with the PDF/A archival standard (ISO 19005).

29A.2. Authors should preferably publish in publications that are archived, satisfying the following criteria as far as is practical (see also Rec. 29A.1):

(a) The material should be placed in multiple trusted online digital repositories, e.g. an ISO-certified repository;

(b) Digital repositories should be in more than one area of the world and preferably on different continents;

(c) Deposition of printed copies in libraries in more than one area of the world and preferably on different continents is also advisable.

Article 30

30.1. Publication by distribution of electronic material does not constitute effective publication before 1 January 2012.

30.2. An electronic publication is not effectively published if there is evidence associated with or within the publication that it is merely a preliminary version that was, or is to be, replaced by a version that the publisher considers final, in which case only that final version is effectively published.

30.3. Publication by indelible autograph before 1 January 1953 is effective. Indelible autograph produced at a later date is not effectively published.

30.4. For the purpose of this Article, indelible autograph is handwritten material reproduced by some mechanical or graphic process (such as lithography, offset, or metallic etching).

30.5. Publication on or after 1 January 1953 in trade catalogues or non-scientific newspapers, and on or after 1 January 1973 in seed-exchange lists, does not constitute effective publication.

30.6. The distribution on or after 1 January 1953 of printed matter accompanying exsiccatae does not constitute effective publication.

Note 1. If the printed matter is also distributed independently of the exsiccata, it is effectively published.

30.7. Publication on or after 1 January 1953 of an independent non-serial work stated to be a thesis submitted to a university or other institute of education for the purpose of obtaining a degree is not effectively published unless it includes an explicit statement (referring to the requirements of the *Code* for effective publication) or other internal evidence that it is regarded as an effective publication by its author or publisher.

Note 2. The presence of an International Standard Book Number (ISBN) or a statement of the name of the printer, publisher, or distributor in the original printed version is regarded as internal evidence that the work was intended to be effectively published.

Recommendation 30A

30A.1. Preliminary and final versions of the same electronic publication should be clearly indicated as such when they are first issued.

30A.2. It is strongly recommended that authors avoid publishing new names and descriptions or diagnoses of new taxa (nomenclatural novelties) in ephemeral printed matter of any kind, in particular printed matter that is multiplied in restricted and uncertain numbers, in which the permanence of the text may be limited, for which effective publication in terms of number of copies is not obvious, or that is unlikely to reach the general public. Authors should also avoid publishing new names and descriptions or diagnoses in popular periodicals, in abstracting journals, or on correction slips.

30A.3. To aid availability through time and place, authors publishing nomenclatural novelties should give preference to periodicals that regularly publish taxonomic articles. **Otherwise, a copy of a publication (whether published as printed or electronic matter) should be sent to an indexing centre appropriate to the taxonomic group, and publications that exist only as printed matter** should be deposited in at least ten, but preferably more, botanical or other generally accessible libraries throughout the world.

30A.4. Authors and editors are encouraged to mention nomenclatural novelties in the summary or abstract, or list them in an index in the publication.

Article 31

31.1. The date of effective publication is the date on which the printed **or electronic** matter became available as defined in Art. 29 and 30. In the absence of proof establishing some other date, the one appearing in the printed **or electronic** matter must be accepted as correct.

[Existing Note 1 replaced by the following:]

31.2. When a publication is issued in parallel electronic and printed versions, these must be treated as effectively published on the same date unless the dates of the versions are different according to Art. 31.1.

31.3. When separates from periodicals or other works placed on sale are issued in advance, the date on the separate is accepted as the date of effective publication unless there is evidence that it is erroneous.

Recommendation 31A

31A.1. The date on which the publisher or publisher's agent delivers printed matter to one of the usual carriers for distribution to the public should be accepted as its date of effective publication.

Best practice

Authors of new names, editors and publishers will all be interested in ensuring that the publications including new names are in accordance with the *Melbourne Code*, so that the names therein are effectively published. We suggest that those publishing in journals or monograph series and books that have online editions communicate with the editors so that best practice can be established across the community as quickly as possible. Many publishers have been carefully addressing the issues involved with the e-publication of novelties for some time (see Knapp and Wright 2010; guidelines in PLoS One [<http://www.plosone.org/static/policies.action#taxon>]) and considerable interest in making these new *Code* changes function effectively has been apparent.

Some practices that we feel will help with the initial stages of e-publication of novelties that are according to the *Melbourne Code* are:

- Having each article bear the date of publication prominently (as is done in many journals, for example *New Phytologist* or *Nature*).
- If an online early version is issued that is not the same as the final version (and thus not the place of effective publication), stamp each article with this fact prominently (for example *American Journal of Botany*).
- Prominent display of the ISSN or ISBN of the publication on each article will help indexers establish effective publication.
- Publication in journals (or monograph series) that participate in the CLOCKSS system (see Knapp and Wright 2010 for a description) or another international archive and preservation system will ensure long-term archiving.
- Authors of new names by electronic means should alert the appropriate indexing center as recommended in Rec. 30A.3 - this will help indexers who may otherwise not be aware of electronically published names.

What these changes do not mean

Although the new Articles and Recommendations use the terms PDF and PDF/A, this does not mean that publications must be issued *only* in that format to be effectively published. For example, some online journals issue papers in Hypertext Markup Language (HTML) format together with a parallel PDF version. In such cases, the PDF version will be effectively published. The stipulation that the General Committee for Botanical Nomenclature will communicate the acceptability of a new international standard format, should PDF ever be succeeded, means authors of novelties and the community using the *Code* can remain informed as to advances in the field and that the *Code* will be protected from obsolescence.

Use of the following means of electronic publication will *not* result in effective publication of novelties under the *Melbourne Code*:

- Publication on websites or in ephemeral documents available over the Internet (there are strict criteria for granting of ISSNs [<http://www.issn.org>]).
- Publication in journals without a registered ISSN or e-ISSN.
- Publication in books without a registered ISBN or e-ISBN.

The Recommendation approved to advise the deposition of a hard copy of any e-publication in a library suggests to botanists an action, but it does not set out standard practice or a protocol for librarians to follow. Librarians are themselves in a complex transition zone between publication modalities (Johnson and Luther 2007), and botanists may find librarians to be unwilling or unable to accommodate single hard copy papers as individual accessions should the volume be great.

Two other important changes to the *Code* relating to the publication of names

The second change to the *Code* approved in Melbourne to take effect from 1 January 2012 is that the description or diagnosis required for valid publication of the name of a new taxon of all organisms falling under the *Code* may be in either English or Latin. This is the current provision for names of plant fossils, but all new non-fossil taxa have required a Latin description or diagnosis (fungi and plants from 1 January 1935; algae [including cyanobacteria, if treated under the *Code*] from 1 January 1958). This has no bearing on the form of scientific names, which continue to be Latin or treated as Latin. Individual journal requirements for Latin and/or English will, of course, be determined by the editors of those journals.

A third change to the *Code* approved in Melbourne relating to publication of names, but one not taking effect until 1 January 2013 (not 1 January 2012 as reported by Miller et al. 2011), is that all new names of organisms treated as fungi must, as an additional requirement for valid publication, include in the protologue (everything associated with a name at its valid publication) the citation of an identifier issued by a recognized repository (such as MycoBank [<http://www.mycobank.org/>]). This will be publicized separately.

The requirement for a unique identifier for new names of fungi on or after 1 January 2013 does *not* apply to plants or algae; there is no need for authors of new names in these groups to request Life Science Identifiers (LSIDs) - or other identifiers - from indexing centers.

Acknowledgements

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To encourage dissemination of the changes made to the International Code of Nomenclature for algae, fungi, and plants, this article will be published in *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, *Plant Diversity and Resources*, *Systematic Botany* and *Taxon*.

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Translation into Chinese of: "Changes to publication requirements made at the XVIII International Botanical Congress in Melbourne – what does e-publication mean for you?". Translated by Li-Bing Zhang

在墨尔本召开的第18届国际植物学大会做出的有关名称发表要求的变化 — 电子出版物对你意味着什么?

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摘要

《国际植物命名法规》的修订由每六年一次的国际植物学大会(IBC)命名分会来决定。第18届国际植物学大会在澳大利亚墨尔本举行；命名分会于2011年7月18日至22日召开，其决议获得7月30日的全体会议通过。“墨尔本法规”有几个重要的变化，将影响新名称的发表。这些变化中的两个将在“墨尔本法规”出版前的几个月，即于2012年1月1日起生效。通过以移动文档格式(Portable Document Format; pdf)在线发表的具有国际标准连续出版物号(ISSN)或国际标准图书编号(ISBN)的电出版物，将构成有效发表。新分类群名称的合格发表所必须的拉丁文描述或特征集要将更改为拉丁文或英文描述或特征集要。此外，自2013年1月1日起，被处理为真菌的生物的新名称必须在原始资料(某一名称合格发表时与之有关的所有资料)中引证一个由一家公认的存储库(例如MycoBank)签发的标识符，才构成合格发表。本文提供了有关电子出版物的新规则的草案文本，并概述了相应的最佳做法。

为便于新的《国际藻类、真菌和植物命名法规》中的变化得到广泛的了解, 本文将发表在 *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, 《植物分类与资源学报》, *Systematic Botany* 和 *Taxon*。

序言

于2011年7月在澳大利亚墨尔本召开的第18届国际植物学大会通过的《国际植物命名法规》(现称为《国际藻类、真菌和植物命名法》规)有两个重要的变化, 并将于2012年1月1日生效。这些变化将影响到每一个发表相关名称的人。由于“墨尔本法规”大约要等到2012年中才能出版, 我们认为将这些变化, 特别是那些有关在电子媒体中有效发表的变化(规则29, 30, 31), 做一概述, 将对我们的读者有所裨益。有关在墨尔本接受的所有变化的一个简明报告, 可参阅 McNeill et al. (2011)。

本文提供了修订后的有关有效发表的规则、注释和辅则的草案, 以帮助编辑和出版商建立为实施本法规的最佳做法。我们这里还概述了这些变化并不包含的意思, 以指导那些希望通过电子方式发表新名称和指定模式的人们。我们促请读者阅读电子发表特别委员会的报告 Chapman et al. 2010 以及国际植物学大会之前的相关提案。有关法规修订的理由在那里有详细的陈述。

修订后的规则29, 30和31, 和辅则29A, 30A及31A的草案

在这里, 我们复制了所有相关的规则、注释和辅则(省去例子), 黑体字指法规中新的变化。这里的措辞只是临时性的, 印刷版的“墨尔本法规”的内容将由2011年12月召开的法规编辑委员会会议来决定。

规则29

29.1. 根据本法规, 只有将印刷品向一般公众发行(通过出售、交换或赠送), 或至少分送给具有普通植物学家可使用的图书馆的植物学研究机构, 这样的发表才是有效发表(effective publication)。通过以移动文档格式(**Portable Document Format(pdf; 也见规则29.3及辅则29A.1)**在线发表的具有国际标准连续出版物号(**International Standard Serial Number; ISSN**)或国际标准图书编号(**International Standard Book Number; ISBN**)的电子发行, 也是有效发表。在公共会议上对新名称的交流, 或将名称置于对公众开放的标本馆或植物园, 或发行由文稿(**manuscript**)、打字稿(**typescripts**)或其他未发表的材料(**unpublished material**)制成的微缩胶片(**microfilm**), 或通过上述电子发表方式之外的电子发表, 均为无效发表。

29.2. 就本规则的实际应用而言,“在线”指的是可通过万维网(World Wide Web)访问的。

29.3. 如果今后移动文档格式(pdf)被取代,可以接受由总委员会(见第三部分)通报的下一个国际标准格式。

29.4. 一个电子出版物首次发行以后,其内容便不能更改。任何更改都是无效发表。对其更正或修改必须独立地发表才构成有效发表。

辅则29A

[现有辅则被下面辅则取代]

29A.1. 以移动文档格式(pdf)的电子发表应遵照pdf/A存档标准(国际标准化组织(ISO)19005)。

29A.2. 在切实可行的情况下,作者在发表存档的出版物时,应该最好满足以下条件(也见辅则29A.1):

(a) 材料应存放在多个值得信赖的在线数字资源库,如国际标准化组织(ISO)认证的存储库;

(b) 数字资源库应放置在这个世界上多个地区,最好在不同的大洲;

(c) 印本应存放在世界上多个地区、最好在不同的大洲的图书馆。

规则30

30.1. 2012年1月1日前电子材料的分发并不构成有效的发表。

30.2. 如果存在跟电子出版物相关的证据或有电子出版物内部的证据显示,该电子出版物仅仅是一个初级的版本或将要被一个出版者所认为的最终版本所取代,该电子出版物便不构成有效发表。在这种情况下,只有最终版本才是有效发表。

30.3. 1953年1月1日之前的擦不掉的手写体(indelible autograph)出版物是有效发表。其后出现的擦不掉的手写体为无效发表。

30.4. 就本规则的具体应用而言,擦不掉的手写体是指通过机械或图像过程(例如平版印刷,胶印,或金属蚀刻)复制的手写材料。

30.5. 1953年1月1日或之后发行的商业目录(trade catalogue)或非学术性报纸,以及1973年1月1日或之后发行的种子交换目录(seed-exchange list),均不构成有效发表。

30.6. 在1953年1月1日或之后随腊叶标本(exsiccatae)而被分发的印刷品不构成有效发表。

注释1. 如果该印刷品在随腊叶标本之外也有分发,则构成有效发表。

30.7. 在1953年1月1日或之后,指明为提交给大学或其它教育机构而为获得某种学位的、独立的、非系列的毕业论文的发表,是无效发表,除非论文中清楚地说明(指本法规中有效发表的必要条件)或其它的内部证据(internal evidence)显示其作者或出版者视它为有效发表。

注释2. 国际标准图书编号(International Standard Book Number; ISBN)的存在, 或在原始印刷版中指出了有关印刷厂、出版者或发行者的名字, 均被视为相关著作有意为有效发表的内部证据。

辅则30A

30A.1. 同一电子出版物的初级和最终版本在第一次发行时, 应清楚地表明它们的版本。

30A.2. 本法规强烈地建议, 作者应竭力避免在任何临时性的印刷品(ephemeral printed matter)中、特别是那些印数有限和不定的印刷品中发表新名称和新分类群的描述或特征集要(命名新材料nomenclatural novelties)。这样的印刷品内容的持久性可能会受到限制, 其有效发表的拷贝数亦不明显, 或者一般公众不太可能接触到。作者也应避免在通俗刊物(popular periodicals)、文摘杂志(abstracting journals)或勘误表(correction slip)上发表新名称和描述或特征集要。

30A.3. 为提高时间和地点方面的可用性, 发表命名新材料的作者应尽量选择经常发表分类学文章的期刊。否则, 应将其文章的拷贝(无论是印本发表或电子发表)寄给适当的与分类群相关的索引中心(indexing centre)。只有印本发表的文章应存于世界上至少10个或最好更多的植物学或其它一般的公共图书馆。

30A.4. 作者和编辑最好在摘要(abstract)或概要(summary)中提及所发表的命名新材料, 或将其列在出版物的索引中。

规则31

31.1. 有效发表的日期是, 根据规则29和30的规定, 印刷品或电子件可被使用的日期。如果没有证据证明不同, 印刷品或电子件上的日期必须被接受为正确的日期。

[现有的注释1被以下规则取代]

31.2. 当一个出版物同时发行在印刷版和电子版上, 必须视印刷版和电子版的有效发表日期相同, 除非根据规则31.1. 印刷版和电子版的有效发表日期不同。

31.3. 当期刊或其它出售品的抽印本被提前发行时, 抽印本上的日期为有效发表日期, 除非有证据显示该日期是错误的。

辅则31A

31A.1. 出版商或其代理将印刷品交付给平常的投递人向公众发行的日期, 应被接受为该印刷品的有效发表日期。

最佳做法

新名称的作者、编辑和出版商都将确保含新名称的出版物符合“墨尔本法规”，以便其中的名称是有效发表。我们建议，含网络版的学术期刊或专著系列和书籍的作者与相关编辑沟通，使最佳做法可以在整个领域尽快建立起来。在有一段时间以来，许多出版商都精心讨论过有关新材料的电子发表问题(见 Knapp and Wright 2010, *PLoS One*指南[<http://www.plosone.org/static/policies.action#taxon>])。对法规的这些修改使其有效地发挥作用，已势在必行。

我们认为，有些做法将有助于符合“墨尔本法规”的电子发表新材料的开始阶段：

- 在每篇文章的醒目位置注明出版日期(象许多杂志所为，例如*New Phytologist*或*Nature*)。
- 如果早期网络版不是最终版(因而不是有效发表的地方)，应在醒目位置注明这一事实(例如*American Journal of Botany*)。
- 突出显示每篇文章所在的出版物的ISSN或ISBN，将有助于索引编写者确定有关名称是否为有效发表。
- 发表在参与CLOCKSS系统(描述见 Knapp and Wright 2010)或其他国际存档和保存系统的期刊(或专著系列)上的文章，将确保其长期归档。
- 通过电子方式发表新名称的作者，应采纳辅则30A.3的建议而提醒适当的索引中心。这将有助于索引编写者意识到其通过电子方式发表的名称。

这些变化不意味着什么

尽管新的规则和辅则使用PDF和PDF / A术语，这并不意味着，为了有效发表就只能发行这种格式。例如，一些在线期刊发行超文本标记语言(Hyper-text Markup Language; HTML)格式的论文，同时还有一个PDF的版本。在这种情况下，PDF版将是有效发表。如果将来PDF格式被取代，植物命名总委员会将通报一个新的国际标准格式的接受情况。这一规定意味着，新材料的作者和使用法规的人们会及时了解到该领域的进展情况，并保护法规不至于过时。

根据“墨尔本法规”，使用下列电子出版方式不构成新材料的有效发表：

- 网页上的发表或在因特网上出现的短暂文件(发放ISSN号有严格的标准 - 见[<http://www.issn.org>])。
- 没有ISSN号或e-ISSN号的期刊上的发表。
- 没有ISSN号或e-ISSN号的书籍中的发表。

获得植物学大会通过的辅则虽建议植物学家们将任何电子出版物的电脑打印件保存在图书馆里，但该辅则并没设定标准做法或需图书馆馆员遵从的规程。图书馆馆员本身处在出版模式之间的复杂的过渡区(Johnson and Luther 2007)。植物学家可能会发现，如果要保存的量很大，图书馆馆员不愿或无法收存个人单篇论文的电脑打印件。

法规中另外两个重要的有关名称发表的变化

在墨尔本获得通过的从2012年1月1日起生效的法规的第二个变化是，法规所管理的所有生物的新分类群名称的合格发表所需的描述或特征集要可以是英文或拉丁文。这是目前对发表植物化石名称的规定，但所有非化石分类群的新名称的发表，目前都需要拉丁文描述或特征集要(真菌和植物从1935年1月1日开始，藻类[包括根据该法规处理的蓝藻]从1958年1月1日开始)。这一变化跟学名的形式没有关系。学名将继续为拉丁词或被处理为拉丁词。当然，至于期刊要求描述或特征集要为英文和/或拉丁文，则由这些期刊的编辑决定。

直到2013年1月1日才生效(不是如Miller et al. 2011 所报道的2012年1月1日)的第三个在墨尔本获得通过的有关名称发表的法规的变化是，作为合格发表的附加要求，被处理为真菌的生物的所有新名称必须在原始资料(某一名称合格发表时与之有关的所有资料)中引证一个由一家公认的存储库(例如 MycoBank [<http://www.mycobank.org/>])签发的标识码。这将另行公布。

2013年1月1日或之后的真菌新名称的独特标识码的规定并不适用于植物或藻类；这些类群的新名称的作者不需要从索引中心申请生命科学标识码(Life Science Identifiers; LSIDs)或其他标识码。

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为便于新的《国际藻类、真菌和植物命名法规》中的变化得到广泛的了解，本文将发表在*BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, 《植物分类与资源学报》, *Systematic Botany*和*Taxon*。

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Translation into Portuguese of: "Changes to publication requirements made at the XVIII International Botanical Congress in Melbourne – what does e-publication mean for you?". Translated by Jefferson Prado, Regina Y. Hirai, and Cíntia Kameyama

Alterações nos requisitos de publicação feitas no XVIII Congresso Internacional de Botânica em Melbourne – o que significa publicação eletrônica para você?

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Resumo

Alterações no *Código Internacional de Nomenclatura Botânica* são decididas a cada seis anos na Sessão de Nomenclatura, associada ao Congresso Internacional de Botânica (CIB). O XVIII CIB foi realizado em Melbourne, Austrália; a Sessão de Nomenclatura ocorreu de 18–22 de julho de 2011 e suas decisões foram aceitas pelo Congresso, em sua sessão plenária em 30 de julho. Como resultado desta reunião, foram decididas várias mudanças importantes no *Código* que afetarão a publicação de novos nomes. Duas dessas mudanças se tornarão efetivas em 1º de janeiro de 2012, alguns meses antes do *Código de Melbourne* ser publicado. Material eletrônico publicado online em Formato de Documento Portátil (PDF) com um Número Padrão Internacional de Séries (ISSN) ou com um Número Padrão Internacional de Livros

(ISBN) constituirão publicação efetiva e o requisito de uma descrição ou diagnose em latim para nomes de táxons novos será substituído por uma descrição ou diagnose em latim ou inglês. Além disso, nomes novos de organismos tratados como fungos devem, a partir de 1º de janeiro de 2013, a fim de ser validamente publicados, incluir no seu protótipo a citação de um número identificador de um indexador de nomes (p.e., MycoBank). O texto preliminar de novos artigos, tratando de publicação eletrônica, é apresentado e o melhor modo de fazer isto é discutido.

Para encorajar a disseminação das mudanças feitas no *Código Internacional de Nomenclatura para algas, fungos e plantas*, este artigo será publicado na *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, *Plant Diversity and Resources*, *Systematic Botany* e *Taxon*.

Introdução

No XVIII Congresso Internacional de Botânica em Melbourne, Austrália, em julho de 2011, duas alterações importantes foram decididas para o *Código Internacional de Nomenclatura Botânica* (agora, o *Código Internacional de Nomenclatura para algas, fungos e plantas*) e se tornarão efetivas a partir de 1º de janeiro de 2012. Essas mudanças afetarão todos aqueles que publicam nomes regidos por este *Código*. Como o *Código de Melbourne* não será publicado até aproximadamente a metade de 2012, nós achamos que seria útil esboçar essas mudanças, particularmente aquelas relacionadas à publicação efetiva em mídia eletrônica (nos Artigos 29, 30 e 31). Um relatório conciso de todas as alterações para o *Código* aceitas em Melbourne, pode ser visto em McNeill et al. (2011).

Um rascunho revisado da redação dos Artigos, Notas e Recomendações sobre publicação efetiva é apresentado para auxiliar os editores e editoras no estabelecimento de boas práticas para implementação deste aspecto do *Código*. Nós também esboçamos aqui o que essas mudanças *não* significam, para guiar aqueles que desejam publicar nomes novos e tipificações por meios eletrônicos. Nós recomendamos aos leitores consultar o relatório do Comitê Especial sobre Publicação Eletrônica que acompanha as mudanças propostas anteriormente ao Congresso (Chapman et al. 2010), onde estão as razões para estas alterações agora aceitas no *Código* e aqui expostas.

Rascunho revisado da redação dos Artigos 29, 30 e 31 e Recomendações 29A, 30A e 31A

Nós reproduzimos aqui a redação de todos os Artigos, Notas e Recomendações relevantes (omitindo os Exemplos), com as mudanças destacadas em **negrito**. A redação aqui é provisória, dependendo da reunião do Comitê Editorial em dezembro de 2011 para finalizar a versão impressa do *Código de Melbourne*.

Artigo 29

29.1. A publicação é efetiva, segundo este *Código*, somente pela distribuição de matéria impressa (por meio de venda, intercâmbio ou doação) ao público em geral ou, pelo menos, às instituições botânicas com bibliotecas acessíveis aos botânicos em geral. **A publicação também é efetiva pela distribuição eletrônica da matéria em Formato de Documento Portátil (PDF; veja também Art. 29.3 e Rec. 29A.1) em uma publicação online com um Número Padrão Internacional de Séries (ISSN) ou com um Número Padrão Internacional de Livros (ISBN).** Não é efetiva pela comunicação de nomes novos em reuniões públicas, pela colocação de nomes em coleções ou jardins abertos ao público, pela produção de microfilme feito a partir de manuscritos, textos datilografados ou outro material não publicado, ou pela distribuição eletrônica ou por qualquer meio eletrônico, **exceto como descrito acima.**

29.2. Para propósito deste Artigo, “online” é definido como acessível eletronicamente via “World Wide Web”.

29.3. Caso o Formato de Documento Portátil (PDF) seja sucedido por um formato padrão internacional, este formato sucessor informado pelo Comitê Geral (veja Div. III), é aceitável.

29.4. O conteúdo de uma publicação eletrônica em particular não deve ser alterado depois dele publicado pela primeira vez. Nenhuma dessas alterações é efetivamente publicada. Correções ou revisões devem ser publicadas separadamente para serem efetivamente publicadas.

Recomendação 29A

[A Recomendação atual será substituída pelas seguintes]

29A.1. A publicação eletrônica em Formato de Documento Portátil (PDF) deveria estar de acordo com o padrão de arquivo PDF/A (ISO 19005).

29A.2. Autores deveriam preferencialmente publicar em publicações que são arquivadas, cumprindo os seguintes critérios tanto quanto possível na prática (veja também Rec. 29A.1):

(a) O material deveria ser colocado em múltiplos repositórios digitais online confiáveis, p.e., um repositório com certificado ISO;

(b) Repositórios digitais deveriam estar em mais de um local do mundo e preferencialmente em diferentes continentes;

(c) É também recomendável o depósito de cópias impressas em bibliotecas em mais de um local do mundo e preferencialmente em diferentes continentes.

Article 30

30.1. Publicação através da distribuição de matéria eletrônica não constitui publicação efetiva antes de 1º de janeiro de 2012.

30.2. Uma publicação eletrônica não é efetivamente publicada caso exista uma evidência associada com ou dentro dela de que ela seja meramente uma versão preliminar, que foi ou que será substituída por uma versão que o editor considera final, neste caso somente a versão final é efetivamente publicada.

30.3. Publicação através de manuscrito indelével é efetiva antes de 1º de janeiro de 1953. Manuscrito indelével produzido em data posterior não é efetivamente publicado.

30.4. Para fins deste artigo, manuscrito indelével é o material manuscrito reproduzido por algum processo mecânico ou gráfico (tal como litografia, 'offset' ou gravação em chapa metálica).

30.5. Publicação em ou a partir de 1º de janeiro de 1953, em catálogos de intercâmbio ou em revistas não-científicas e em ou a partir de 1º de janeiro de 1973, em listas de intercâmbio de sementes, não constitui publicação efetiva.

30.6. A distribuição em ou a partir de 1º de janeiro de 1953, de material impressa que acompanhe exsicatas não constitui publicação efetiva.

Nota 1. Se a matéria impressa também for distribuída independente da exsicata, constitui publicação efetiva.

30.7. Publicação em ou a partir de 1º de janeiro de 1953, de um trabalho independente, não seriado, definido como uma tese submetida a uma Universidade ou outro instituto de educação com o propósito de obtenção de grau, não é efetivamente publicada, a menos que inclua uma declaração explícita (referente aos requisitos do *Código* para publicação efetiva) ou outra evidência interna de que seja entendida como uma publicação efetiva por seu autor ou editor.

Nota 2. A presença de um Número Padrão Internacional de Livros (ISBN) ou a colocação do nome da gráfica, da editora ou distribuidor na versão impressa original é entendido como evidência interna de que o trabalho foi definido como efetivamente publicado.

Recommendation 30A

30A.1. Versões preliminares e finais da mesma publicação eletrônica deveriam ser claramente indicadas tal como quando são publicadas pela primeira vez.

30A.2. É fortemente recomendado que os autores evitem publicar nomes novos e descrições ou diagnoses de táxons novos (novidades nomenclaturais) em matéria impressa de qualquer tipo que seja efêmera, em matéria impressa particular que seja multiplicada em números restritos e incertos, nos quais a permanência do texto possa ser limitada, para os quais a publicação efetiva em termos de número

de cópias não seja óbvia ou que seja improvável que alcance o público em geral. Os autores deveriam também evitar nomes novos e descrições ou diagnoses em revistas populares, em revistas de resumos ('abstracting journals') ou em etiquetas de correção.

30A.3. Para ajudar na disponibilidade em termos de tempo e lugar, os autores ao publicar novidades nomenclaturais, deveriam dar preferência a revistas periódicas que regularmente publiquem artigos taxonômicos. **Por outro lado, uma cópia da publicação (se publicada como matéria eletrônica ou impressa) deveria ser enviada para um centro indexador apropriado do grupo taxonômico e publicações que existirem somente como matéria impressa** deveriam ser depositadas em, pelo menos dez, mas preferivelmente em mais bibliotecas botânicas ou outras geralmente acessíveis em todo o mundo.

30A.4. Autores e editores são encorajados a mencionar as novidades nomenclaturais no resumo ou no 'abstract' ou listá-las num índice na própria publicação.

Article 31

31.1. A data de publicação efetiva é a data na qual a matéria impressa **ou eletrônica** tornou-se disponível conforme definido nos Art. 29 e 30. Na ausência de prova estabelecendo alguma outra data, a data que aparece na matéria impressa **ou eletrônica** deve ser aceita como correta.

[A Nota 1 atual será substituída pelo seguinte]

31.2. Quando uma publicação é lançada paralelamente em versões eletrônica e impressa, estas devem ser tratadas como efetivamente publicadas na mesma data a menos que as datas das versões sejam diferentes de acordo com o Art. 31.1.

31.3. Quando separatas de periódicos ou outros trabalhos colocados à venda são distribuídos antes, a data na separata é aceita como a data da publicação efetiva, a menos que haja evidência de que esteja errada.

Recomendação 31A

31A.1. A data na qual o editor ou o agente do publicador distribuiu a matéria impressa a um dos transportadores usuais para distribuição ao público deveria ser aceita como a data de publicação efetiva.

Boas práticas

Autores de nomes novos, editores e editoras estarão todos interessados em assegurar que as publicações incluindo nomes novos estejam de acordo com o *Código de Mel-*

bourne, de tal modo que os nomes sejam efetivamente publicados. Nós sugerimos que aqueles que publicam, em periódicos ou monografias seriadas e livros que tenham edições online, se comuniquem com os editores de modo que as boas práticas possam ser estabelecidas na comunidade, o mais rápido possível. Já há algum tempo, muitos editores tem sido cuidadosamente orientados sobre as novidades relacionadas às publicações eletrônicas (veja Knapp and Wright 2010; guia para autores em PLoS One [<http://www.plosone.org/static/policies.action#taxon>] e eles tem, aparentemente, um considerável interesse em tornar essas novas mudanças do *Código* efetivas.

Nós acreditamos que algumas práticas que ajudarão nos estágios iniciais das publicações eletrônicas de novidades, que estão de acordo com o *Código de Melbourne*, são:

- Cada artigo ter a data de publicação bem evidente (como é feito em vários periódicos, p.e., *New Phytologist* ou *Nature*).
- Se uma versão anterior online é publicada e esta não for igual à versão final (e deste modo não é o local de publicação efetiva), estampar em cada artigo esta informação de forma bem evidente (p.e., *American Journal of Botany*).
- A exposição bem evidente do ISSN ou ISBN da publicação em cada artigo ajudará os indexadores estabelecer a publicação efetiva.
- A publicação em periódicos (ou monografias seriadas) que participam do sistema CLOCKSS (veja Knapp and Wright 2010 para uma descrição) ou de outro sistema internacional de arquivo e preservação garantirá o arquivamento a longo prazo.
- Autores de nomes novos por meio eletrônico deveriam alertar o centro indexador apropriado como recomendado na Rec. 30A.3 – isto ajudará os indexadores que poderiam não estar cientes dos nomes publicados eletronicamente.

O que essas mudanças não significam

Embora os novos Artigos e Recomendações usem os termos PDF e PDF/A, isto não significa que as publicações devam ser lançadas *somente* neste formato para ser efetivamente publicadas. Por exemplo, alguns periódicos online publicam trabalhos em formato HTML (Linguagem de Marcação de Hipertexto) junto com uma versão paralela em PDF. Nestes casos, a versão PDF será a efetivamente publicada. A determinação de que o Comitê Geral para Nomenclatura Botânica informará a aceitação de um novo formato padrão internacional, que poderá suceder o PDF, significa que autores de novidades e a comunidade que usam o *Código* permanecerão informados sobre os avanços na área e que o *Código* estará protegido da obsolescência.

O uso dos seguintes meios de publicação eletrônica *não* resultará em publicação efetiva de novidades sob o *Código* de Melbourne:

- A publicação em sítios na Web ou em documentos efêmeros disponíveis na Internet (há critérios estritos para concessão de ISSNs [<http://www.issn.org>]).
- A publicação em periódicos sem um ISSN ou e-ISSN registrado.
- A publicação em livros sem um ISBN ou e-ISBN registrado.

A Recomendação aprovada para orientar o depósito de uma cópia impressa de qualquer publicação eletrônica em uma biblioteca sugere aos botânicos uma ação, mas isto não estabelece uma prática padrão ou um protocolo para os bibliotecários seguirem. Os bibliotecários encontram-se em uma zona de transição complexa entre modalidades de publicação (Johnson and Luther 2007) e os botânicos podem encontrá-los não dispostos ou capacitados para acomodar cópias impressas avulsas de trabalhos como entradas pontuais, se o volume for grande.

Outras duas mudanças importantes para o *Código* relacionadas à publicação de nomes

A segunda mudança para o *Código*, aprovada em Melbourne, que entrará em vigor a partir de 1º de janeiro de 2012 é que a descrição ou diagnose, requerida para publicação válida de um nome de um novo táxon de todos os organismos, sob este *Código*, pode ser em inglês ou em latim. Esta é uma provisão corrente para nomes de plantas fósseis, porém todos os táxons novos não-fósseis requeriam uma diagnose ou descrição em latim (fungos e plantas desde 1º de janeiro de 1935; algas [incluindo cianobactérias, se tratadas sob este *Código*] desde 1º de janeiro de 1958). Isto não se refere à forma de nomes científicos, que continuam sendo em latim ou tratados em latim. Os requisitos de cada periódico para latim e/ou inglês, deverão, claro, ser determinados pelos editores desses periódicos.

A terceira mudança para o *Código* aprovada em Melbourne está relacionada à publicação de nomes, porém não terá efeito até 1º de janeiro de 2013 (não em 1º de janeiro de 2012 como relatado por Miller et al. 2011), é que todos os nomes novos de organismos tratados como fungos devem, como um requisito adicional para publicação válida, incluir no protólogo (tudo associado com o nome na sua publicação válida) a citação de um número identificador de um repositório reconhecido (p.e., MycoBank [<http://www.mycobank.org/>]). Isto será divulgado à parte.

O requisito para um único identificador para nomes novos de fungos em ou a partir de 1º de janeiro de 2013 *não* se aplica a plantas ou algas; não há necessidade que autores de nomes novos nesses grupos requeram “Life Science Identifiers” (LSIDs) – ou outros identificadores – de centros indexadores.

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Para encorajar a disseminação das mudanças feitas no *Código Internacional de Nomenclatura para algas, fungos e plantas*, este artigo será publicado na *BMC Evolutionary*

Biology, Botanical Journal of the Linnean Society, Brittonia, Cladistics, MycoKeys, Myco-taxon, New Phytologist, North American Fungi, Novon, Opuscula Philolichenum, PhytoK-ey, Phytoneuron, Phytotaxa, Plant Diversity and Resources, Systematic Botany e Taxon.

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Translation into Russian of: “Changes to publication requirements made at the XVIII International Botanical Congress in Melbourne – what does e-publication mean for you?” Translated by Irina V. Belyaeva and Maria S. Vorontsova

Изменения требований к обнародованию, принятые на XVIII Международном Ботаническом Конгрессе в Мельбурне – что означает электронное обнародование?

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Резюме

Решения по изменениям *Международного Кодекса Ботанической Номенклатуры* принимаются каждые 6 лет на заседании Номенклатурной Секции Международного Ботанического Конгресса (МБК). XVIII МБК состоялся в Мельбурне, Австралия; Номенклатурная Секция заседала 18–22 июля 2011 г., и ее решения были утверждены Конгрессом на пленарном заседании 30 июля. В ходе этого заседания было сделано несколько важных изменений в *Кодексе*, которые затрагивают обнародо-

вание новых названий. Два из этих изменений вступят в действие с 1 января 2012 г., несколькими месяцами раньше, чем *Мельбурнский Кодекс* будет опубликован. Электронные материалы, опубликованные онлайн в формате PDF (Portable Document Format) с Международным Стандартным Серийным Номером ISSN (International Standard Serial Number) или с Международным Стандартным Книжным Номером ISBN (International Standard Book Number) будут считаться эффективно обнародованными, а требование наличия латинского описания или диагноза при обнародовании новых названий будет заменено требованием наличия описания на латинском или английском языке. В дополнение к этому, чтобы быть эффективно и действительно обнародованными, с 1 января 2013 г. новые названия организмов, считающихся грибами, должны цитировать в протологе (все, что связано с названием при его действительной публикации) идентификационный номер (идентификатор), присвоенный признанным банком данных (например, MycoBank). Приводятся предварительные тексты новых статей *Кодекса*, касающихся электронной публикации и предложены наилучшие пути их практического применения.

С тем, чтобы ускорить распространение информации об изменениях, сделанных в *Международном Кодексе Номенклатуры водорослей, грибов и растений*, эта статья будет напечатана в журналах: *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Noron*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, *Plant Diversity and Resources*, *Systematic Botany* и *Taxon*.

Введение

На XVIII Международном Ботаническом Конгрессе в Мельбурне, Австралии, в июле 2011 года, были сделаны два важных изменения в *Международном Кодексе Ботанической Номенклатуры* (теперь — *Международный Кодекс Номенклатуры водорослей, грибов и растений*), которые начнут действовать с 1 января 2012 г.. Эти изменения будут касаться всех, кто публикует названия соответственно этому *Кодексу*. Поскольку *Кодекс*, принятый в Мельбурне, не будет опубликован примерно до середины 2012 г., мы полагаем, что было бы полезно описать эти изменения, в частности те, которые касаются эффективной публикации с помощью электронных средств массовой информации (в статьях 29, 30 и 31). Краткий отчет обо всех изменениях, принятых в Мельбурне, см. в McNeill et al. (2011).

Предварительные тексты измененных Статей, Примечаний и Советов *Кодекса* об эффективном обнародовании приведены с тем, чтобы помочь редакторам и издателям разработать наилучшие пути применения *Кодекса* в этом аспекте. Мы также разъясняем здесь, что эти изменения не означают, чтобы помочь тем, кто хочет обнародовать новые названия и типификации в электронном виде. Мы настоятельно советуем читателям сверяться с отчетом Специального Комитета по Электронным Публикациям (Charman et al. 2010), где объясняются причины изменений, предложенных перед Конгрессом, и принятых теперь в *Кодексе*.

Предварительный текст измененных Статей 29, 30 и 31 и Советов 29А, 30А и 31А

Здесь мы приводим текст всех относящихся к случаю Статей, Примечаний и Советов (пропуская Примеры) с изменениями, выделенными **жирным шрифтом**. Предложенный текст – предварительный, в ожидании заседания Редакционного Комитета в декабре 2011 г. и утверждения копии для печати *Мельбурнского Кодекса*.

Статья 29

29.1. Эффективное обнародование осуществляется, согласно настоящему *Кодексу*, через распространение печатного материала (посредством продажи, обмена или дарения) среди широкой публики или, по крайней мере, в ботанические учреждения с доступными для ботаников библиотеками. **Эффективное обнародование осуществляется также посредством распространения материала в электронном виде в формате PDF (см. также Ст. 29.3 и Сов. 29А.1), опубликованном онлайн с Международным Стандартным Серийным Номером (ISSN) или с Международным Стандартным Книжным Номером (ISBN).** Эффективное обнародование не производится путем сообщения новых названий на публичных заседаниях, указанием названий в открытых для публики коллекциях или садах, путем выпуска микрофильмов, сделанных с рукописей, машинописных текстов или других неопубликованных материалов, а также распространением названий на электронных носителях **иным путем, чем описано выше.**

29.2. Для целей этой статьи, термин «онлайн» определен как электронно доступный через Международную Мировую Сеть - Интернет (World Wide Web).

29.3. В случае изменения формата PDF принимается последующий международный стандартный формат, сообщенный Генеральным Комитетом (см. Разд. III).

29.4. Содержание конкретной электронной публикации не должно исправляться после того, как она была впервые обнародована. Любые поправки не являются эффективно обнародованными. Для эффективного обнародования исправления или изменения должны быть опубликованы отдельно.

Совет 29A

[Существующий Совет заменен следующим:]

29A.1. Электронная публикация в формате PDF должна быть совместима со стандартом для архивирования PDF/A (ISO 19005).

29A.2. Авторы должны отдавать предпочтение обнародованию в публикациях, которые архивируются соответственно следующим критериям настолько, насколько возможно (см. также Сов. 29A.1):

(a) Материал должен быть размещен в нескольких заслуживающих доверия электронных онлайн-банках данных, например, ISO-сертифицированный репозиторий;

(b) Цифровые банки информации должны быть размещены в более чем одном регионе и, предпочтительно, на разных континентах;

(c) Также рекомендуется рассылка печатных копий в библиотеки в более чем один регион мира и, предпочтительно, на разные континенты.

Статья 30

30.1. Обнародование, осуществляемое посредством распространения электронных материалов до 1 января 2012 г., не является эффективным.

30.2. Обнародование не является эффективным, если существуют факты, связанные с публикацией или содержанием публикации, свидетельствующие тому, что эта публикация является только предварительной версией, которая была или будет заменена версией, которую издатель считает окончательной; в этом случае только окончательная версия является эффективно обнародованной.

30.3. Обнародование до 1 января 1953 г. посредством несмываемой автографии является эффективным. Несмываемая автография, произведенная позднее этой даты не является эффективно обнародованной.

30.4. Применительно к настоящей статье, несмываемой автографией является рукописный материал, воспроизведенный каким-либо механическим или графическим способом (таким как литография, офсет или гравирование на металле).

30.5. Начиная с 1 января 1953 г., обнародование в торговых каталогах или в ненаучных информационных изданиях, а с 1 января 1973 г. и в обменных списках семян, не является эффективным обнародованием.

30.6. Начиная с 1 января 1953 г., распространение печатного материала, сопровождающего эксикаты (*exsiccatae*), не является эффективным обнародованием.

Примечание 1. Если печатный материал распространяется также и отдельно от эксикат, это является эффективным обнародованием.

30.7. Начиная с 1 января 1953 г., публикация отдельной несериальной работы с указанием, что она является диссертацией, представленной университету или другому образовательному учреждению с целью получения ученой степени, не является эффективным обнародованием, если в самой работе не содержится ясного указания (со ссылкой на требования *Кодекса* к эффективному обнародованию) или другого внутреннего (содержащегося в самой работе – *Прим. пер.*) свидетельства, что эта публикация предназначена для эффективного обнародования ее автором или издателем.

Примечание 2. Наличие ISBN (International Standard Book Number) или указание названия типографии, издательства или распространителя в оригинальной печатной версии рассматривается как внутреннее свидетельство того, что работа была предназначена для эффективного обнародования.

Совет 30А

30А.1. Предварительная и окончательная версии той же самой электронной публикации должны быть ясно обозначены как таковые при их первом издании.

30А.2. Авторам настоятельно рекомендуется избегать обнародования новых названий и описаний или диагнозов новых таксонов (номенклатурных новаций) в недолговечных печатных материалах любого рода, в частности, в таких, которые воспроизводятся в ограниченном и неопределенном количестве, в которых долговечность текста может быть ограниченной, для которых эффективное обнародование, исходя из количества экземпляров, не является очевидным, или в таких материалах, которые, скорее всего, не дойдут до широкой публики. Авторы должны также избегать обнародования новых названий и описаний или диагнозов в популярной периодике, реферативных журналах или в списках исправлений, прилагаемых к изданиям.

30А.3. Для того, чтобы обеспечить доступность во времени и пространстве, авторы, обнародующие номенклатурные новации, должны отдавать предпочтение периодическим изданиям, которые регулярно публикуют таксономические статьи. **В противном случае, копия публикации (опубликованной в печатном или электронном варианте) должна быть послана в центр индексации по соответствующей таксономической группе, а публикации, существующие только в печатном варианте,** должны быть помещены, по крайней мере, в десять, но предпочтительно большее число ботанических или других общедоступных библиотек во всем мире.

30А.4. Авторам и редакторам рекомендуется сообщать о номенклатурных новациях в резюме, реферате или перечислять их в указателе публикации.

Статья 31

31.1. Датой эффективного обнародования является дата, в которую печатный или **электронный** материал стал доступным, как определено в Ст. 29 и 30. При отсутствии доказательств, устанавливающих какую-либо другую дату, правильной следует считать дату, указанную на печатной или **электронной** копии.

[Существующее Примечание 1 заменено следующим:]

31.2. Если обнародование осуществлено параллельным выпуском электронной и печатной версий, это является эффективным обнародованием с одной и той же датой, если даты на копиях не разные, соответственно Ст. 31.1.

31.3. Если отдельные оттиски из периодических изданий или других работ, поступающих в продажу, выпускаются раньше этих публикаций, то дата оттиска принимается как дата эффективного обнародования, если нет доказательств, что она ошибочна.

Совет 31A

31A.1. За дату эффективного обнародования печатного произведения следует принимать ту дату, в которую издатель или его представитель выпускает это произведение в свет одним из обычных способов.

Рекомендации

Авторы новых названий, редакторы и издатели будут заинтересованы в обеспечении того, чтобы публикации, включающие новые названия, соответствовали *Мельбурнскому Кодексу* и чтобы названия в них были эффективно обнародованы. Мы предлагаем авторам публикаций в журналах или серийных монографиях и книгах, издаваемых онлайн, обмениваться информацией с редакторами, чтобы, как можно быстрее, внедрить лучшие методы в научном сообществе. В течение некоторого времени многие издатели внимательно адресовали проблемы, связанные с электронной публикацией новаций (см. Knapp and Wright 2010; руководство в PLoS One [<http://www.plosone.org/static/policies.action#taxon>]), и значительный интерес к внедрению этих изменений в *Кодекс* был очевидным.

Некоторые рекомендации, которые, мы надеемся, смогут помочь на начальной стадии электронной публикации новаций соответственно *Мельбурнскому Кодексу* приведены ниже:

- Рекомендуется выделять в каждой статье даты публикации (как это сделано в большинстве журналов, например, *New Phytologist* или *Nature*).

- Если более ранний выпуск онлайн-версии не является таким же, как окончательная версия (и поэтому не является эффективно обнародованным), рекомендуется отметить этот факт штампом (пример - *American Journal of Botany*).
- Включение и выделение ISSN или ISBN публикации в каждой статье поможет регистрирующему персоналу установить, эффективна ли публикация.
- Публикации в журналах (или серийных монографиях), участвующих в системе CLOCKSS (см. описание Knapp and Wright 2010) или в других международных архивах и системах хранения данных, обеспечат долгосрочное хранение.
- Авторы электронно обнародуемых новых названий должны уведомлять соответствующие центры индексации, как рекомендовано в Сов.30.A.3 – это поможет регистрирующему персоналу, который, иначе, может не знать об электронно обнародованных названиях.

Что эти изменения не означают

Не смотря на то, что новые Статьи и Рекомендации *Кодекса* используют термины PDF и PDF/A, это не означает, что публикации должны быть изданы *только* в этом формате с тем, чтобы быть эффективно опубликованными. Например, некоторые онлайн-журналы издаются параллельно в формате HTML (Hypertext Markup Language) вместе с PDF версией. В таких случаях PDF версия будет эффективно опубликована. Соглашение о том, что Генеральный Комитет по Ботанической Номенклатуре будет сообщать о новом приемлемом международном стандартном формате, в случае, если PDF будет заменен, означает, что авторы новаций и научная общественность, использующие *Кодекс*, будут информированы о новшествах в этой области, и *Кодекс* будет защищен от устаревания.

Новации, опубликованные ниже перечисленными способами *не* будут эффективно обнародованы согласно *Мельбурнскому Кодексу*:

- Публикации на веб-сайтах или в недолговечных документах, доступных в Интернет (существуют строгие критерии получения ISSN [<http://www.issn.org>]).
- Публикации в журналах без зарегистрированного ISSN или e-ISSN.
- Публикации в книгах без зарегистрированного ISBN или e-ISBN.

Совет о том, что печатную копию каждой электронной публикации следует помещать в библиотеку рекомендует ботаникам, как поступать, но не устанавливает стандарты или протокол действий для сотрудников библиотек. Библиотекари находятся в сложном переходном состоянии между разными методами публикации (Johnson and Luther 2007), и, в случае большого объема присылаемого материала, ботаники могут оказаться в ситуации, когда работники библиотек откажутся принять печатные оттиски отдельных статей.

Два других важных изменения в Кодексе, относящихся к обнародованию названий

Второе изменение в *Кодексе*, утвержденное в Мельбурне и вступающее в действие с 1 января 2012 г. гласит, что описание или диагноз, требуемые для действительного обнародования названия нового таксона для всех организмов, попадающих под действие *Кодекса*, могут быть опубликованы на любом из двух языков, английском, либо латинском. В настоящее время это положение действует для ископаемых растений, но для всех не ископаемых таксонов требуются латинские описание или диагноз (грибы и растения с 1 января 1958; водоросли [включая цианобактерии, попадающие под действие *Кодекса*] с 1 января 1958 г.). Это не относится к форме научных названий, которые остаются латинскими или принимаются как латинские. Требования отдельных журналов относительно латинского или английского языков, будет определяться, конечно же, редакторами этих журналов.

Третье изменение в *Кодексе*, утвержденное в Мельбурне и относящееся к обнародованию названий, но не вступающее в действие до 1 января 2013 г. (а не 1 января 2012 г. как ошибочно отмечено Миллером и др. (Miller et al. 2011)) гласит, что для всех новых названий организмов, понимаемых как грибы, в качестве дополнительного требования для действительного обнародования необходимо цитировать в протологе (все, что связано с названием и его действительным обнародованием) идентификационный номер, выданный международно признанным банком данных (таким, как MycoBank [<http://www.mycobank.org/>]). Об этом пойдет речь в отдельной публикации.

Требование наличия уникального идентификатора для новых названий грибов, начиная с 1 января 2013 г., не касается растений и водорослей; авторам новых названий для этих групп не нужно запрашивать LSIDs (Life Science Identifiers) или другие идентификаторы в центрах по индексации.

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С тем, чтобы ускорить распространение информации об изменениях, сделанных в *Международном Кодексе Номенклатуры водорослей, грибов и растений*, эта статья будет напечатана в журналах: *BMC Evolutionary Biology*, *Botanical Journal of the*

* И. Беляева и М. Воронцова благодарят Bentham-Moxton Trust за финансовую поддержку их участия в XVIII МБК в Мельбурне.

Linnean Society, Brittonia, Cladistics, MycoKeys, Mycotaxon, New Phytologist, North American Fungi, Novon, Opuscula Philolichenum, PhytoKeys, Phytoneuron, Phytotaxa, Plant Diversity and Resources, Systematic Botany и Taxon.

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Translation into Spanish of: “Changes to publication requirements made at the XVIII International Botanical Congress in Melbourne – what does e-publication mean for you?”. Translated by Carmen Ulloa Ulloa, Lourdes Rico Arce, and Renée H. Fortunato

Cambios a los requisitos para publicar realizados en el XVIII Congreso Internacional de Botánica en Melbourne – ¿qué significado tiene la publicación electrónica para usted?

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Resumen

Los cambios al *Código Internacional de Nomenclatura Botánica* se deciden cada seis años en las Secciones de Nomenclatura asociadas a los Congresos Internacionales de Botánica. El XVIII Congreso Internacional de Botánica se llevó a cabo en Melbourne, Australia; la Sección de Nomenclatura se efectuó desde el 18 al 22 de julio de 2011 y sus decisiones fueron aceptadas por el Congreso en la asamblea plenaria del 30 de julio. Como resultado de esta reunión se hicieron varios cambios importantes al *Código* que afectarán la publicación de nuevos nombres. Dos de estos cambios entrarán en vigencia a partir del 1 de enero de 2012, meses antes de la edición del *Código de Melbourne*. El material electrónico publicado en línea en Formato de

Documento Portátil (PDF) con un Número Internacional Normalizado de Publicaciones Seriadas (ISSN) o con un Número Internacional Normalizado de Libro (ISBN) constituirá una publicación efectiva; y el requisito para una descripción o diagnóstico en latín para los nombres de nuevos taxones será cambiado a un requisito de una descripción o diagnóstico en los idiomas latín o inglés. Asimismo, a partir del 1 de enero de 2013, los nuevos nombres de organismos tratados como hongos, para ser publicados en forma válida, deberán incluir en el protólogo (todo lo asociado con el nombre en su publicación válida) la cita de un identificador provisto por un repositorio reconocido (como MycoBank). Se presenta un texto borrador de los nuevos artículos que tratan con publicación electrónica y se provee las mejores prácticas descritas.

Para incentivar la difusión de los cambios realizados en el *Código Internacional de Nomenclatura para algas, hongos y plantas*, este artículo se publicará en: *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, *Plant Diversity and Resources*, *Systematic Botany* y *Taxon*.

Introducción

En julio de 2011, durante el XVIII Congreso Internacional de Botánica en Melbourne, Australia, se hicieron dos cambios importantes en el *Código Internacional de Nomenclatura Botánica* (ahora llamado el *Código Internacional de Nomenclatura para algas, hongos y plantas*) que entrarán en vigencia a partir del 1 de enero de 2012. Estos cambios afectarán a todos los autores que publican nombres regidos por este *Código*. Como el *Código de Melbourne* no será editado hasta aproximadamente mediados del 2012, se ha pensado que sería útil actualizar estos cambios, particularmente aquellos relacionados a la publicación efectiva por medios electrónicos (artículos 29, 30 y 31). Para un informe conciso de todos los cambios al *Código* aceptados en Melbourne, ver McNeill et al. (2011).

Un borrador revisado del texto de los Artículos, Notas y Recomendaciones sobre publicación efectiva se proporciona a los editores y comités editoriales como ayuda en el establecimiento de las mejores prácticas descritas para la aplicación del *Código*. También se describe lo que estos cambios *no* significan, a fin de orientar a aquellos que deseen publicar nuevos nombres y tipificaciones por medios electrónicos. Se solicita a los lectores consultar el informe del Comité Especial sobre Publicación Electrónica que acompaña los cambios propuestos previamente al XVIII Congreso (Chapman et al. 2010); en ellos se expone el razonamiento para los cambios ahora aceptados en el *Código*.

Borrador revisado del texto de los Artículos 29, 30 y 31 y Recomendaciones 29A, 30A, y 31A

Se reproduce el texto de todos los Artículos, Notas y Recomendaciones pertinentes (omitiendo los ejemplos), con los cambios resaltados en **negritas**. El presente texto

es provisional, en espera de la reunión del Comité Editorial para finalizar la versión impresa del *Código de Melbourne* en diciembre del 2011.

Artículo 29

29.1. De acuerdo con este *Código*, una publicación se hace efectiva por distribución de material impreso (por venta, intercambio o donación) al público o, al menos, a instituciones botánicas con bibliotecas accesibles generalmente a botánicos. **La publicación es también efectiva por la distribución electrónica de material en Formato de Documento Portátil (siglas en inglés PDF; véase también Art. 29.3 y Rec. 29A.1) en una publicación en línea con un Número Internacional Normalizado de Publicaciones Seriadas (siglas en inglés ISSN) o un Número Internacional Normalizado de Libro (siglas en inglés ISBN).** Una publicación no se hace efectiva en comunicaciones de nombres nuevos durante reuniones públicas, al colocar los nombres en colecciones o jardines abiertos al público, en la edición de microfilmes confeccionados a partir de manuscritos u originales mecanografiados o en otro material no publicado, o en otra distribución electrónica que no sea como la anteriormente descrita.

29.2. A efectos de este Artículo, "en línea" se define como accesible electrónicamente a través de la Red Informática Mundial o "World Wide Web".

29.3. En el caso de tener un reemplazo del Formato de Documento Portátil (PDF), el formato estándar internacional sucesor será comunicado por el Comité General (véase Div. III).

29.4. El contenido de una publicación electrónica en particular no deberá ser modificada después de ser emitido por primera vez. Tales alteraciones no son efectivamente publicadas. Las correcciones o revisiones deberán ser expedidas por separado para ser efectivamente publicadas.

Recomendación 29A

[La Recomendación actual se reemplaza por lo siguiente:]

29A.1. La publicación electrónica en Formato de Documento Portátil (PDF) debe cumplir con el estándar de archivo PDF/A (ISO 19005).

29A.2. Los autores deberían preferiblemente publicar en publicaciones que se archiven, satisfaciendo en la medida de lo posible los siguientes criterios (véase también Rec. 29A.1):

(a) El material debe colocarse en varios repositorios de confianza digitales en línea, ej. un repositorio con certificación ISO;

(b) Los repositorios digitales deben ser en más de un área del mundo y preferiblemente en diferentes continentes;

(c) También es recomendable depositar copias impresas en bibliotecas en más de un área del mundo y preferiblemente en diferentes continentes.

Artículo 30

30.1. La distribución de una publicación por medio de material electrónico no constituye una publicación efectiva antes del 1 de enero de 2012.

30.2. Una publicación electrónica no se hace efectiva si hay pruebas asociadas con o dentro de la publicación que indiquen que es simplemente una versión preliminar que fue, o que será, reemplazada por una versión que el editor considere final, en cuyo caso sólo esa versión final es publicada en forma efectiva.

30.3. La publicación con autografía indeleble es considerada efectiva, antes del 1 de enero de 1953. La autografía indeleble producida en una fecha posterior no se considera una publicación efectiva.

30.4. A efectos de este Artículo, la autografía indeleble es el material escrito a mano reproducido por algún proceso mecánico o gráfico (como litografía, offset o grabado metálico).

30.5. La publicación, desde o después del 1 de enero de 1953, en catálogos comerciales o periódicos no científicos, y desde o después el 1 de enero de 1973 en listas de intercambio de semillas, no constituye una publicación efectiva.

30.6. La distribución desde o después del 1 de enero de 1953 de material impreso acompañando ejemplares de herbario (exsiccatae) no constituye una publicación efectiva.

Nota 1. Si el material impreso es también distribuido independientemente de los ejemplares de herbario (exsiccatae), sí está efectivamente publicado.

30.7. La publicación desde o después del 1 de enero de 1953, de una obra que no forma parte de una serie y que dice ser una tesis presentada a una universidad u otro instituto de educación con el fin de obtener un título, no es efectivamente publicada a menos que incluya una declaración explícita (refiriéndose a los requisitos del *Código* para su publicación efectiva) u otra evidencia interna que sea considerada como una publicación efectiva por su autor o editor.

Nota 2. La presencia de un Número Internacional Normalizado de Libro (ISBN) o una declaración del nombre de la imprenta, editor o distribuidor en la versión impresa original es considerada como evidencia interna que el trabajo tenía la intención de ser publicado en forma efectiva.

Recomendación 30A

30A.1. Versiones preliminares y finales de la misma publicación electrónica deben indicarse claramente como tal cuando se emiten por primera vez.

30A.2. Se recomienda enfáticamente que los autores eviten la publicación de nuevos nombres y descripciones o diagnosis de nuevos taxones (novedades nomenclaturales) en material impreso efímero de cualquier tipo, en particular material impreso que se publica en tiradas cortas e inciertas, donde la permanencia del texto puede ser limitada, para el que la publicación efectiva por lo que se refiere al número de copias no es evidente, o que es improbable que llegue al público en general. Los autores también deberían evitar la publicación de nuevos nombres y descripciones o diagnosis en revistas populares, en revistas o publicaciones de resúmenes, o en etiquetas de corrección.

30A.3. Para facilitar la disponibilidad a través de tiempo y lugar, los autores que publican novedades nomenclaturales deben dar preferencia a revistas periódicas que publican regularmente artículos taxonómicos. **De lo contrario, una copia de una publicación (ya sea impresa o electrónica) debe ser enviada a un centro de indexación apropiado para el grupo taxonómico, y las publicaciones que sólo existen como material impreso** deben ser depositadas en al menos diez, aunque preferiblemente más, bibliotecas botánicas u otras que estén generalmente accesibles en todo el mundo.

30A.4. Se recomienda a los autores y editores que mencionen las novedades nomenclaturales en el sumario o resumen, o que las inserten en un índice en la publicación.

Artículo 31

31.1. La fecha de publicación efectiva es la fecha en que el material impreso o **electrónico** comenzó a estar disponible, tal como se define en los Arts. 29 y 30. En ausencia de prueba que establezca otra fecha, debe aceptarse como correcta la que aparece en el material impreso o **electrónico**.

[Nota 1 existente se sustituirá por lo siguiente:]

31.2. **Cuando una publicación se emite en versiones paralelas electrónica e impresa, estas deben tratarse como publicadas en forma efectiva en la misma fecha, a menos que las fechas de las versiones sean diferentes de acuerdo con el Art. 31.1.**

31.3. Cuando separatas de revistas periódicas, o de otras obras a la venta se distribuyen por adelantado, la fecha de las separatas se acepta como la fecha de publicación efectiva, a menos que haya evidencias de que sea errónea.

Recomendación 31A

31A.1. La fecha en la cual el editor o su agente entrega el material impreso a uno de los correos usuales para su distribución al público debería aceptarse como la fecha de publicación efectiva.

Mejores prácticas

Los autores de nuevos nombres, los editores y las editoriales estarán interesados en garantizar que las publicaciones que incluyen nuevos nombres estén en conformidad con el *Código de Melbourne*, para que los nombres en ellos incluidos sean efectivamente publicados. Se sugiere que aquellos que publiquen en revistas periódicas o series monográficas y libros que tienen ediciones en línea se comuniquen con los editores de manera que las normas prácticas se puedan establecer en toda la comunidad lo antes posible. Varios editores ya han estado abordando cuidadosamente los temas relacionados con la publicación electrónica de novedades (véase Knapp and Wright 2010; normas para autores en PLoS One [<http://www.plosone.org/static/policies.action#taxon>]) y ha sido evidente el considerable interés en hacer que los cambios al *Código* funcionen efectivamente.

Algunas prácticas que consideramos ayudarán en las etapas iniciales de la publicación electrónica de novedades de acuerdo con el *Código de Melbourne* son:

- Que en cada artículo figure destacada la fecha de publicación (como se hace en muchas revistas, por ejemplo, *New Phytologist* o *Nature*).
- Si se emite una versión en línea que no es la misma que la versión final (y por lo tanto no da lugar a una publicación efectiva) sellar cada artículo con este hecho en forma destacada (véase por ejemplo, *American Journal of Botany*).
- La visualización prominente del ISSN o ISBN de la publicación de cada artículo ayudará a los indizadores a establecer si el artículo está efectivamente publicado o si no lo está.
- La publicación en revistas (o series monográficas) que participan en el sistema CLOCKSS (véase Knapp and Wright 2010, para obtener una descripción) o de otro sistema internacional de archivo y sistema de conservación garantizará el archivo a largo plazo.
- Autores de nuevos nombres por medios electrónicos deben notificar al centro de indexación adecuado como se recomienda en la Rec 30A.3; esto ayudará a los indizadores, quienes de lo contrario, podrían no darse cuenta de los nombres publicados electrónicamente.

Lo que estos cambios no significan

Aunque los nuevos Artículos y Recomendaciones utilicen los términos PDF y PDF/A, esto no significa que las publicaciones deben ser emitidas *sólo* en ese formato para ser efectivamente publicadas. Por ejemplo, algunas revistas en línea emiten documentos en formato de Lenguaje de Marcado de Hipertexto (siglas en inglés HTML) junto con una versión paralela de PDF. En tales casos, la versión PDF será la publicada de manera efectiva. La cláusula de que el Comité General de Nomenclatura Botánica comunicará la aceptación de un nuevo formato estándar internacional, en caso de que el PDF sea reemplazado, significa que los autores de novedades y la comunidad que usa el *Código*

puedan permanecer informados sobre avances en el área y que el *Código* sea protegido de quedar obsoleto.

De acuerdo al *Código de Melbourne* el uso de los siguientes medios de publicación electrónica no resultará en una publicación efectiva de novedades.

- Publicación en sitios Web o en documentos efímeros disponibles en Internet (hay criterios estrictos para la concesión de un ISSN [<http://www.issn.org>]).
- Publicación en revistas sin un ISSN o e-ISSN registrado.
- Publicación en libros sin un ISBN o e-ISBN registrado.

La Recomendación aprobada para aconsejar que se deposite una copia impresa de cualquier publicación electrónica en una biblioteca sugiere que los botánicos tomen una acción, pero no establece una práctica estándar o un protocolo a seguir por los bibliotecarios. Los bibliotecarios, están en una etapa de transición compleja entre las modalidades de publicación (Johnson and Luther 2007), por lo cual los botánicos pueden encontrar que los bibliotecarios no quieran o no puedan acomodar una sola copia de documentos impresos como ficheros individuales si el volumen es muy grande.

Otros dos cambios importantes en el *Código* relativos a la publicación de nombres

El segundo cambio en el *Código* aprobado en Melbourne que entrará en vigencia a partir del 1 de enero de 2012 es que la descripción o la diagnosis requerida para la publicación válida de un nombre de un taxón nuevo, de cualquiera de los organismos comprendidos en el *Código*, puede ser en idioma inglés o latín. Esta es la disposición que actualmente aplica para los nombres de plantas fósiles, mientras que todos los taxones nuevos que no son fósiles han requerido una descripción o diagnosis en latín (hongos y plantas desde el 1 de enero de 1935; algas [incluyendo cianobacterias, también tratadas bajo el *Código*] desde el 1 de enero de 1958). Esto no tiene ninguna relación para los nombres científicos, que siguen siendo en latín o tratados como latín. Los requisitos individuales de las revistas periódicas de latín y/o inglés serán determinados, por supuesto, por los editores de las mismas.

Un tercer cambio al *Código* aprobado en Melbourne relativo a la publicación de los nombres, pero que no tomará efecto hasta el 1 de enero de 2013 (no a partir del 1 de enero de 2012 como fue registrado según Miller et al. 2011), es en el cual todos los nuevos nombres de organismos tratados como hongos tendrán, como un requisito adicional para que la publicación sea válida, que incluir en el protólogo (todo lo asociado con un nombre en su publicación válida) la cita de un identificador emitido por un repositorio reconocido (como MycoBank [<http://www.mycobank.org/>]). Este tema será publicitado por separado.

El requisito de un identificador único para nuevos nombres de hongos desde o después del 1 de enero de 2013 *no* se aplica a plantas o algas; no hay necesidad para autores de nuevos nombres en estos grupos solicitar LSIDs (siglas en inglés de *Life*

Science Identifiers, Identificadores de Ciencias de la Vida), u otros identificadores de centros de indexación.

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Para incentivar la difusión de los cambios realizados en el *Código Internacional de Nomenclatura para algas, hongos y plantas*, este artículo se publicará en: *BMC Evolutionary Biology*, *Botanical Journal of the Linnean Society*, *Brittonia*, *Cladistics*, *MycoKeys*, *Mycotaxon*, *New Phytologist*, *North American Fungi*, *Novon*, *Opuscula Philolichenum*, *PhytoKeys*, *Phytoneuron*, *Phytotaxa*, *Plant Diversity and Resources*, *Systematic Botany* y *Taxon*.

Nota de traducción: texto en español del *Código* adaptado de Kiesling 2002.

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Testing the phylogenetic utility of *MCM7* in the Ascomycota

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Abstract

The Ascomycota are a group of filamentous fungi that occur as saprobes, pathogens, and symbionts. They are of immense industrial, medical, ecological, and economical importance. The search for new markers appropriate for molecular phylogenetic analysis of Ascomycota remains a challenging problem. In this study, we explore the phylogenetic utility of a single copy protein-coding gene, *MCM7*; newly recognized as useful for inferring phylogenetic relationships among the major classes of the Ascomycota. Our specific goals were to: 1) test the phylogenetic utility of *MCM7* for estimating phylogenies at various taxonomic ranks (class and below) with an emphasis on non-lichenized ascomycetes; and, 2) compare the congruence, robustness and resolving power of *MCM7*-based phylogenies with that of nuclear large subunit rDNA (LSU)-based phylogenies for the same taxon set. A dataset of sequence data for *MCM7* as well as LSU was assembled for 80 species belonging to 63 genera of lichenized and non-lichenized ascomycetes in the classes Dothideomycetes, Eurotiomycetes, Geoglossomycetes, Lecanoromycetes, Leotiomycetes, and Sordariomycetes. We obtained 93 new sequences of which 65 are *MCM7* and 28 are LSU. Maximum-Likelihood and Bayesian analyses were performed using single as well as combined gene datasets and partitions. We also assessed substitution saturation for the *MCM7* gene. Results indicate that *MCM7* can be used successfully for determining phylogenetic relationships of ascomycetes and provided good resolution and support at half the cost compared to LSU. Phylogenetic informativeness profiles showed that *MCM7* was more phylogenetically informative than LSU. The *MCM7* gene is also a valuable phylogenetic marker for both lower as well as higher level phylogenetic analyses within the Ascomycota, especially when used in

combination with the LSU gene. We found that although the third codon position of *MCM7* is saturated, it was better to analyze the dataset with all codon positions included. Phylogenetic performance of *MCM7* with and without the third codon position is discussed.

Key words

Fungi, Leotiomyceta, MS456, non-lichenized ascomycetes, systematics, 28S nrDNA

Introduction

The Ascomycota, commonly referred to as the sac-fungi (Eriksson 2009), is the largest and most phylogenetically diverse group of organisms within the Kingdom Fungi and consists of an estimated 64,000 described species (Kirk et al. 2008). Currently the Ascomycota comprises three subphyla, 15 classes and 68 orders (Kirk et al. 2008). Species belonging to the Ascomycota can be found in all ecosystems where they inhabit a diverse array of ecological niches, acting as saprobes that decay dead organic matter, pathogens of plants and animals, as well as mutualists (lichen-forming fungi) and endophytes. In addition, numerous taxa within the Ascomycota are of industrial, medical and economical importance. A large proportion of taxa that reside within the Ascomycota are known only from their mitosporic or asexual states (Gams and Seifert 2008), thereby, making it difficult to determine phylogenetic and evolutionary relationships within this mega diverse group of fungi. The advent of molecular systematics has revolutionized our knowledge of the phylogenetics of the Ascomycota.

Early fungal phylogenetic studies used DNA sequences from nuclear ribosomal genes such as small subunit (18S) and large subunit (28S) rDNA genes (Bruns et al. 1991, 1992, Berbee and Taylor 1995, Spatafora 1995, Taylor et al. 1994, Tehler et al. 2000). Due to the presence of a large number of copies within the genome being subjected to concerted evolution (Zimmer et al. 1990), and due to their ease of amplification (Hills and Dixon 1991), 18S and 28S sequence data were used early on and still dominate the fungal sequence data in GenBank (Begerow et al. 2010, Lutzoni et al. 2004). Recently, however, fungal systematists have started using a number of single-copy protein-coding genes for investigating deep phylogenetic relationships among the fungi. This has largely become possible due to the advent of fungal phylogenomics (Galagan et al. 2005). This task has been achieved due in part to the efforts of research consortiums among fungal systematists such as “Assembling the Fungal Tree of Life” (Hibbett et al. 2007, Lutzoni et al. 2004) and “Deep Hypha” (Blackwell et al. 2006).

Phylogenetic relationships among taxa of Ascomycota (Schoch et al. 2009a, Spatafora et al. 2006) have been inferred using a variety of protein-coding genes such as the mitochondrial ATP synthase-subunit 6 (Castlebury et al. 2004, Sung et al. 2007), β -tubulin (Ayliffe et al. 2001, Hansen et al. 2005, Huang et al. 2009, Hsieh et al. 2010, Miller and Huhndorf 2004, Tang et al. 2007), alpha-actin (Hsieh et al., 2010), glyceraldehyde 3-phosphate dehydrogenase (Berbee et al. 1999, Smith 1989) RNA polymerase including the largest and second largest subunits (*RPB1*, *RPB2*; Liu et al.

1999, Liu and Hall 2004, Zhang and Blackwell 2002, Tang et al. 2007, Schmitt et al. 2009a, Hsieh et al. 2010), and translation elongation factor alpha *TEF1* (Mugambi and Huhndorf 2009a, 2009b, Rehner and Buckley 2005). Use of these protein-coding genes has become increasingly common in systematic studies within the fungal kingdom (Blackwell et al. 2006, James et al. 2006, Lutzoni et al. 2004).

Despite their widely accepted use in inferring evolutionary relationships among the ascomycete fungi, a number of protein-coding genes have been shown to perform variably (Aguileta et al. 2008). In fact a number of studies have attempted to use varying definitions of phylogenetic informativeness to compare various genes to one another. In addition to the aforementioned study by Aguileta et al. (2008), which compared gene based trees to an ideal tree, Townsend et al. (2007) used character rates, Graybeal et al. (1994) used empirical saturation plots and Collins et al. (2005) used base compositional stationarity, amongst others. The Townsend et al. (2007) measure of selecting genes with an optimal rate as it is projected backwards in time was applied to a taxon set comprising all major classes in the Ascomycota for DNA sequences from three ribosomal genes (two nuclear, one mitochondrial) and three protein-coding genes by Schoch et al. (2009a). These studies showed how different genes behave differently for discovering older versus younger divergences. In the majority of cases the selected protein-coding genes were more informative than the ribosomal genes over all time periods. Using different criteria, Aguileta et al. (2008) showed that several protein-coding genes used routinely in fungal phylogenetic studies were not among the best performing genes when tested against 246 single-copy orthologous genes extracted from 30 fungal genomes (see supplementary material in Aguileta et al. 2008). The authors discovered two ortholog single-copy protein coding gene loci, MS277 and MS456, which outperformed all other protein-coding genes in their study. MS456, commonly referred to as *MCM7*, codes for a licensing factor required for DNA replication initiation and cell proliferation. The protein encoded by this gene is one of the highly conserved mini-chromosome maintenance proteins (MCM) that are essential for the initiation of eukaryotic genome replication (Kearsey and Labib 1998).

Schmitt et al. (2009b) subsequently developed fungal-specific primers for these two loci and tested their phylogenetic utility across a wide range of classes from the Ascomycota with a majority of taxa sampled from within the lichenized fungi in the Lecanoromycetes. Notably, the large and diverse class Dothideomycetes did not have representatives in this study. Data from this study suggested that, compared to MS277 (*TSR1*), the *MCM7* primers were able to amplify a greater number of diverse taxa within the Ascomycota. However, the authors did not compare *MCM7* with any other gene commonly used for fungal phylogenies. This includes the 28S large-subunit nuclear ribosomal DNA (LSU), which is currently one of the most widely used ribosomal genes for assessing phylogenetic relationships at the class level and below for Fungi (Begerow et al. 2010, Lutzoni et al. 2004).

The major objectives of this study, therefore, were to: 1) test the phylogenetic utility of *MCM7* for estimating phylogenies at various taxonomic ranks (class and below) with a focus on non-lichenized ascomycetes; 2) expand use of the *MCM7* gene

to include taxa in the Dothideomycetes, Geoglossomycetes, Leotiomyces, and Sordariomycetes; and, 3) compare the congruence, robustness and resolving power of *MCM7*-based phylogenies with that of LSU-based phylogenies for the same taxon set. Comparing the phylogenetic utility of the new gene with that of existing ones helps build robust and well-resolved phylogenies among ascomycete fungi while improving cost management of molecular studies.

Materials and methods

Taxon sampling

Taxa used in this study are listed in Table 1, along with information on the source of the isolates as well as their country of origin, where available. The focus of our taxon sampling was to include non-lichenized ascomycetes representing terrestrial and freshwater ascomycete taxa from the Dothideomycetes, Geoglossomycetes, Leotiomyces, and Sordariomycetes for both *MCM7* and LSU genes. We assembled datasets of each gene for the same 89 taxa. Six classes from within the rankless taxon Leotiomyces (Schoch et al. 2009b): Dothideomycetes, Eurotiomycetes, Geoglossomycetes, Lecanoromycetes, Leotiomyces, and Sordariomycetes, were sampled. Based on results of previous phylogenetic analyses (James et al. 2006, Lutzoni et al. 2004, Spatafora et al. 2006), one representative each from Saccharomycotina and Taphrinomycotina was used as outgroup taxa for all analyses. For some taxa, more than one representative was sequenced for both genes to verify its identity as well as to assess the utility of *MCM7* in comparison to LSU at lower taxonomic levels. Newly generated sequences are deposited in GenBank and their accession numbers are listed in Table 1.

Molecular Methods (DNA extraction, primers and sequencing)

Total genomic DNA from terrestrial ascomycetes was extracted using methods outlined in Promputtha and Miller (2010), whereas DNA from freshwater ascomycete taxa was extracted from axenic cultures obtained from single-spore isolates following Campbell et al. (2007). PCR reactions were carried out using known LSU and *MCM7* primers (Rehner and Samuels 1995, Schmitt et al. 2009b, Vilgalys and Hester 1990). The LSU gene was amplified using thermocycler conditions outlined in Miller and Huhndorf (2004) and *MCM7* was amplified using the following thermocycler conditions: initial denaturing at 94 °C for 5 min; 30 cycles of denaturing at 94 °C for 45 sec, annealing at 50–56 °C for 50 sec; extension at 72 °C for 1 min; and a final extension step of 72 °C for 5 min. For taxa which were difficult to amplify, the annealing temperature was decreased to 45 °C. PCR reactions using Illustra Ready-To-Go™ PCR Beads (GE Healthcare, Waukesha, WI) contained 1–5 µl genomic DNA, 2.5 µL of BSA (bovine serum albumin, New England Biolabs, Ipswich, MA) and/or 2.5 µL of DMSO (dimethyl

Table 1. Species used in this study along with their source, localities and accession numbers.

Taxon	Source**	Locality	GenBank Accession Numbers	
			28S nuc-rDNA	<i>MCM7</i>
<i>Ajellomyces capsulatus</i>	GenBank/Genome	–	AAJI01002781	XM_001538714
<i>Aliquandostipite crystallinus</i>	F83-1	USA	GU266239	JN672963
<i>Aliquandostipite khaoyaiensis</i>	AF276-1	Costa Rica	JN673028	JN672964
<i>Aliquandostipite khaoyaiensis</i>	F89-1	USA	EF175647	JN672965
<i>Aliquandostipite khaoyaiensis</i>	CBS 118232	Thailand	GU301796	JN672966
<i>Alternaria alternata</i>	CBS 916.96	–	DQ678082	JN672967
<i>Anguillospora longissima</i>	CCM-F10304	–	JN673029	JN672968
<i>Anguillospora longissima</i>	CS869-1D	USA	GU266240	JN672969
<i>Apiosporina collinsii</i>	CBS 118973	–	GU301798	JN672970
<i>Arctomia delicatula</i>	GenBank	Sweden	AY853355	GQ272388
<i>Arctomia teretiuscula</i>	GenBank	China	DQ007346	GQ272389
<i>Aspergillus clavatus</i>	GenBank/Genome	–	AF454152	XM_001275314
<i>Aspergillus fumigatus</i>	GenBank/Genome	–	AAHF01000000	XM_750254
<i>Aspergillus niger</i>	GenBank	–	NT_166520	XM_001397760
<i>Aspergillus oryzae</i>	GenBank	–	AP_007172	XM_001826176
<i>Aspicilia caesiocinerea</i>	GenBank	USA	DQ780303	GQ272390
<i>Aspicilia cinerea</i>	GenBank	USA	DQ780304	GQ272390
<i>Bisporella citrina</i>	VPH-IL0501	USA, IL	JN673031	JN672971
<i>Botryotinia fuckeliana</i>	GenBank/Genome	–	AAID01003173.1	XM_001556412
<i>Brachiosphaera tropicalis</i>	E192-1	Panama	EF175653	JN672972
<i>Bulbothrix apophysata</i>	GenBank	Costa Rica	EU562670	GQ272392
<i>Camarops polysperma</i>	Hanson 2006-747	Sweden	JN673030	JN672973
<i>Camarops lutea</i>	Hanson 2008-222	Sweden	JN673032	JN672974
<i>Camarops plana</i>	Pouzar s.n.	–	JN673033	JN672975
<i>Camarops scleroderma</i>	MP 4464	Panama	JN673034	JN672976
<i>Camarops</i> sp.	CH 08-570	China	JN673035	JN672977
<i>Cercophora aquatica</i>	JF 06314	France	JN673036	JN672978
<i>Cercophora arenicola</i>	ANM1080	GSMNP	JN673037	JN672979
<i>Cercophora</i> sp.	JF 09214	France	JN673038	JN672980
<i>Chaetomium globosum</i>	GenBank	–	AAFU01000612	XM_001220296
<i>Chaetosphaeria lateriphiala</i>	ANM1079	GSMNP	JN673039	JN672984
<i>Chlorencoelia torta</i>	ANM2124	GSMNP	JN673040	JN672985
<i>Coccidioides immitis</i>	GenBank/Genome	–	AAEC03000009	XM_001240385
<i>Coniochaeta</i> sp.	ANM1174	GSMNP	JN673041	JN672986
<i>Corynespora casicola</i>	CBS 100822	–	GU301808	JN672981
<i>Creosphaeria sassafras</i>	ANM1978	Indiana	JN673042	JN672987
<i>Cudoniella clavus</i>	ANM2087	GSMNP	JN012006	JN672988
<i>Delitschia winteri</i>	CBS 116.29	–	DQ678077	JN672982
<i>Dermatocarpon minutum</i>	GenBank	Germany	AY607733	GQ272394
<i>Farlowiella carmichaelina</i>	CBS 206.36	–	GU301791	JN672983
<i>Geoglossum diffforme</i>	VPH 25	GSMNP	JN673043	JN672989
<i>Geoglossum diffforme</i>	ANM2169	GSMNP	JN673044	JN672990
<i>Geoglossum simile</i>	ANM2173	GSMNP	JN673045	JN672991
<i>Gibberella zeae</i>	GenBank/Genome	–	AACM02000312	XM_387281
<i>Gloniopsis smilacis</i>	CBS 114601	–	FJ161174	JN672992
<i>Graddonina coracina</i>	ANM2018	GSMNP	JN012009	JN672993

Taxon	Source**	Locality	GenBank Accession Numbers	
			28S nuc-rDNA	MCM7
<i>Graddonina coracina</i>	Hanson 2007-208	Sweden	JN012010	JN672994
<i>Graddonina coracina</i>	JF 09318	France	JN012011	JN672995
<i>Hyalorostratum brunneisporum</i>	A573-2b	USA	HM191720	JN672996
<i>Hymenoscyphus fructigenus</i>	ASM10619	Russia	JN673046	JN672997
<i>Hypoxyylon crocopenum</i>	ANM1118	GSMNP	JN673047	JN672998
<i>Jahnula aquatica</i>	R68-1	USA	EF175655	JN672999
<i>Jahnula bipileata</i>	MYA 4173	USA	EF175657	JN673000
<i>Jahnula bipileata</i>	AF220-1	Ecuador	EF175656	JN673001
<i>Jahnula rostrata</i>	MYA 4176	USA	EF175660	JN673002
<i>Jahnula sangamonensis</i>	MYA 4174	USA	EF175662	JN673003
<i>Jahnula sangamonensis</i>	MYA 4175	USA	EF175663	JN673004
<i>Lachnellula</i> sp.	ANM1992	GSMNP	JN673048	JN673005
<i>Lasiosphaeria lanuginosa</i>	SMH3819	–	AY436412	JN673006
<i>Lasiosphaeria lanuginosa</i>	SMH4925	–	JN673049	JN673007
<i>Lasiosphaeria ovina</i>	ANM1295	Louisiana	JN673050	JN673008
<i>Lasiosphaeria hirsuta</i>	ANM1066	GSMNP	JN673051	JN673009
<i>Leptosphaeria dryadis</i>	CBS 473.64	–	GU301828	JN673010
<i>Lobothallia radiosa</i>	GenBank	Switzerland	DQ780306	GQ272397
<i>Magnaporthe grisea</i>	GenBank/Genome	–	DQ493955	XM_364455
<i>Megalohypha aqua-dulces</i>	AF005-2a	Panama	EF175667	JN673011
<i>Microthyrium microscopicum</i>	CBS 115976	–	GU301846	JN673012
<i>Montagnula opulenta</i>	CBS 168.34	–	DQ678086	JN673013
<i>Mycosphaerella punctiformis</i>	CBS 113265	–	DQ470968	JN673014
<i>Myriangium hispanicum</i>	CBS 247.33	–	GU301854	JN673015
<i>Mytilinidium mytilinellum</i>	EB 0386	–	GU397347	JN673016
<i>Neosartorya fischeri</i>	GenBank/Genome	–	EF669936	XM_001260497
<i>Neurospora crassa</i>	GenBank/Genome	–	AF286411	XM_958785
<i>Phaeosclera dermatoides</i>	CBS 157.81	–	GU301858	JN673017
<i>Psiloparmelia denotata</i>	GenBank	Peru	EF105426	GQ272413
<i>Pyrenula subpraelucida</i>	GenBank	Costa Rica	DQ329015	GQ272414
<i>Pyrgillus javanicus</i>	GenBank	Australia	AY605078	GQ272415
<i>Saccharomyces cerevisiae</i>	GenBank		AB212638	NM_001178550
<i>Schizosaccharomyces pombe</i>	GenBank		Z19136	NP_596545
<i>Scoria spongiosa</i>	CBS 325.33		DQ678075	JN673018
<i>Strossmayeria basitricha</i>	ANM2055	GSMNP	JN673052	JN673019
<i>Sydowia polyspora</i>	CBS 116.29	–	DQ678085	JN673020
<i>Tenatosphaeria associata</i>	CBS 112224	–	GU301874	JN673021
<i>Trichoglossum walteri</i>	ANM2203	GSMNP	JN673053	JN673022
<i>Vibrisea filisporia</i> f. <i>filisporia</i>	ANM2064	GSMNP	JN012017	JN673023
<i>Westerdykella angulata</i>	CBS 610.74	–	DQ384105	JN673024
<i>Xylaria frustulosa</i>	ANM1300	Louisiana	JN673055	JN673025
<i>Xylomyces chlamydosporus</i>	H58-4	USA	EF175669	JN673026
<i>Xylomyces-like</i>	H58-5	USA	JN673054	JN673027

** A, Carol Shearer, ascomycetes; AF, Astrid Ferrer; ASM, Andrew S. Methven; ANM, Andrew N. Miller; CS, Carol Shearer hyphomycetes (mitosporic fungi); CBS, Centraalbureau voor Schimmelcultures; CH, China; E, Astrid Ferrer hyphomycetes; EB, Eric Boehm ascomycetes; F, Florida, freshwater ascomycetes; GSMNP, Great Smoky Mountain National Park; H, Huzefa Raja, hyphomycetes; MP, Meike Piepenbring; MYA, American Type Culture Collection; R, Huzefa Raja, ascomycetes; SMH, Sabine M. Huhndorf; JF, Jack Fournier; VPH, Vince P. Hustad.

sulfoxide, Fisher Scientific, Pittsburgh, PA), 1 μ L of each 10mM primer, and enough distilled water to bring the reaction volume to 25 μ L. Purified PCR products were used in 11 μ L sequencing reactions with BigDye Terminators v. 3.1 (Applied Biosystems, Foster City, CA) in combination with the following LSU primers: LROR, LR3, LR3R, LR6 and *MCM7* primers: Mcm7-709for, Mcm7-1384rev. Sequences were generated on an ABI Applied Biosystems 3730XL high-throughput DNA capillary sequencer at the UIUC Keck Center for Comparative and Functional Genomics.

Sequence alignment

Each sequence fragment was subjected to an individual BLAST search to verify its identity. *MCM7* sequences from the GenBank were assembled and aligned with newly obtained sequences using Sequencher 4.9 (Gene Codes Corp.), optimized by eye, and manually corrected. For the LSU data, the newly obtained sequences were aligned with sequences from GenBank using the multiple sequence alignment program, MUSCLE[®] (Edgar 2004), with default parameters in operation. MUSCLE[®] was implemented using the program Seaview v. 4.1 (Gouy et al. 2010). The LSU sequences were aligned in MUSCLE[®] using a previous (trusted) alignment made by eye in Sequencher v. 4.9 based on a method called “jump-starting alignment” (Morrisson 2006). The final alignment was again optimized by eye and manually corrected using MacClade v. 4.08 (Maddison and Maddison 2000) and Se-Al v. 2.0a8 (Rambaut 1996). The separate and combined alignments are available from the authors upon request.

Maximum likelihood and Bayesian search strategies for phylogenetic analyses

Maximum likelihood (ML) and Bayesian Inference (BI) methods were used in phylogenetic analyses for both the *MCM7* and LSU datasets. The Akaike Information Criterion (AIC) (Posada and Buckley 2004) as implemented in Modeltest v. 3.7 (Posada and Crandall 1998) was used to determine the best-fit model of evolution for each data set for both ML and BI. For the separate and combined datasets, the best-fit model of evolution was the GTR + I + G model. Likelihood analyses were conducted using PhyML (Guindon and Gascuel 2003) under the following parameters: GTR model was implemented with six rate classes and invariable sites. Across site variations were fixed with parameter values obtained from Modeltest and 1000 bootstrap replicates were performed from a BioNJ starting tree employing the best of nearest neighbor interchange (NNI) and subtree pruning and regrafting (SPR) branch swapping. Maximum likelihood analyses were also performed using RAxML v. 7.0.4 (Stamatakis 2006) run on the CIPRES Portal v. 2.0 (Miller et al. 2010) with the default rapid hill-climbing algorithm and GTR model employing 1000 fast bootstrap searches. Clades with bootstrap values $\geq 70\%$ were considered significant and strongly supported (Hills and Bull 1993). Bayesian analyses employing a Markov Chain Monte Carlo (MCMC)

algorithm were run with MrBayes v. 3.1 (Huelsenbeck and Ronquist 2001) on the CIPRES Portal v. 2.0 as an additional means of assessing branch support. These analyses incorporated the general time reversible model (Rodríguez et al. 1991) including an estimation of invariant sites and assuming a gamma distribution parameter (GTR + I + G) with six rate categories. Four independent chains of MCMC were run for 50 million generations to insure that the same tree space was being sampled during each analysis and that the trees were not trapped in local optima. Trees were sampled every 1000th generation resulting in 50,000 total trees. Bayesian posterior probabilities (BPP) were determined from a consensus tree generated from the remaining 40,000 trees in PAUP * 4.0b10 (Swofford 2002) after the first 10,000 trees, which extended beyond the burn-in phase in each analysis, were discarded. Clades with posterior probability $\geq 95\%$ were considered significant and strongly supported.

Combined analyses and test for conflict

The individual LSU and *MCM7* datasets were examined for potential conflict before they were combined into a single dataset for total evidence analyses (Eernisse and Kluge 1993, Kluge 1989). Since previous studies have shown that the incongruence length difference (ILD) test performs poorly (Barker and Lutzoni 2002, Dolphin et al. 2000, Dowton and Austin 2002, Yoder et al. 2001), a simple test was used for comparing and assessing the combinability of the data from individual datasets. The individual gene phylogenies were considered to be incongruent if clades with significant ML bootstrap support and BI BPP (i.e. $\geq 70\%$ BS or $\geq 95\%$ BPP) were conflicting in the tree topologies (Alfaro et al. 2003, Weins 1998, Lutzoni et al. 2004). Incongruent clades with $< 70\%$ BS and $< 95\%$ BPP suggest the conflict is statistically unsupported. If there is no conflict based on the above assumptions, it supports the argument that the individual genes possess similar phylogenetic histories and can be combined. Since no significant conflict was observed among clades in each of the individual datasets, they were combined to achieve maximum phylogenetic resolution and support. The combined dataset was analyzed with the same parameters as above except that the protein coding dataset was partitioned based on codon positions. For BI we used flat priors and unlinked model parameters across partitions. The combined datasets were partitioned and analyzed so as to allow separate parameter estimation for each gene as well as for each codon position for *MCM7*.

Substitution saturation test

All of the 89 sequences from the *MCM7* alignment were used to assess transitions/transversions (ti/tv) substitution saturation of first, second, and third-codon positions. Observed ti/tv was plotted against Jukes Cantor JC89 corrected distance (Jukes and Cantor 1969) for each codon position separately as well as combined

using the program DAMBE (Xia and Xia 2001, Xia 2009). Transition and transversion of each codon position can be considered saturated if the scatter points on the two-dimensional plot appear to level off with an increase in sequence divergence. In addition, the I_{ss} statistic, which is a measure of substitution saturation in molecular phylogenetic datasets developed by Xia et al. (2003) and implemented in DAMBE, was also used to detect saturation. Nucleotide statistics for both genes were calculated in PAUP* 4.0b10 (Swofford 2002), SeqState v. 1.4.1 (Müller 2005), and Mega v. 4 (Tamura et al. 2007).

Phylogenetic Informativeness

We performed a phylogenetic informativeness (PI) measure on our combined dataset as proposed by Townsend (2007) using the PhyDesign online tool developed by López-Giráldez and Townsend (2011). PhyDesign measures per-site estimates to project the utility of a particular gene for resolving phylogeny related questions across historical time. This method allows for a comparison of different genes and loci used for phylogenetics by providing an estimate of the cost effectiveness of character sampling for specific time units. The time units used herein are relative time periods. Schoch et al. (2009a) compared PI for the Ascomycota using a 6-gene phylogeny, but *MCM7* was not evaluated in their study.

Results

Taxon sampling

A total of 89 taxa were included in the study, which comprises 80 species belonging to 63 genera of lichenized and non-lichenized ascomycetes in the classes Dothideomycetes, Eurotiomycetes, Geoglossomycetes, Lecanoromycetes, Leotiomycetes, and Sordariomycetes (Table 1).

New taxa sequenced

We report 93 new sequences of which 65 are *MCM7* and 28 are LSU (Table 1). Table 1 provides accession numbers for sequences used from GenBank in addition to those newly generated in this study. Most of the newly generated data for both *MCM7* and LSU are from ascomycetes that occur as saprobes on wood in terrestrial (Miller and Huhndorf 2009) or freshwater habitats (Shearer and Raja 2010). Our study resulted in a > 80% sequencing success rate for *MCM7*, which is comparable to that found by Schmitt et al. (2009b). We obtained the best PCR amplification results for *MCM7* with about 5 µl of total genomic DNA concentration per 25 µl of PCR reaction.

Both LSU and *MCM7* alignments consisted of the same 89-taxon dataset. The original LSU dataset had a total of 1484 nucleotides. After aligning in MUSCLE and excluding nucleotides from the 5' and 3' ends due to missing data in most sequences, the LSU dataset consisted of 1141 nucleotides. The final LSU dataset after excluding 57 ambiguous characters and two short intron regions from *Saccharomyces cerevisiae* consisted of 1076 nucleotides. The LSU dataset had 551 constant characters, 123 variable characters, and 402 parsimony informative characters (Table 2). The *MCM7* dataset consisted of a total of 642 nucleotides (193 constant, 449 variable); there were no missing characters, ambiguous regions, or introns. The majority of informative characters were in third codon positions (Table 2). The GC content of *MCM7* was slightly higher than LSU, although nucleotide percentages were somewhat similar in both datasets (Table 2). Although *MCM7* had fewer nucleotides analyzed, it had a higher percent (62%) of parsimony informative characters than LSU (37%) (Table 2). The final LSU and *MCM7* combined dataset had 1718 nucleotides.

Table 2. Comparison of datasets and trees in phylogenetic analyses.

Datasets	Genes		
	LSU (28S nrDNA) (DNA)	MCM7 (MS456) (DNA)	Combined LSU and MCM7
No. of taxa	89	89	89
No. of primers used to sequence region	4	2	4 + 2
No. of total characters ^a	1141	642	1783
No. of ambiguous characters	57	None	-
No. of characters in introns	8	None	-
No. of characters analysed	1076 (range 889–1064)	642 (range 641-642)	1718 (range 1531-1706)
No. of constant characters	551	193	744
No. of parsimony informative characters ^b	402 (37%)	108, 79, 212 (399) (62%)	801 (47%)
No. of variable parsimony uninformative characters	123 (11%)	50 (8%)	173 (11%)
%GC	50.852	51.493	51.096
%A	25.914	25.345	25.697
%C	21.525	24.967	23.601
%G	29.327	24.526	27.495
%T	23.233	23.162	23.207
(-ln)L score using PhyML	14971	24325	39965
No. of clades with ≥ 70% bootstrap support in PhyML analyses with 1000 bootstrap replicates	46	38	62
No. of clades with ≥ 70% bootstrap support in RAxML analyses with 1000 bootstrap replicates	52	39	63
No. of clades with ≥ 95% Bayesian posterior probability	62	46	61

^a Excluding sites at 5' and 3' ends
^b Divided into first, second, and third codon positions for *MCM7*; total shown in parentheses

Phylogenetic analyses

The estimated model parameter values obtained from AIC with modeltest are listed in Table 3. Application of separate models on the different codon positions for *MCM7* did not affect the topology and posterior probabilities of clades (data not shown). Since PhyML and BI analyses produced trees with nearly identical topologies, only PhyML phylograms are shown (Figs 1–3).

Class-level relationships: The overall tree topologies of LSU and *MCM7* genes were identical with the represented classes of fungi occurring as monophyletic (Figs 1 and 2). A total of 46 clades received strong support ($\geq 70\%$ BS and $\geq 95\%$ BPP) with PhyBS, 52 for RAxBS, and 62 for BPP for LSU, whereas, 38, 39, and 46 clades were strongly supported for PhyBS, RAxBS, and BPP, respectively, for *MCM7* (Table 2).

Table 3. Maximum likelihood best-fit evolutionary models and parameters for separate and combined data sets selected by Akaike Information Criterion.

Datasets	Genes			
	LSU (28S nrDNA) (DNA)	MCM7 (MS456) (DNA)	Combined LSU and MCM7	MCM7 (1-2 codon positions)
Number of sites	1076	642	1718	428
Model	GTR + I + G ^a	GTR + I + G	GTR+ I + G	GTR+ I + G
-L (ln)	15101	24434	40100	7407
Base frequencies				
A	0.2601	0.2462	0.2444	0.3359
C	0.2234	0.2798	0.2598	0.2314
G	0.2929	0.2288	0.2620	0.2187
T	0.2236	0.2452	0.2337	0.2140
Substitution model rate matrix				
[A–C]	0.7196	3.8836	1.6263	3.3571
[A–G]	1.8621	11.6510	4.4131	4.4215
[A–T]	1.1078	2.9992	1.6638	2.3969
[C–G]	0.7829	2.4761	1.1231	1.5438
[C–T]	5.0397	13.6071	6.9837	5.9435
[G–T]	1.0000	1.0000	1.0000	1.0000
Among site variation				
I ^b	0.3527	0.2723	0.3754	0.3490
G ^c	0.5727	0.6444	0.5916	0.7948

^a General Time Reversible model (Rodríguez et al. 1990) with unequal base frequencies, gamma distribution with among site variation and a proportion of sites are invariable.

^b Proportion of invariable sites

^c Variable sites gamma distribution parameter

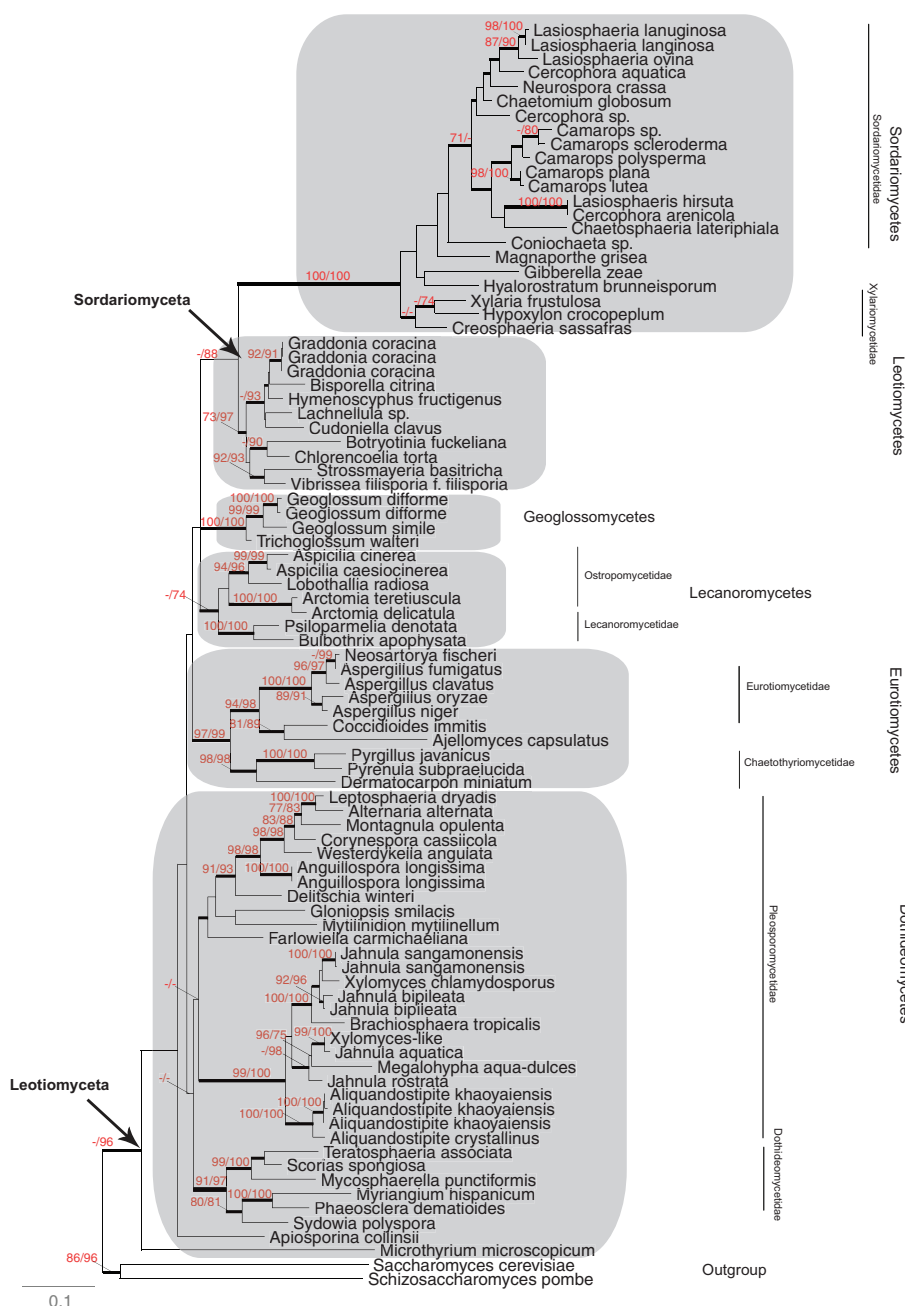


Figure 1. Maximum Likelihood phylogeny of Leotiomyces (Ascomycota) based on 28S nrDNA large subunit data set (1141 bp) of 89 taxa using PhyML ((-ln)L score 14971). Thickened branches indicate significant Bayesian posterior probabilities $\geq 95\%$; numbers refer to PhyML/RAXML bootstrap support values $\geq 70\%$ based on 1000 replicates. One representative each from Saccharomycotina and Taphrinomycotina was used as outgroup taxa. The major classes are shaded in grey. Classification following Hibbett et al. (2007) is shown on the right.

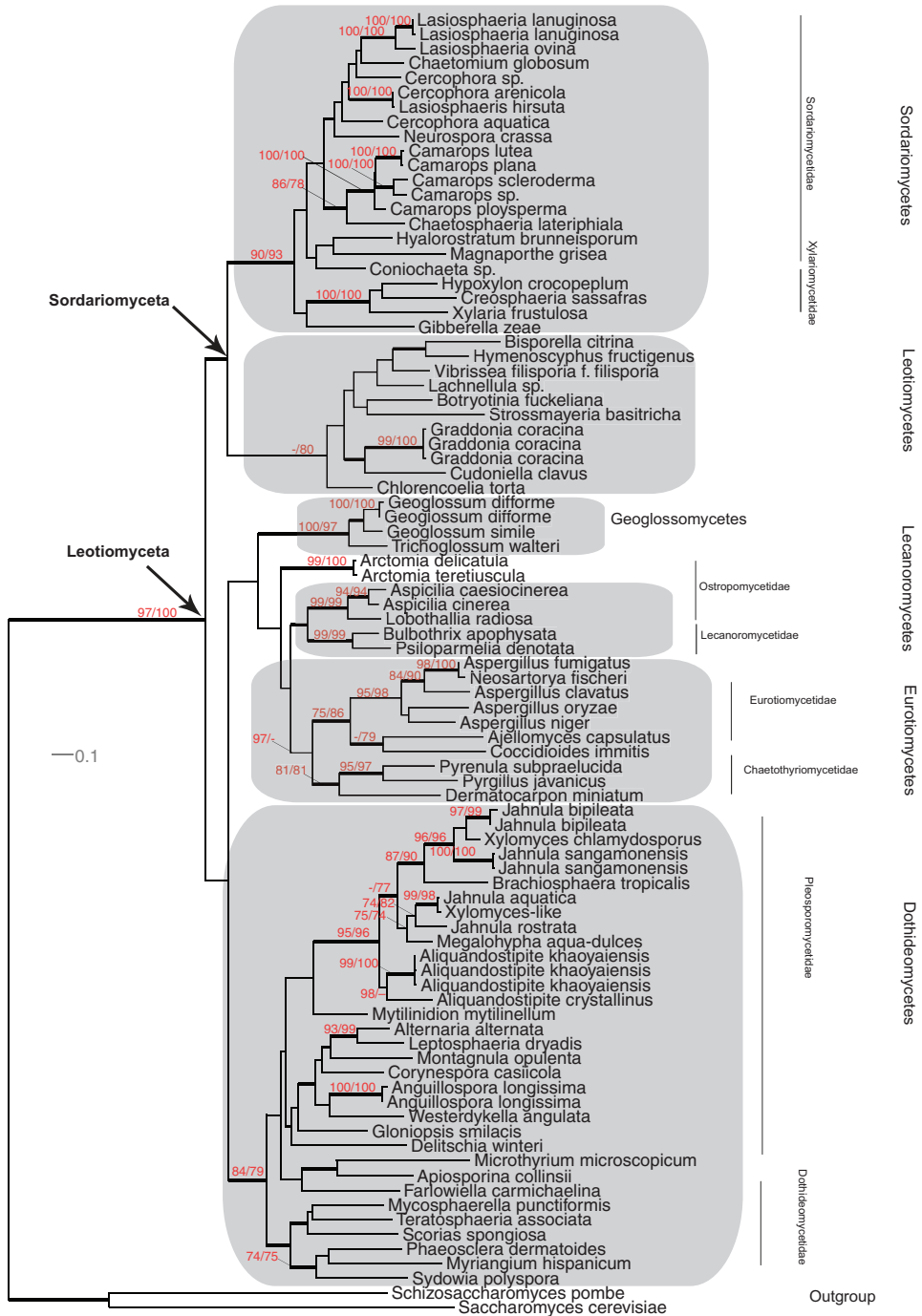


Figure 2. Maximum Likelihood phylogeny of Leotiomyceta (Ascomycota) based on *MCM7* data set (642 bp) of 89 taxa using PhyML ($-\ln L$ score 24325). Support values, shading and classification as in Fig. 1.

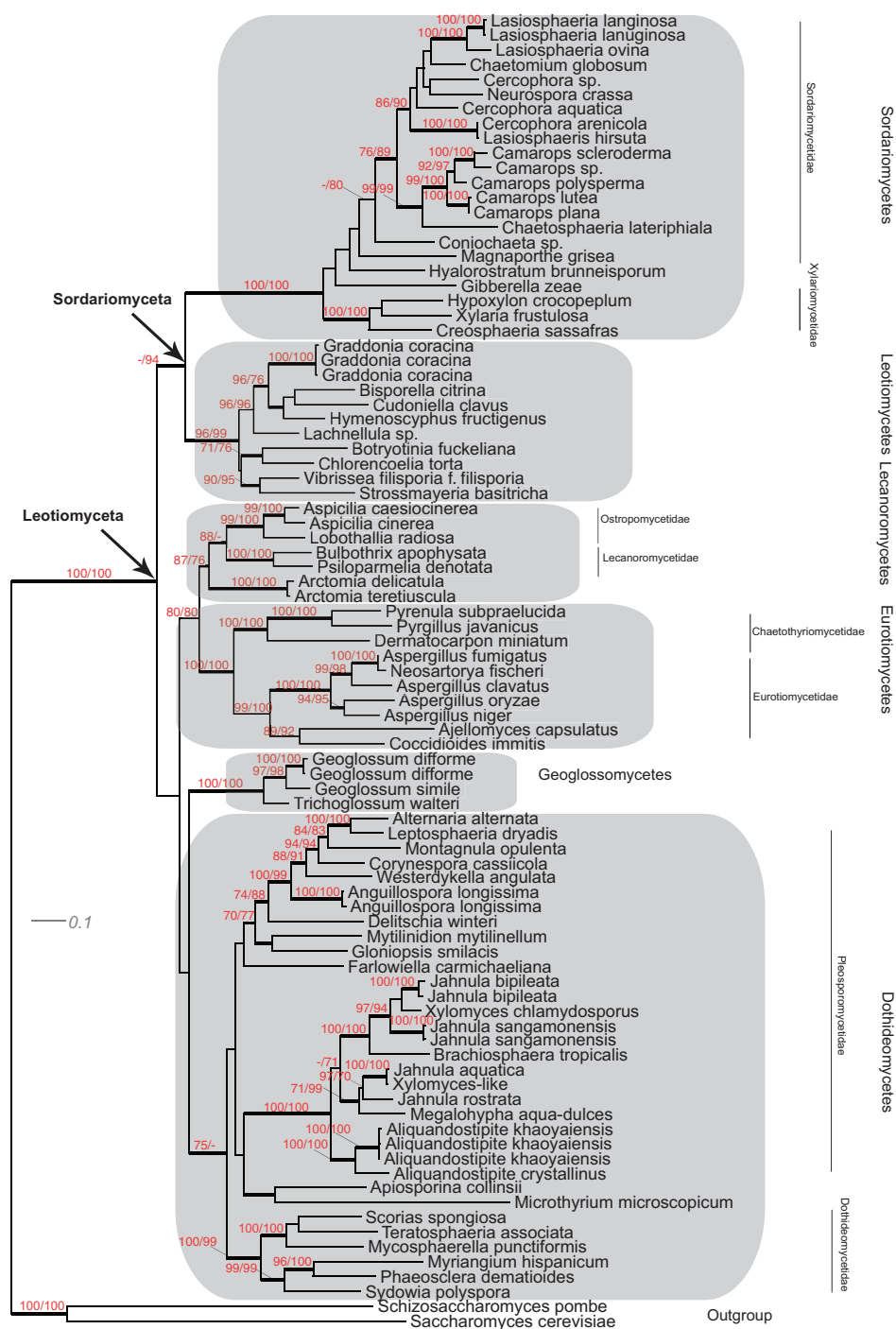


Figure 3. Maximum Likelihood phylogeny of Leotiomyceta (Ascomycota) based on a combined 28S nrDNA large subunit and *MCM7* data set (1718 bp) of 89 taxa using PhyML ((-ln) L score 39965). Support values, shading and classification as in Fig. 1.

More major lineages within the Ascomycota were more strongly supported with LSU compared to *MCM7* data. For LSU, nine nodes were strongly supported with PhyBS and ten with RAxBS, while twelve were strongly supported with BPP (Table 4). For *MCM7*, ten nodes were strongly supported with PhyBS and RAxBS, while only nine were strongly supported based on BPP (Table 4). The somewhat higher support for the LSU gene may be due to the greater sequence length for LSU when compared to *MCM7* in the present study. Min and Hickey (2007) have shown that reducing sequence length can have a profound effect on the resolution of resulting phylogenetic trees. The net PI profile, which is based on sequence length, also shows the LSU gene has slightly higher phylogenetic informativeness at older nodes across relative older dates compared to *MCM7* (Table 5, Fig. 6).

Genus and species level relationships: Within the Dothideomycetes, Eurotiomycetes, Geoglossomycetes, and Sordariomycetes, we selected more than one species/strain within a genus to assess the performance of *MCM7* (MS456) versus LSU. Our data shows that *MCM7* can be used for assessing interspecific relationships of taxa within genera such as *Camarops*, *Lasiosphaeria*, (Sordariomycetes), *Aspergillus* (Eurotiomycetes), *Geoglossum* (Geoglossomycetes), and *Aliquandostipite* (Dothideomycetes). The above taxa sampled from their different classes within the Leotiomyceta each formed a monophyletic clade with high internal resolution and support based on MLBS and BPP values in each gene tree (see Figs 1 and 2, and Table 5). However, the combined gene tree showed even better resolution of relationships and clade support for the above genera (Fig. 3, Table 5). Removing the third codon position had a slight negative effect on clade support within genera (Fig. 5, Table 5).

Combined analysis

Since no significant conflict occurred among well-supported clades in each tree topology, we concatenated the two gene regions. The combined LSU-*MCM7* gene tree (Fig. 3) had a total of 801 parsimony informative characters (Table 2) and provided a more robust phylogenetic hypothesis of the Ascomycota (Fig. 3) than either individual tree topology. A total of 62 clades were strongly supported with PhyBS, 63 with RAxBS, and 61 with BPP (Table 2). The combined tree also received higher nodal support for the major lineages included with 13 strongly supported lineages with PhyBS, twelve with RAxBS, and twelve with BPP (Table 4). The nodal support for the combined data set was higher for the total number of strongly supported clades as well as for the number of nodes strongly supported for the major lineages in comparison to the separate gene analyses (see Table 3, 4 and Figs 1–3). A number of nodes that were moderately (< 70 % BS and < 95% BPP) or poorly (< 50 % BS and < 70% BPP) supported in the separate gene analyses received strong support in the combined gene analyses (Table 4).

Table 4. Comparison of PhyML bootstrap support (PhyBS), RAxML bootstrap support (RAxBS), and Bayesian posterior probabilities (BPP) of all lineages within the Leotiomyceta (Ascomycota) included in the present study obtained from separate and combined data partitions of LSU rDNA and MCM7 sequence data. Only values > 70% BS, and > 95% BPP are shown.

Lineages	LSU rDNA			MCM7 (1, 2, 3 codon positions)			LSU_MCM7 (1, 2, 3 codon positions)			MCM7 (1, 2 codon positions)		
	PhyBS	RAxBS	BPP	PhyBS	RAxBS	BPP	PhyBS	RAxBS	BPP	PhyBS	RAxBS	BPP
Sordariomycetes ¹	100	100	> 95	90	98	> 95	100	100	> 95	86	90	> 95
<i>Sordariomycetidae</i> ²	–	–	–	–	–	–	–	–	–	–	–	–
<i>Xylariomycetidae</i>	–	–	> 95	100	100	> 95	100	100	> 95	99	100	> 95
Leotiomycetes	73	97	> 95	–	80	–	96	99	> 95	90	94	> 95
Geoglossomycetes	100	100	> 95	100	97	> 95	100	100	> 95	96	96	100
Lecanoromycetes	–	74	> 95	–	–	–	87	76	> 95	–	–	–
<i>Ostropomycetidae</i>	94	96	> 95	99	99	> 95	99	100	> 95	84	88	> 95
<i>Lecanoromycetidae</i>	100	100	> 95	99	99	> 95	100	100	> 95	93	95	> 95
Eurotiomycetes	97	99	> 95	97	–	–	100	100	> 95	–	–	–
<i>Eurotiomycetidae</i>	94	98	> 95	75	86	> 95	99	100	–	94	96	> 95
<i>Chaetothyriomycetidae</i>	98	98	> 95	81	81	> 95	100	100	> 95	86	90	> 95
Dothideomycetes	–	–	–	84	79	> 95	75	–	> 95	–	–	–
<i>Pleosporomycetidae</i>	–	–	> 95	–	–	–	70 ^a	77	> 95	–	–	–
<i>Dothideomycetidae</i>	91	97	> 95	74	75	> 95	100	99	> 95	74	86	> 95
Total class lineages supported	4	5	5	4	4	3	6	5	6	3	3	3
Total subclass lineages supported	5	5	7	6	6	6	7	7	6	6	6	6
Total nodes supported	9	10	12	10	10	9	13	12	12	9	9	9

^a excluding *Farlowiella carmichaeliana*
¹ Class lineages are given in bold
² Subclass lineages are given in italics

Table 5. Genus level relationships among selected genera used in the present study. Support values and analyses are same as in Table 4.

Lineages	LSU rDNA			MCM7 (1, 2, 3 codon positions)			LSU_MCM7 (1, 2, 3 codon positions)			MCM7 (1, 2 codon positions)		
	PhyBS	RAXBS	BPP	PhyBS	RAXBS	BPP	PhyBS	RAXBS	BPP	PhyBS	RAXBS	BPP
Sordariomycetes												
<i>Camarops</i>	–	–	> 95	100	100	> 95	99	100	> 95	99	100	> 95
<i>Lasiosphaeria</i>	87	90	> 95	100	100	> 95	100	100	> 95	99	100	–
Leotiomycetes												
<i>Graddonia</i>	92	91	> 95	99	100	> 95	100	100	> 95	99	100	> 95
Eurotiomycetes												
<i>Aspergillus</i>	100	100	> 95	95	98	–	100	100	> 95	94	96	> 95
Dothideomycetes												
<i>Aliquandostipite</i>	100	100	> 95	98	–	–	100	100	> 95	–	–	–
Total nodes supported	4	4	5	5	4	3	5	5	5	4	4	3

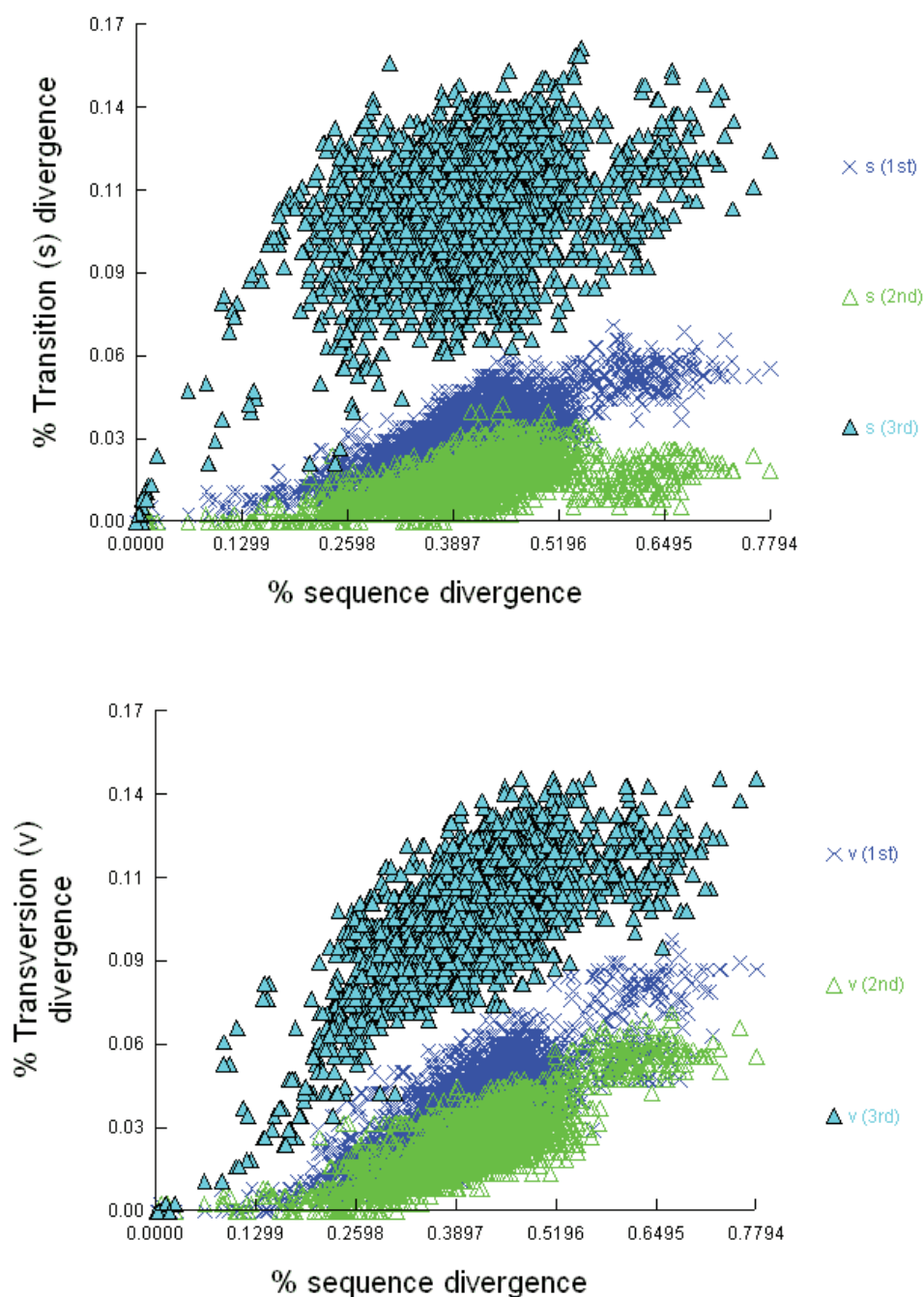
Substitution saturation

There is no indication of substitution saturation in the first or second codon positions (Fig. 4). However, for the third codon position, it is evident that there is leveling off in the scatter plot when transition/transversion divergence are plotted against pairwise sequence divergence (Fig. 4). It is also clear that third codon position transitions reach a plateau. Saturation tests therefore indicate poor phylogenetic signal at the third codon position, and transitions appear to be saturated on a plot of substitution type against JC corrected genetic distances. The test of Xia et al. (2003) suggested that for the first and second codon positions of *MCM7* sequences, the values for the index of substitution saturation I_{ss} were 0.253 and 0.152, respectively, for 32 OTUs, and the critical $I_{ss,C}$ values were 0.659 and 0.658. This suggests that there were no significant levels of substitution saturation at the first and second positions ($I_{ss} < I_{ss,C}$, $P < 0.0001$). However, for the third codon position of *MCM7*, the observed I_{ss} value of 0.807 is significantly greater than the $I_{ss,C}$ value of 0.658, suggesting that the third codon position has experienced substitution saturation (Xia et al. 2003). This statistical test therefore corroborates the scatter plot data and suggests that the third codon position is saturated and therefore might possess a poor phylogenetic signal. Therefore, we carried out an additional set of ML and BI analyses using a method called site stripping (Verbruggen and Theriot 2008), where we entirely removed the third codon position in order to assess the effects of saturated third codon position on the tree topology and statistical clade support.

The PhyML tree resulting from an analysis of only first and second codon positions for *MCM7* is presented in Fig. 5. The topology of this phylogenetic tree is not congruent with the LSU and *MCM7* trees or the combined gene trees. One major difference was that the Xylariomycetidae clade nested within the Sordariomycetidae clade. In addition the nodal support for the major lineages was quite poor for the first and second codon position tree when compared to the separate LSU and *MCM7* gene trees or the combined gene tree (Table 4). For example, Dothideomycetes and Eurotiomycetes did not receive support with PhyBS, RAxBS, or BPP (Table 4). However, the *MCM7* gene tree with all codon positions included showed strong support for the Dothideomycetes and the Eurotiomycetes lineage was strongly supported with PhyBS (Table 4).

Phylogenetic Informativeness

We derived the profiles from rates of evolution of sites within genes using PhyDesign, an online platform for profiling PI (López-Giráldez and Townsend 2011, see also Townsend 2007), which provides a unique empirical metric for guiding marker selection and facilitates locus prioritization. The net PI correlates with the degree of nodal support, while the per site PI compares the relative power of gene performance without confounding effects of gene length (Townsend 2007, López-Giráldez and Townsend 2011). Net PI showed a higher pulse for *MCM7* than LSU. However, LSU



Figures 4a, b. Nucleotide substitution saturation plots: The proportion of transitions (s) and transversions (v) were plotted against sequence divergence using Jukes-Cantor evolutionary distance in the program DAMBE.

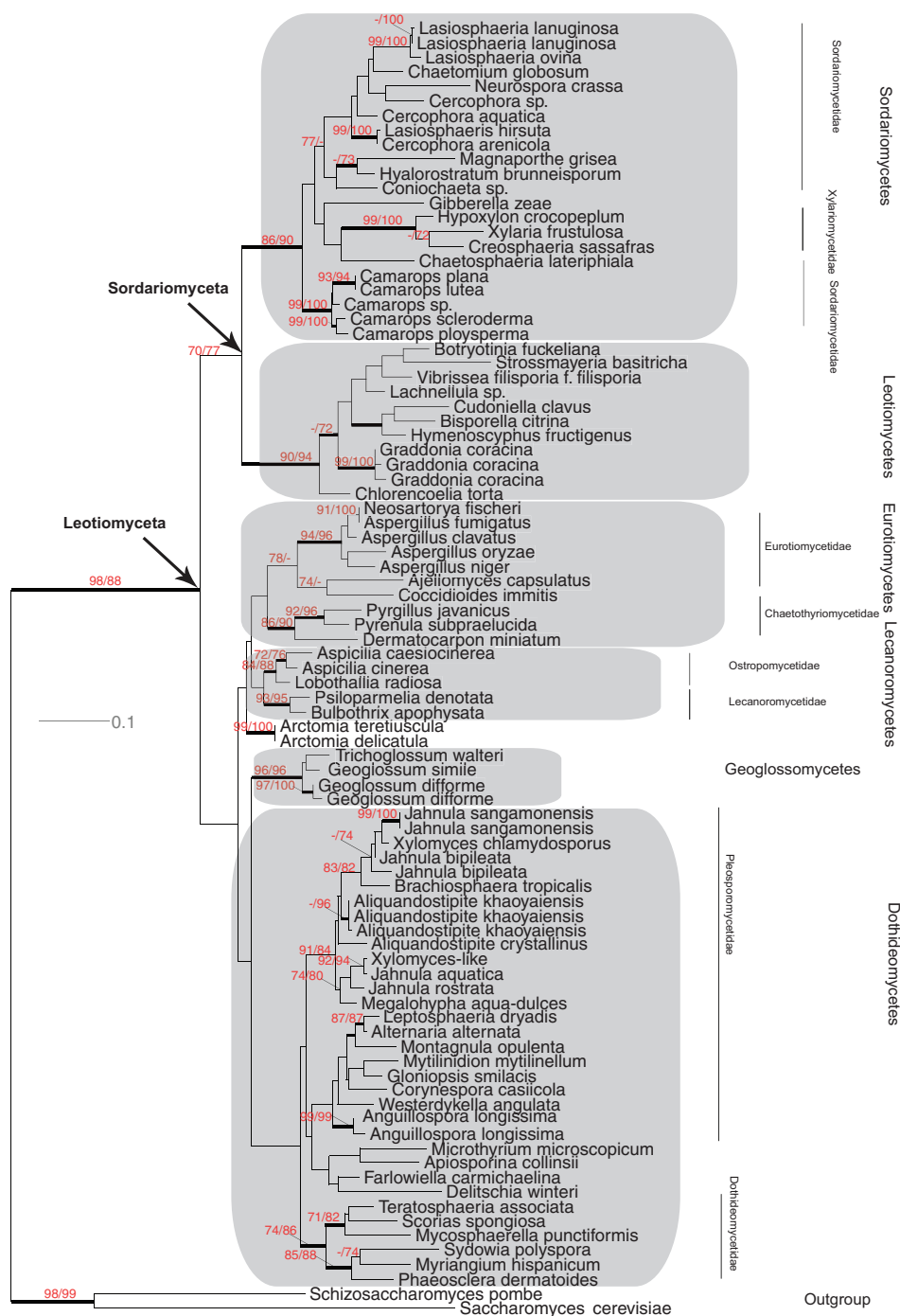


Figure 5. Maximum Likelihood phylogeny of Leotiomyces (Ascomycota) based on 1-2 codon position of *MCM7* data set (428 bp) of 89 taxa using PhyML ((-ln)L score 7352). Support values, shading and classification as in Fig. 1.

had a higher pulse of PI for older time units (beyond 0.4) (Fig. 6). Based on a per-site comparison, the *MCM7* gene fragment (642 bp) produced a pulse of higher PI across relative time units compared to LSU (Fig. 6).

Discussion

Class-level relationships

The topologies of the major classes obtained using the LSU gene (Fig. 1) as well as the *MCM7* gene (Fig. 2) broadly agrees with previously published multi-gene phylogenies of Ascomycota (James et al. 2006, Lutzoni et al. 2004, Schoch et al. 2009a, Spatafora et al. 2006). We show that all classes in the present study are monophyletic, which corroborates earlier hypotheses by Eriksson and Winka (1997). Recently, Schoch et al. (2009b) proposed a new class, Geoglossomycetes, based on a multi-gene phylogeny. Our results for the *MCM7* gene are in agreement with Schoch et al.'s study as Geoglossomycetes is shown as a monophyletic group with strong MLBS and BPP support (Fig 2, Table 4), but, however, without strong support for its placement in relation to other classes of Leotiomyceta as noted previously (Schoch et al. 2009b). We did not recover support for the expanded subclass Pleosporomycetidae as found in a previous multi-gene study focused only on Dothideomycetes (Schoch et al. 2009c) and the influence of additional gene data and improved taxon sampling cannot be ruled out. In spite of this, results of our study are also in agreement with those of Aguilera et al. (2008), who showed that *MCM7* is a reliable marker for establishing phylogenetic relationships among fungi, and concur with Schmitt et al.'s (2009b) results regarding the phylogenetic utility of *MCM7* for resolving relationships among the Ascomycota.

Genus and species-level relationships

We included more than one species or isolate of various genera such as *Camarops*, *Lasiochaeria* (Sordariomycetes), *Graddonina* (Leotiomycetes), *Aspergillus* (Eurotiomycetes), and *Aliquandostipite* (Dothideomycetes) to test how *MCM7* would perform in resolving relationships at the genus-level. Although several species of *Jahnula* were included in our study, we do not discuss results for this genus in more detail since independent data strongly suggest the genus may be polyphyletic within the order Jahnulales (Campbell et al. 2007, Suetrong et al. 2010). Currently, the ribosomal 18S small subunit and 28S large subunit are widely used genes for placing newly described genera of fungi within a class in the Ascomycota (see Begerow et al. 2010). Here we show *MCM7* can be used along with LSU to resolve genus-level relationships. In general, we found slightly better resolution and support with likelihood BP and BPP for the aforementioned genera with *MCM7* in comparison with LSU (Figs 1 and 2; Table 5). All clades within these genera were highly supported based on the combined gene analysis (Fig. 3; Table 5).

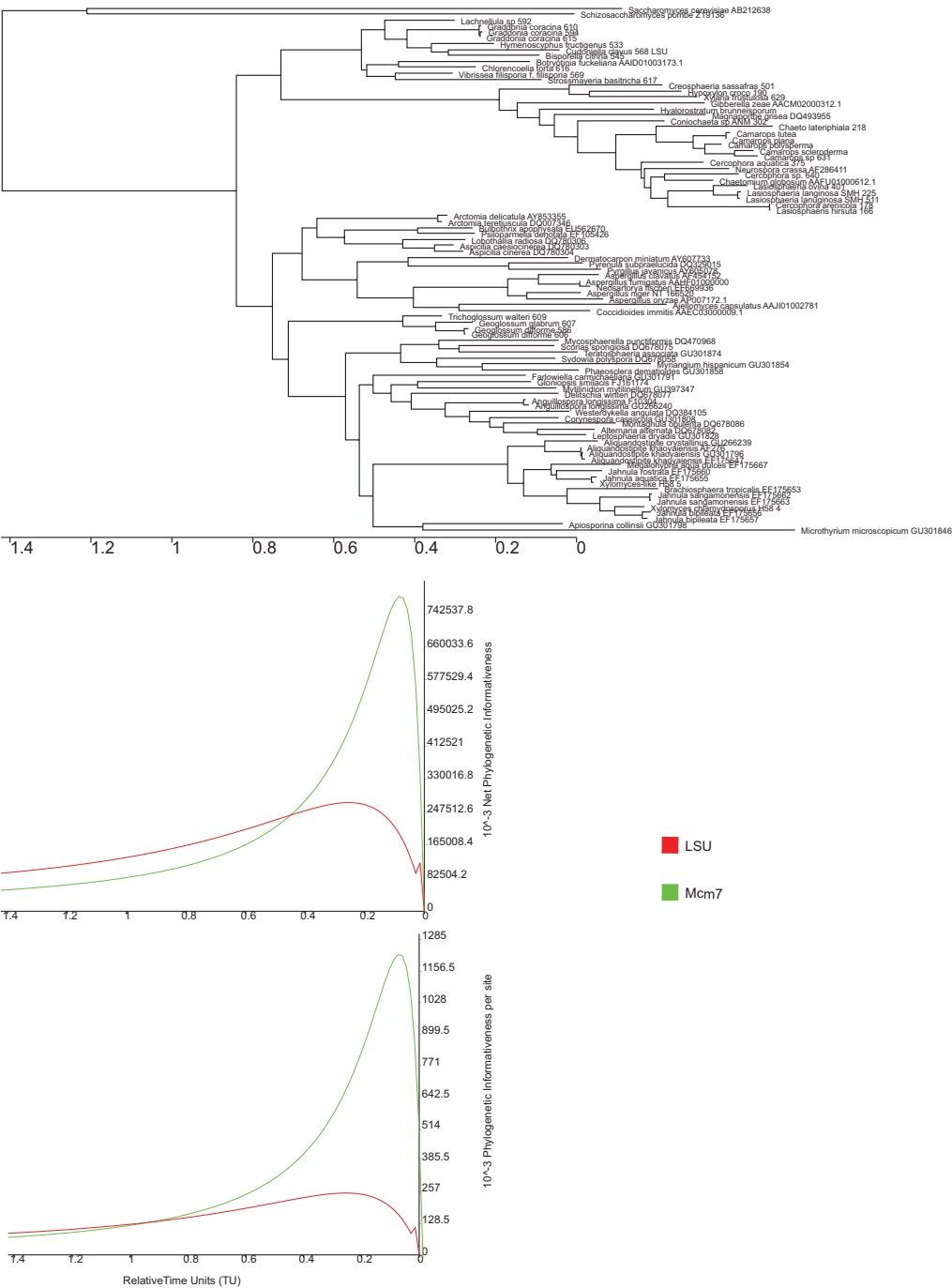


Figure 6. Phylogenetic informativeness profiles for two genes LSU (1076 bp) and *MCM7* (642 bp) through 1.4 time units using PhyDesign online tool. Tree was obtained with PHYML. The relative time units are shown on the X-axis and profiles of net and per-site phylogenetic informativeness is shown on the Y-axis. Profiles of LSU gene are shown in red and *MCM7* are shown in green.

Our results are in agreement with those of Schmitt et al. (2009b), who showed the utility of *MCM7* at the genus level for taxa such as *Aspergillus*, *Lecanora*, and *Malcomiella*. Peterson et al. (2010) also used *MCM7* successfully with other protein coding genes such as *RPB2* and *TSR1* to resolve phylogenetic relationships of the genus *Hamigera*, an ascomycete fungus belonging to the Eurotiomycetes. The *MCM7* gene was also recently used in species delimitation of a lichen forming fungus, *Xanthoparmelia* (Leavitt et al. 2011). The authors reported high parsimony informative variable characters in *MCM7* compared to other protein coding (Beta-tubulin) as well as other ribosomal gene markers (ITS, LSU). More recently, Spribille et al. (2011) used *MCM7* for phylogenetic analysis of the boreal lichen *Mycoblastus sanguinarius*. Although *MCM7* was reported as being highly variable and showed good phylogenetic signal, it showed a higher level of transition saturation at the third codon position (Spribille et al. 2011). The authors concluded that caution must be taken when using *MCM7* to recover gene phylogenies. Although we did not find a significant difference in the nodal support between the *MCM7* and LSU genes (Table 5), overall, based on our study and results of some recent studies, it seems likely that *MCM7* shows good potential as a candidate gene for evaluating interspecific relationships among the Ascomycota.

Combine gene analyses

Combining datasets generally provides better resolution and nodal support for clades in phylogenetic analyses of the fungal kingdom (Lutzoni et al. 2004). Our combined LSU and *MCM7* dataset showed enhanced phylogenetic resolution (Fig. 3) and increased nodal support for clades that were not strongly supported when analyzed separately (Table 4). Our data are in agreement with other Ascomycota studies that have shown that combining protein-coding data with nuclear ribosomal genes (either LSU or SSU) provides an increased number of supported nodes in phylogenetic analyses (Geiser et al. 2006, Hansen et al. 2005, Miller and Huhndorf 2005, Schoch et al. 2006, Spatafora et al. 2006, Tang et al. 2007). Hofstetter et al. (2007) concluded that for better resolution and support of clades in phylogenetic analyses of fungi more characters and protein-coding genes in particular are important. Our study also supports the prediction by Schmitt et al. (2009b) who suggested that *MCM7* has a higher potential to resolve phylogenetic relationships between fungi when analyzed in combination with other commonly used genes such as LSU. In addition, our PI analyses using PhyDesign shows that *MCM7* was a more phylogenetically informative gene than LSU. Schoch et al. (2009a) also found that protein-coding genes had better PI profiles than those of rDNA genes.

MCM7 codon saturation

In this study the third codon position in *MCM7* appears to be saturated based on scatter plots of substitution saturation curves (Fig. 4), which agrees with results of

empirical tests by Xia et al. (2003). Spribille et al. (2011) also showed a higher level of transition-saturation at the third codon position for *MCM7* gene in their phylogenetic analyses. Substitution saturation appears to be a common problem among protein-coding genes routinely used for inferring phylogenetic relationships among fungi (Liu et al. 1999, Hansen et al. 2005, Matheny et al. 2007, Miller and Huhndorf 2005, Sung et al. 2007). There are currently two schools of thought regarding the inclusion or exclusion of third codon positions from saturated protein-coding genes and their method of utilization for phylogenetic analyses. One group is of the opinion that third codon positions should be excluded in ML analysis because these fast evolving, saturated characters can decrease the signal/noise ratio, thus providing misleading interpretations of evolutionary relationships (Blouin et al. 1998, Swofford et al. 1996, Xia et al. 2003). Conversely, the other group suggests the inclusion of the third codon position since the presence of more phylogenetically informative characters helps with potentially decreasing stochastic errors and increases branch-support values (Edwards et al. 1991, Källersjö et al. 1998, Müller et al. 2006, Simmons et al. 2006). Björklund (1999), however, suggests that unless one finds evidence that third codon positions are significantly misleading they should not be eliminated from analyses *a priori*.

Based on our analyses of the *MCM7* dataset with and without third codon positions (Fig. 2, all codon positions included, and Fig. 5, third codon positions excluded), we found that exclusion of third codon positions did not have a major effect on the monophyly of the classes, except that the subclass Xylariomycetidae was nested within the Sordariomycetidae when third codon positions were excluded (Fig. 5). However, exclusion of third codon positions led to a loss of nodal support (MLBS and BPP) for several clades both at the class and genus level (Table 4, 5). These results are in agreement with those found by Edwards et al. (1991), who found that removal of third codon positions in mitochondrial genes in a group of birds resulted in “biological unreasonable” groupings as well as loss of BS for one of the branches in their phylogenetic tree. Hackett (1996) also found that removal of saturated third codon positions from mitochondrial genes in another bird study resulted in a loss of phylogenetically informative transversions. Therefore, for our 89-taxon *MCM7* gene phylogeny it seems appropriate to include the third codon positions in order to retain appropriate tree topology as well as MLBS and BPP nodal support. We concur with the conclusions of Simmons et al. (2006) that despite indications of saturation, third codon positions must be included in phylogenetic analyses since they contain a large number of phylogenetically informative characters.

Conclusions

We have presented evidence for the phylogenetic utility of *MCM7* among the Ascomycota. Results of the PI profiles show that *MCM7* was more informative than LSU. Here we show that this locus can also be used successfully for determining phylogenetic relationships of non-lichenized ascomycetes and provides good resolution

and support at half the cost compared to LSU because we used only two primers to sequence the *MCM7* gene as opposed to four primers used routinely for LSU. In addition, no introns were present in the *MCM7* gene for the taxa sequenced in our study. *MCM7* seems to qualitatively contribute to better resolution of higher as well as lower taxonomic level clades. We also show that combined LSU and *MCM7* gene phylogeny had superior resolving power for both class and genus level relationships since all major classes received high BS in both PhyML and RAxML bootstrap analyses as well as high BPP values. We report that although the third codon position of *MCM7* is saturated, it may be better to analyze the dataset with all codon positions included. Exclusion of third codon positions compromised the overall topology of the tree and, in some clades, resulted in poor nodal support with MLBS and BPP, perhaps due to exclusion of a significant number of phylogenetically informative characters. Lutzoni et al. (2004) suggested “there is a great need for housekeeping protein-coding genes to be sequenced and combined with other loci to assemble the fungal tree of life”. The results from this study suggest that *MCM7* will make an important contribution toward such an effort.

Future Directions

MCM7 shows good potential to be a candidate gene for fungal phylogeny reconstruction, especially for the Ascomycota. However, future studies comparing *MCM7* with *RPB1*, *RPB2*, and *EF1* alpha are warranted for the Ascomycota to better understand which single copy protein coding locus is easiest to PCR amplify and sequence, while at the same time also provides the greatest amount of phylogenetic informativeness.

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