

The Amsterdam Declaration on Fungal Nomenclature

David L. Hawksworth¹, Pedro W. Crous², Scott A. Redhead³, Don R. Reynolds⁴, Robert A. Samson², Keith A. Seifert³, John W. Taylor⁵, Michael J. Wingfield⁶*, Özlem Abaci⁷, Catherine Aime⁸, Ahmet Asan⁹, Feng-Yan Bai¹⁰, Z. Wilhelm de Beer⁶, Dominik Begerow¹¹, Derya Berikten¹², Teun Boekhout², Peter K. Buchanan¹³, Treena Burgess¹⁴, Walter Buzina¹⁵, Lei Cai¹⁶, Paul F. Cannon¹⁷, J. Leland Crane³⁸, Ulrike Damm², Heide-Marie Daniel¹⁸, Anne D. van Diepeningen², Irina Druzhinina¹⁹, Paul S. Dyer²⁰, Ursula Eberhardt², Jack W. Fell²¹, Jens C. Frisvad²², David M. Geiser²³, József Geml²⁴, Chirlei Glienke²⁵, Tom Gräfenhan²⁶, Johannes Z. Groenewald², Marizeth Groenewald², Johannes de Gruyter²⁷, Eveline Guého-Kellermann²⁸, Liang-Dong Guo¹⁰, David S. Hibbett²⁹, Seung-Beom Hong³⁰, G. Sybren de Hoog², Jos Houbraken², Sabine M. Huhndorf³¹, Kevin D. Hyde³², Ahmed Ismail², Peter R. Johnston¹³, Duygu G. Kadaifciler³³, Paul M. Kirk³⁴, Urmaz Köljalg³⁵, Cletus P. Kurtzman³⁶, Paul-Emile Lagneau³⁷, C. André Lévesque³, Xingzhong Liu¹⁰, Lorenzo Lombard², Wieland Meyer³⁸, Andrew Miller³⁹, David W. Minter⁴⁰, Mohammad Javad Najafzadeh⁴¹, Lorelei Norvell⁴², Svetlana M. Ozerskaya⁴³, Rasime Öziç⁴⁴, Shaun R. Pennycook¹³, Stephen W. Peterson³⁶, Olga V. Pettersson⁴⁵, William Quaedvlieg², Vincent A. Robert², Constantino Ruibal¹, Johan Schnürer⁴⁵, Hans-Josef Schroers⁴⁶, Roger Shivas⁴⁷, Bernard Slippers⁶, Henk Spierenburg², Masako Takashima⁴⁸, Evrim Taşkın⁴⁹, Marco Thines⁵⁰, Ulf Thrane²², Alev Haliki Uztan⁵¹, Marcel van Raak²⁷, János Varga⁵², Aida Vasco⁵³, Gerard Verkley², Sandra I.R. Videira², Ronald P. de Vries², Bevan S. Weir¹³, Neriman Yilmaz², Andrey Yurkov⁵⁴, and Ning Zhang⁵⁵

Abstract: The Amsterdam Declaration on Fungal Nomenclature was agreed at an international symposium convened in Amsterdam on 19–20 April 2011 under the auspices of the International Commission on the Taxonomy of Fungi (ICTF). The purpose of the symposium was to address the issue of whether or how the current system of naming pleomorphic fungi should be maintained or changed now that molecular data are routinely available. The issue is urgent as mycologists currently follow different practices, and no consensus was achieved by a Special Committee appointed in 2005 by the International Botanical Congress to advise on the problem. The Declaration recognizes the need for an orderly transition to a single-name nomenclatural system for all fungi, and to provide mechanisms to protect names that otherwise then become endangered. That is, meaning that priority should be given to the first described name, except where that is a younger name in general use when the first author to select a name of a pleomorphic monophyletic genus is to be followed, and suggests controversial cases are referred to a body, such as the ICTF, which will report to the Committee for Fungi. If appropriate, the ICTF could be mandated to promote the implementation of the Declaration. In addition, but not forming part of the Declaration, are reports of discussions held during the symposium on the governance of the nomenclature of fungi, and the naming of fungi known only from an environmental nucleic acid sequence in particular. Possible amendments to the *Draft BioCode* (2011) to allow for the needs of mycologists are suggested for further consideration, and a possible example of how a fungus only known from the environment might be described is presented.

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¹Departamento de Biología Vegetal II, Facultad de Farmacia, Universidad Complutense de Madrid, Plaza Ramón y Cajal, E-28040 Madrid, Spain; and Department of Botany, Natural History Museum, Cromwell Road, London SW7 5BD, UK; corresponding author e-mail: d.hawksworth@nhm.ac.uk. ²CBS-KNAW Fungal Biodiversity Centre, Uppsalalaan 8, 3584 CT Utrecht, The Netherlands; p.crous@cbs.knaw.nl. ³National Mycological Herbarium, Agriculture and Agri-Food Canada, Neatby Building, 960 Carling Avenue, Ottawa, Ontario K1A 0C6, Canada. ⁴Herbarium, University of California Berkeley, 1001 Valley Life Sciences Building 2465, Berkeley, CA 94720-2465, USA. ⁵Department of Plant and Microbial Biology, University of California, Berkeley, CA 94720-3102, USA. ⁶Forestry and Agricultural Biotechnology Institute (FABI), University of Pretoria, Private bag X20, Hatfield 0028, Pretoria 0002, South Africa. ⁷Department of Biology, Basic and Industrial Microbiology Section, Faculty of Science, Ege University,

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İzmir, Turkey. ⁸Department of Plant Pathology and Crop Physiology, Louisiana State University, Agricultural Center, 302 Life Sciences Building, Baton Rouge, LA 70803, USA. ⁹Department of Biology, Trakya University, 22030 Edirne, Turkey. ¹⁰State Key Laboratory of Mycology, Institute of Microbiology, Chinese Academy of Sciences, No.3, 1st Beichen West Road, Chaoyang District, Beijing 100101, China. ¹¹AG Geobotanik, Ruhr-Universität Bochum, Universitätsstraße 150, D-44780 Bochum, Germany. ¹²Department of Biology, Anadolu University, TR-26470 Eskisehir, Turkey. ¹³Landcare Research, Private Bag 92170, Auckland 1142, New Zealand. ¹⁴School of Biological Sciences and Biotechnology, Murdoch University, South St, Perth, 6150, Australia. ¹⁵Institute of Hygiene, Microbiology and Environmental Medicine, Medical University Graz, Universitaetsplatz 4, A 8010 Graz, Austria. ¹⁶Key Laboratory of Systematic Mycology & Lichenology, Institute of Microbiology, Chinese Academy of Sciences, No.10, North 4th Ring Road West (BeiSiHuanXiLu), HaiDian District, Beijing 100190, China. ¹⁷CABI Europe – UK and Royal Botanic Gardens Kew, Jodrell Laboratory, Royal Botanic Gardens, Kew, Richmond, Surrey TW9 3AB, UK. ¹⁸BCCM/MUCL, Earth and Life Institute, Applied Microbiology, Mycology, Université catholique de Louvain, Croix du Sud 3, bte 6, B-1348 Louvain-la-Neuve, Belgium. ¹⁹Area Gene Technology and Applied Biochemistry, Institute of Chemical Engineering, Vienna University of Technology, 1060 Vienna, Austria. ²⁰School of Biology, University of Nottingham, University Park, Nottingham NG7 2RD, UK. ²¹RSMAS/University of Miami, 4600 Rickenbacker Causeway, Key Biscayne, FL 33149, USA. ²²Center for Microbial Biotechnology, Department of Systems Biology, Technical University of Denmark, Søtofts Plads B. 221, DK-2800 Kgs. Lyngby, Denmark. ²³Fusarium Research Center, Department of Plant Pathology, The Pennsylvania State University, University Park, Pennsylvania, PA 16802, USA. ²⁴National Herbarium of the Netherlands, Netherlands Centre for Biodiversity Naturalis, Leiden University, P.O. Box 9514, Einsteinweg 2, 2300 RA Leiden, The Netherlands. ²⁵Departament of Genetics, Federal University of Parana Curitiba – Brazil, PO Box 19071, 815310990 Brazil. ²⁶Grain Research Laboratory, Canadian Grain Commission, 1404-303 Main Street, Winnipeg, Manitoba R3C 3G8, Canada. ²⁷Plant Protection Service, P.O. Box 9102, 6700 HC Wageningen, The Netherlands. ²⁸5 Rue de la Huchette, 61400 Mauves sur Huisne, France. ²⁹Biology Department, Clark University, Worcester, MA 01610, USA. ³⁰National Academy of Agricultural Science, Suwon, 441-707, Korea. ³¹Department of Botany, The Field Museum, 400 South Lake Shore Drive, Chicago, IL 60605-2496, USA. ³²PO Box 58, Bandoo Post Office, Muang, Chiang Rai 57100, Thailand. ³³Department of Biology, Faculty of Science, Istanbul University, 34134 Vezneciler-Istanbul, Turkey. ³⁴CABI - Europe, Bakeham Lane, Egham, Surrey TW20 9TY, UK. ³⁵Institute of Ecology and Earth Sciences, University of Tartu, 40 Lai Street, EE-51005 Tartu, Estonia. ³⁶National Center for Agricultural Utilization Research, ARS, USDA, 1815 North University Street, Peoria, IL 61604-3999 USA. ³⁷Regional Association for Health and Animal Identification, Drève du Prophète 2, B-7000 Mons, Belgium. ³⁸Molecular Mycology Research Laboratory, Westmead Millennium Institute, Sydney Medical School - Westmead, University of Sydney Centre for Infectious Diseases and Microbiology, ICPMR, Level 3, Room 3114A, Darcy Road, Westmead Hospital, Westmead, NSW 2145, Australia. ³⁹Illinois Natural History Survey, University of Illinois, 1816 South Oak Street, Champaign, IL 61820-6970, USA. ⁴⁰Cybertruffle, 4 Esk Terrace, Whitby, North Yorkshire YO21 1PA, UK; CAB International, Bakeham Lane, Egham, Surrey, TW20 9TY, UK. ⁴¹Mashhad University of Medical Sciences, Mashhad, Iran. ⁴²6720 NW Skyline Boulevard, Portland, OR 97229-1309, USA. ⁴³All-Russian Collection of Microorganisms, G.K.Skryabin Institute of Biochemistry and Physiology of Microorganisms, Prospect Nauki 5, Pushchino, Russia 142290. ⁴⁴Department of Biology, Faculty of Science, Anadolu University, TR-26470 Eskişehir, Turkey. ⁴⁵Department of Microbiology, Uppsala Biocenter, Swedish University of Agricultural Sciences, P.O. Box 7025, SE-750 07, Uppsala, Sweden. ⁴⁶Agricultural Institute of Slovenia, Hacquetova 17, 1000 Ljubljana, Slovenia. ⁴⁷Plant Pathology Herbarium (BRIP), Ecosciences Precinct, Department of Employment, Economic Development and Innovation, 41 Boggo Road, Dutton Park, Qld 4102, Australia. ⁴⁸Japan Collection of Microorganisms, RIKEN BioResource Center, 2-1 Hirosawa, Wako, Saitama 351-0198, Japan. ⁴⁹Biology Department, Faculty of Arts and Sciences, Celal Bayar University, 45140 Muradiye /Manisa, Turkey. ⁵⁰Biodiversity and Climate Research Centre (BiK-F), Senckenberganlage 25, D-60325 Frankfurt (Main), Germany; and Institute of Ecology, Evolution and Diversity, Goethe University, Siesmayerstrasse 70, D-60323 Frankfurt (Main), Germany. ⁵¹Basic and Industrial Microbiology Section, Biology Department, Ege University, Bornova/Izmir, Turkey. ⁵²Department of Microbiology, Faculty of Science and Informatics, University of Szeged, H-6726 Szeged, Közép fasor 52, Hungary. ⁵³Laboratorio de Taxonomía y Ecología de Hongos, Instituto de Biología, Facultad de Ciencias Exactas y Naturales, Universidad de Antioquia, A.A.1226 Medellín, Colombia. ⁵⁴AG Geobotanik, Ruhr-Universität Bochum, Universitätsstraße 150, 44780 Bochum, Germany. ⁵⁵Department of Plant Biology and Pathology, Rutgers University, 59 Dudley Road, New Brunswick, NJ 08901, USA.

*The first eight authors undertook the finalization of this text, taking into account comments and suggestions from the others listed here.

BACKGROUND

The International Code of Botanical Nomenclature (ICBN) and its predecessors¹ have regulated the nomenclature of fungi since 1867. The ICBN is now revised at each six-yearly International Botanical Congress. The ICBN currently in force is that adopted at the Vienna Congress in 2005 (McNeill *et al.* 2006), and published proposals to further modify the ICBN will be voted on at the XVIIIth Congress in Melbourne in July 2011 (McNeill & Turland 2011). The ICBN includes several special provisions for aspects of the nomenclature of fungi. Amongst those provisions, that permitting the separate naming of different morphs of the same species in non-

lichenized ascomycetes (*Ascomycota*) and basidiomycetes (*Basidiomycota*), has been a cause of on-going controversy and passionate debates between mycologists, and also of nomenclatural instability – for over 80 years. Aspects of the early history of the problem are summarized by Weresub & Pirozynski (1979).

The instability in fungal names as a consequence of these provisions has arisen because of the periodic major changes

¹ *The International Rules of Nomenclature* ([1905]–1935), the *American Code of Botanical Nomenclature* (1907), and the *Lois de la Nomenclature Botanique* (1867).

in the ICBN and dissatisfied mycologists who do not follow the prescribed rules. With authors implementing the rules in different ways, the situation had become so unsatisfactory by the 1970s that a committee to investigate the matter was appointed under the auspices of the Nomenclatural Secretariat of the International Mycological Association (IMA). The resultant proposals, endorsed by the 2nd International Mycological Congress (IMC2) in Tampa (FL) in 1977 (Van Warmelo 1979) and adopted at the subsequent International Botanical Congress (IBC) in Sydney in 1981, simplified the system then in force. However, as anticipated by Hawksworth & Sutton (1974), this action led to numerous changes in names in economically important groups of fungi, some of which have never been adopted by those working with these organisms in applied fields. Many mycologists remained dissatisfied and frustrated with the changes.

As molecular data became available in the early 1990s (Ozerskaya *et al.* 2010), the need for reinterpreting Art. 59 of the ICBN, which permits the dual nomenclature of pleomorphic fungi, became apparent. At that time even the option of deleting the special provisions allowing for alternate names for fungi was floated (Reynolds & Taylor 1991, 1992). However, an international symposium convened in Newport (OR) in August 1992 to consider the matter further remained conservative and failed to reach a consensus on the substantive issues (Reynolds & Taylor 1993). The matter was revisited at a symposium during the XVIth IBC in St Louis (MO) in 1999 and a workshop at the IXth IUMS Congress of Mycology in Sydney the same year (Seifert *et al.* 2000), leading to a well-attended debate at IMC7 in Oslo in 2002 where 84 voted for a one name for one fungus system, and 121 against (Seifert 2003). As molecular data accumulation accelerated, so did the desire for change. Rossman & Samuels (2005) went so far as to propose deletion of the pertinent Article, Art. 59, a suggestion strongly opposed by Gams (2005), while Hawksworth (2005) suggested limitation and future prohibition. The 2005 Vienna IBC introduced the concept of a special kind of typification using teleomorphs and established a Special Committee to report on the matter. In the meantime the desire for change was increasing; 84 % of those voting at three different mycological meetings in Baton Rouge (USA), St Petersburg (Russia), and Léon (Spain) favoured having only one name for each fungus (Hawksworth 2007).

The results of a questionnaire circulated at IMC9 in Edinburgh in 2010, revealed 73 % favouring a progressive movement to one name for each fungus, and 58 % favouring deletion of Art. 59, provided that retroactive invalidation of existing names was avoided (Norvell *et al.* 2010). The Special Committee appointed in 2005, however, failed to reach consensus, with 21 % supporting deletion of the Article in its entirety, 16.5 % for returning to the St Louis Code of 1999, and 62.5 % for continuing work on modifications of the Article (Redhead 2010a). The Secretary of that Committee independently published proposals (primarily based on those of Hawksworth 2005), for modification to move the situation forward (Redhead 2010b), while alternative formal proposals

were made (Gams *et al.* 2010). Although ultimately the Committee for Fungi (Norvell 2011) and the Special Committee (cf. McNeill & Turland 2011) supported the complicated patches to Art. 59 (Redhead 2010b), few mycologists are expected to understand fully the intricacies of a further modified Art. 59 following decades of repeated change.

This lack of consensus leaves the issue in an unacceptable state which is urgently in need of resolution. Impatient with the current situation, different mycologists are increasingly operating as they consider most appropriate, with many ignoring the current ICBN. Indeed, contributors to one recent single multi-authored work followed *five* different practices in the various chapters (Rossman & Seifert 2011). The situation needs to be addressed now to give guidance to mycologists as how to proceed over the short term. However, while the nomenclature of fungi continues to be covered under the ICBN, if changes are not made at the upcoming XVIIIth IBC in Melbourne in July 2011, there will be no opportunity to make any formal change until the XIXth IBC in Beijing in 2017 – and possibly those would not become effective until 2019. Furthermore, even if changes are made, more could be expected in the following cycle. Increasing numbers of mycologists will continue to ignore, or personally interpret the current rules. If this matter is allowed merely to drift, uncertainty and confusion will inevitably increase and be compounded. This will be to the detriment not only of mycologists but of all users of fungal names. Recognizing the imperative for action at the 2011 Congress, the International Commission on the Taxonomy of Fungi (ICTF) encouraged the CBS-KNAW Fungal Biodiversity Centre to select the topic for a special symposium they were planning. The result was the international symposium on “One Fungus = One Name (1F = 1N)” held in the rooms of the Royal Netherlands Academy of Arts and Sciences (Koninklijke Nederlandse Akademie van Wetenschappen) on 19–20 April 2011. The symposium was attended by 90 mycologists from 23 countries.

Following presentations on the problems in naming a wide range of fungi of economic and medical importance under the current rules and after open discussion, the following Declaration was made, with only three dissenting. This Declaration is presented here also with the support of several mycologists who though unable to attend the Amsterdam meeting learned of its development from colleagues, and whose names are now included amongst the list of authors.

In addition to the Declaration, there was considerable discussion and some proposals made on aspects of fungal nomenclature other than those concerned with the naming of pleomorphic fungi. These included the governance of fungal nomenclature and the need to develop a method of recognizing fungi only known from environmental nucleic acid sequences. The key points and suggestions made on these and some additional minor matters are summarized following the Declaration. However, there were considerable differences of opinion on these two matters. We stress that they are independent from the Declaration, do not reflect the views of all of us, and present them here only as a record and to provide material to be considered in future arenas.

THE AMSTERDAM DECLARATION ON FUNGAL NOMENCLATURE

Enacted in Amsterdam, 20 April 2011

One Fungus = One Name

Recognizing the desire of mycologists to progress to a system of adopting one name for each fungal species expressed at the 9th International Mycological Congress in 2010,

noting the proposals so far made to that end, and

considering the urgent need for mycologists to have immediate guidance on this matter, as articulated following the “One Fungus = One Name” symposium held in Amsterdam, The Netherlands, on 19-20 April 2011, which was convened under the auspices of the International Committee on the Taxonomy of Fungi (ICTF), we, authors of this paper

recommend the following steps for the orderly transition towards a single-name nomenclatural system for all fungi.

1. **Follow**, except when it is contrary to the items listed below, the rules of the International Code of Botanical Nomenclature (ICBN) until such time as mycological nomenclature is governed by a unified *BioCode*, or by a code specifically implemented for fungi.

2. **Remember** that following the ICBN (2006): (a) legitimately and validly published names of monomorphic fungi, whether anamorphic or teleomorphic, can be transferred to any other validly published legitimate generic name and remain nomenclaturally legitimate (if not contrary to other provisions); and (b) that it is possible under the ICBN to epitypify (teleotypify) names with an anamorphic type by material exhibiting the teleomorph.

² See Hawksworth *et al.* (2010) for further information on the proposals to be voted on at the IBC in Melbourne in July 2011.

³ See Redhead (2010b) for the detailed proposal made.

3. **Refrain** from proposing new names for newly discovered morphs of validly published and legitimately named species, and where necessary refer to the newly discovered morphs by an informal cross reference name in lower case Roman type, e.g. *Niesslia exilis* (monocillium-morph), *Aspergillus fumigatus* (neosartorya-morph).

4. **Follow** the Principle of Priority of publication of the ICBN when selecting the generic name to adopt. This means that authors should choose the oldest generic name, irrespective of whether it is typified by a species name with a teleomorphic or an anamorphic type, except where the younger generic name is far better known (in cases of doubt the appropriately mandated body should be consulted).

5. **Follow** the author(s), or working groups of mycologists, who first choose the generic name to be adopted. Authors should consider it mandatory to register the choice in a recognized repository, as proposed for scientific names of fungi (e.g. *Index Fungorum*, *MycBank*)², and then be followed. However, in cases where the first selection appears not to be in the interests of most users of fungal names, a case to overturn the choice may be submitted to the appropriately mandated international body.

6. **Encourage** individuals, or working groups of mycologists, to prepare lists of names to be preferentially used for any groups of fungi to be published (e.g. in *Mycotaxon*, *IMA Fungus*, or monographs), for endorsement by the ICTF or one of its Subcommissions.

In addition we **encourage** the enactment of appropriate changes in the ICBN, or any future code governing the nomenclature of fungi, to accommodate these practices. We also **endorse** the proposal already made to declare simultaneously published anamorph-typified and teleomorph-typified names for a species illegitimate after 1 January 2013³.

Note: The meeting felt that the ICTF, and its Subcommissions where established, was probably the most “appropriately mandated body” for this task. It could then report its decisions to the Committee for Fungi for formal adoption under the ICBN.

The views expressed in the above Declaration were subsequently endorsed by majority votes of the International Mycological Association (Executive Committee), International Commission on the Taxonomy of Fungi, Nomenclature Committee for Fungi, International Society for Fungal Conservation (Council), European Mycological Association (Council), and the African Mycological Association. This endorsement relates only to the Declaration enclosed in this box.

THE GOVERNANCE OF FUNGAL NOMENCLATURE

Although not formally on the agenda for the Amsterdam symposium, the participants were also strongly in favour of increased autonomy for the governance of fungal nomenclature. IMC9 approved the proposals already made (Hawksworth *et al.* 2009) to continue the current practice of dealing with the nomenclature of fungi within the ICBN, but with the transfer of decision-making on matters solely related to fungi from International Botanical Congresses to International Mycological Congresses (Norvell *et al.* 2010).

Subsequent to IMC9, a new version of the *BioCode* was released, the *Draft BioCode* (2011) (Greuter *et al.* 2011), which it is envisaged will eventually oversee the naming of organisms of all kinds. There was strong support at the symposium for the view that the *BioCode* model provided a satisfactory framework for the future governance of fungal nomenclature, and that mycologists should contribute to its development. Also, if the finalization and implementation of the *BioCode* became protracted, and the idea of a *MycoCode* independent from the ICBN came to be supported by mycologists as a whole, that could be based on the new *BioCode* model.

In order to suit the needs of mycologists, a *MycoCode* would need to define the scope of organisms considered to be *Fungi* and other organisms studied by mycologists. The participants recommended that the appropriately mandated body propose amendments to the *Draft BioCode* (2011) to accommodate the needs of mycologists in relation to: (1) the naming of pleomorphic fungi (as proposed in the Declaration above); (2) the operation of electronic repositories of key nomenclatural information (e.g. *Index Fungorum*, *MycoBank*); and (3) the naming of environmental sequences or taxa distinguished only by nucleic acid sequences. In the event that the *BioCode* does not progress towards implementation by the end of 2012 or fails to accommodate the requirements of mycologists, and especially if the International Botanical Congress does not agree to the changes supported at IMC9, the meeting further recommended that mycologists consider developing a *MycoCode* based on the *Draft BioCode* (2011) for approval by the IMA through an e-mail ballot of its members.

Drafts for two possible paragraphs for the *Draft BioCode* (2011), or for a possible future *MycoCode* were, however, agreed:

(1) To define fungi

Fungi are defined to include the monophyletic kingdom *Fungi* and other groups of organisms traditionally studied by mycologists, including *Dictyosteliomycota*, *Myxogasteromycota*, *Protosteliomycota*, *Acrasiomycota*, *Labyrinthulomycota*, *Oomycota*, and *Plasmodiophoromycota*. *Microsporidia* under the *BioCode* would maintain names that were assigned under the International Code of Zoological Nomenclature (ICZN).

(2) To revise Article 31 Notes

Note 1. Fungi that bear more than one name due to their pleomorphy shall be known by one name. In selecting the name to represent fungi that bear more than one name, attention should be given to priority, regardless of the morph named, except where a name other than the oldest one is far more widely recognized.

Note 2. Where a pleomorphic fungus bears just one name, proposals to provide new names for other morphs are prohibited.

Note 3. It is emphasized that, as in the ICBN (2006) and the *Draft BioCode* (2011): (a) legitimately and validly published names of monomorphic fungi, whether anamorph-typified or teleomorph-typified, can be transferred to any other legitimately and validly published generic name and remain nomenclaturally legitimate and valid; that (b) it is possible under the *BioCode* to epitypify (teleomorphic) names with an anamorphic type by material exhibiting the teleomorph; and that (c) if, in the opinion of mycologists, a poor choice is made for the name to represent a pleomorphic fungus previously bearing more than one name, the option remains to submit a case to overturn the choice to the appropriately mandated international body.

ENVIRONMENTAL SEQUENCE DATA

The need to provide an internationally agreed method of referring to fungi only known from environmental nucleic acid sequences, and not from preserved specimens or cultures was repeatedly mentioned during the symposium. However, while there was no consensus at the symposium as to how best this task should be done, it was felt that consideration should be given to the naming of fungi known from environmental nucleic acid sequences in the revision of the *Draft BioCode* (2011) or an eventual *MycoCode*. Possible criteria, previously advanced by Hibbett *et al.* (2011), were commended by John Taylor to provide for the naming of a fungus known only through the sequencing of nucleic acids from environmental samples, commonly known as a Molecular Operational Taxonomic Unit (MOTU). These were modified in subsequent exchanges and the following have been suggested as minimum criteria required for naming a fungus known only from nucleic acid sequence:

(1) The genetic marker used must be or include the barcode standard designated for *Fungi*.

(2) Representation by at least two full-length sequences of the genomic regions, each of which is derived from independent studies, with one sequence designated as the reference sequence; the use of genomic regions in addition to the barcode standard is encouraged.

(3) A published phylogenetic analysis demonstrating monophyly, and considering all relevant, publicly available sequences retrieved using BLAST or a similar method.

(4) The application of chimera checking software and other

quality-control measures.

(5) Provision of locality data (including GPS co-ordinates) and ecological/substrate/host data, at least for the reference sequence.

(6) Registration in a recognized public-access online data repository (e.g. *Mycobank*).

In the event that a name based only on a nucleic acid sequence subsequently proves to belong to the same taxon as a species previously described from a specimen (or culture) that had not then been sequenced, priority would be given to the first-published name.

Some participants felt that if scientific names were to be based only on sequence data, these should be “flagged” in some way. This could be done, for example, by the use of the prefix “*Candidatus*” as had become the practice in bacteriology (Murray & Stackebrandt 1995, Jezbera *et al.* 2009). However, as the prefix could be confused with a generic name, use as a suffix could be a better option. The idea of adding “ENAS” (environmental nucleic acid sequence) after the name was another option suggested. One possible example of how the format for the introduction of such an entity might appear, based on the model of Hibbett *et al.* (2011) is appended (Annex A).

It was also questioned whether just a single ITS (Internal Transcribed Spacer) sequence, even if found twice, should be sufficient for the recognition of an MOTU, and noted that confusion could arise from the occurrence of non-orthologous copies of nuclear rDNA ITS sequences in the same fungus. Mention was also made of the prospect of obtaining single cell genomes rather than metagenomes from environmental samples in the near future, and it was suggested that any provisions should also permit a genome to serve as a nomenclatural “type”. It was further suggested that (1) and (2) be extended to apply also to new species described from specimens or cultures where that was technically feasible. Clearly, all of these matters need to be explored further before requirements become formalized.

OTHER MATTERS

An implicit assumption made throughout the discussions at the symposium was that the forthcoming IBC in Melbourne will accept the proposals (Hawksworth *et al.* 2010) to make the deposit of key nomenclatural information in a recognized repository (e.g. *Index Fungorum*, *Mycobank*) a mandatory requirement for the valid publication of fungal names. Those proposals were overwhelmingly supported at the Nomenclature Sessions convened during IMC9 (Norvell *et al.* 2010).

Also raised at the symposium was the issue of using author citations after scientific names. There was a consensus that, in accordance with Article 46.1 of the ICBN, which was revised at the St Louis IBC in 1999, their use should be limited to formal taxonomic and nomenclatural works. This information is now freely available online through the *Mycobank* and *Index Fungorum* databases should it be required. Where it

was pertinent to cite the originators of a scientific name, it was considered better to refer to the original publication and include the full bibliographic citation in lists of references. Adoption of that practice would acknowledge more equitably the important research performed by fungal systematists.

ACTION POINTS

In order to effect the desired changes in the ICBN necessary to implement the Declaration on “One fungus = One name” presented above, formal proposals need to be prepared by the ICTF and proposed from the floor to the meeting of the Nomenclature Section of the XVIIIth IBC in Melbourne in July 2011 so as to: (a) delete the current provisions of Art. 59 in the ICBN; (b) extend the principle of following the first reviser (as already used in lecto-, neo-, and epitypifications) to the choice of names when anamorph-typified and teleomorph-typified generic or specific names are united; and (c) introduce other changes to avoid previously proposed teleomorph-typified or anamorph-typified names being automatically ruled as invalid or illegitimate. In order to advise mycologists as to the most appropriate names to use where the situation is unclear, or to rule on controversial choices that have been made, mechanisms and procedures will need to be developed by the ICTF in consultation with the Committee for Fungi.

With respect to the governance of the nomenclature of fungi, the ICTF will need to consider: (a) what modifications of the *Draft BioCode* (2011) should be proposed to ensure that it will meet the future needs of mycologists; (b) the implications of the results of the voting at the ICB in Melbourne on the proposals to change the name and governance of the ICBN with respect to fungi (Hawksworth *et al.* 2009), which have already been endorsed by IMC9 (Norvell *et al.* 2010); and (c) initiating work towards a separate *Mycocode*, should it become necessary, outside of, or preferably within, the *BioCode* framework.

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ANNEX A

An example of a possible format for a description of a new fungal species known only from molecular sequence data (adapted from Hibbett *et al.* 2011) discussed at the Symposium

Inocybe narae Hibbett & P.M. Kirk, **sp. nov.**¹

Mycobank no.: MBXXXXXX

Etymology: The epithet honours Kazuhide Nara, who obtained the reference sequence.

Diagnosis: The least inclusive group containing organisms with nuclear rDNA ITS sequences with GenBank accessions AB244041 and DQ054545.

Reference phylogeny: M Ryberg *et al.* (*BMC Evolutionary Biology* **8**: 50, 2008; additional file 1, fig. A).

*Nucleic acid type and reference sequence*²: GenBank AB244041 (K Nara, *New Phytologist* **171**: 187–198, 2006).

Other included sequences: GenBank DQ054545 (Wilson *et al.* 2008). Sequence similarity: 99.09 % (ITS1), 98.92 % (ITS2).

*Nomenclatural sample*³: Soil sample and *Larix kaempferi* root tips, collected by Nara in October, 2010, preserved in the Kew fungarium K(M) nnnnnn.

Quality control: Chimera checker (Nilsson *et al.* 2009b) results negative for both included sequences. Boundaries of 18S, 25S, and 5.8S rRNA coding regions identified with ITS extractor (Nilsson *et al.* 2010). The sequence contains no DNA ambiguity symbols.

Reference sequence locality: Japan: Shizuoka, Gotenba, Mt Fuji, alt. 1450–1600 m asl⁴.

Synonyms: *Inocybe* sp. 2 (Ryberg *et al.* 2008); *Inocybe* sp. 3 (Nara 2006).

Phylogenetic notes: Strongly supported as monophyletic (parsimony bootstrap 1/4 100 %). Environmental sequence AY702727 was placed as the sister group (parsimony bootstrap 1/4 95 %).

Ecological notes: The reference sequence was obtained from an ectomycorrhizal root tip of *Larix kaempferi* in the “volcanic desert” of Mt Fuji, Japan. Nara considered this to be a later-stage species in succession. The other included sequence was obtained from soil⁵ at ca 50 cm depth under beech and chestnut at ca 1000 m asl on the extinct volcano, Monte Amiata, Tuscany, Italy. The closely related undescribed sequence AY702727 was obtained from ectomycorrhizal root tips of *Abies* sp. at 2600 m asl in the Sierra National Forest, California, USA (Izzo *et al.* 2005).

¹ Some of those present at the symposium favoured the association of the term “*Candidatus*” as a suffix to the species name, or the use of the suffix “ENAS” (environmental nucleic acid sequence); “*nara*” is changed to “*narae*” in accordance with Latin usage.

² The phrase, “Nucleic acid type” is placed before the term “Reference sequence” to make it clear that the sequence itself serves as the nomenclatural type.

³ The phrase “Nomenclatural type” is changed to “Nomenclatural sample” to distinguish it from the nucleic acid type and to broaden the definition of the sample to include an environmental sample, e.g. soil or plant material, as well as nucleic acid extracted from or amplified from an environmental sample.

⁴ GPS latitude and longitude co-ordinates, or national grid references where available, should ideally also be added.

⁵ The type of “soil” should be specified, using the terminology adopted in published surveys of soil types in the region where they are available.