Reply to Kidd et al., "Inconsistencies within the proposed framework for stabilizing fungal nomenclature risk further confusion"

Sybren de Hoog, Thomas J Walsh, Sarah A Ahmed, Ana Alastruey-Izquierdo, Barbara D Alexander, Maiken Cavling Arendrup, Esther Babady, Feng-Yan Bai, Joan-Miquel Balada-Llasat, Andrew Borman, et al.

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Reply

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Sybren de Hoog,[1,2,3,4,5,6] Thomas J. Walsh,[6,7,8,9,10,11,12,13,14,15] Sarah A. Ahmed,[1,2,6] Ana Alastruey-Izquierdo,[6,16,17] Barbara D. Alexander,[10,14,18] Maiken Cavling Arendrup,[19,20,21] Esther Babady,[10,22] Feng-Yan Bai,[23,24,25,26,27,28] Joan-Miquel Balada-Llasat,[10,29] Andrew Borman,[30] Anuradha Chowdhary,[17,31] Andrew Clark,[10,32] Robert C. Colgrove,[33,34] Oliver A. Cornely,[12,17,35,36] Tanis C. Dingle,[10,13,37] Philippe J. Dufresne,[10,13,38] Jeff Fuller,[10,39] Jean-Pierre Gangneux,[12,40] Connie Gibas,[41] Heather Glasgow,[10,13,42] Yvonne Graser,[43] Jacques Guillot,[27,44] Andreas H. Groll,[17,45] Gerhard Haase,[46] Kimberly Hanson,[10,47] Amanda Harrington,[10,48] David L. Hawksworth,[49,50,51,52,53,54] Randall T. Hayden,[10,13,42] Martin Hoenigl,[11,12,55,56,57] Vit Hubka,[58] Kristie Johnson,[10,59] Julianne V. Kus,[10,60,61] Ruoyu Li,[3,5,15,17,21,25] Jacques F. Meis,[1,15,35,36] Michaela Lackner,[6,62] Fanny Lanternier,[63] Sixto M. Leal Jr.,[10,11,13,64] Francesca Lee,[10,32] Shawn R. Lockhart,[1,10,57,65] Paul Luethy,[10,59] Isabella Martin,[10,66] Kyung J. Kwon-Chung,[67] Wieland Meyer,[9,68] M. Hong Nguyen,[10,11,14,69] Luis Ostrosky-Zeichner,[11,70] Elizabeth Palavecino,[10,71] Preeti Pancholi,[10,29] Peter G. Pappas,[10,11,64] Gary W. Procop,[10,13,72,73] Scott A. Redhead,[9,74] Daniel D. Rhoads,[75,76,77] Stefan Riedel,[10,78] Bryan Stevens,[10,69] Kaede Ota Sullivan,[10,79] Paschalis Vergidis,[10,80] Emmanuel Roilides,[6,12,17,81] Amir Seyedmousavi,[10,17,27,82] Lili Tao,[10,83] Vania A. Vicente,[4] Roxana G. Vitale,[84,85] Qi-Ming Wang,[86] Nancy L. Wengenack,[10,80] Lars Westblade,[10,87] Nathan Wiederhold,[10,11,13,14,41] Lewis White,[88] Christina M. Wojewoda,[89] Sean X. Zhang[6,10,90]

AUTHOR AFFILIATIONS See affiliation list on p. 2.

We would like to thank Kidd et al. for their thoughtful comments on our manuscript about a proposed global consensus guideline for fungal name changes published in the *Journal of Clinical Microbiology* (1). We would also like to take this opportunity to further explain our position and clarify the intent of this work. The proposed International Nomenclature Committee for Clinical Fungi neither wishes to impede name changes, nor prescribe or arbitrate nomenclatural questions.

Our main goal is to achieve broad acceptance of changes that are beneficial to science and patient care. We strongly believe that the best means to achieve this important objective is to consider the clinical utility of nomenclature, provide an understanding of the reasons for the change, and how it could improve clinical management. In particular, the needs of clinical laboratories, which are important stakeholders dealing with the consequences of fungal name changes on a daily basis, have been largely neglected to date. Early and collaborative involvement of all stakeholders leads to faster acceptance, while sudden and unexplained name changes, even when necessary, lead to reluctance and clinical risk. We acknowledge different viewpoints toward fungal nomenclature and taxonomy. This underlines the proposal to form an open, international nomenclatural Working Group/Committee for clinical fungi which will provide the clinical user with the rationale for name changes and their relevance to patient care.

The nomenclatural database is made with the same intention. Existing databases such as MycoBank, Species Fungorum, and Index Fungorum cover the entire fungal Kingdom and follow the latest taxonomic literature. The clinical database was founded to bring taxonomy closer to clinical needs, which may occasionally deviate from existing databases. An illustrative example is *Trichophyton indotineae* (1). From a strictly phylogenetic perspective, this is a member of the *Trichophyton mentagrophytes* complex. Complexes, as used in clinical routine practice, are composed of sibling lineages with identical biology, having epidemiological rather than clinical significance. *Trichophyton indotineae*, although just a few barcode SNPs remote from other *Trichophyton*

Editor Alexander J. McAdam, Boston Children's Hospital, Boston, Massachusetts, USA

Address correspondence to Sean X. Zhang, szhang28@jhmi.edu, Thomas J. Walsh, thomaswalshmd@gmail.com, or Sybren de Hoog, Sybren.deHoog@radboudumc.nl.

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mentagrophytes lineages, is clinically different from other members of the complex due to its high virulence and a high degree of antifungal resistance, and is phenotypically often urease negative. It is therefore recommended to be identified as an individual species. This certainly is a dilemma, and the decision of Tang et al to retain T. *indotineae* as a haplotype of the *T. mentagrophytes* complex (2) may be debatable; we are open to anyone's opinion.

We respectfully disagree with the statement from Kidd et al. that includes "the recommended option to continue using prior (now obsolete) *Candida* names appears inconsistent with the statement that the '[Candida] genus in the traditional sense is untenable.'" These new names, which may be valid, do not make old names obsolete, particularly within a clinical context where antifungal susceptibility testing and treatment guidelines maintain the continuity of patient care. Another misunderstanding concerns the "recommending two names is against established One Fungus One Name rule." The "one fungus one name" concept addresses the unification of the anamorph and teleomorph phase of a fungus. Our proposal of reporting both old and new names (irrespective of life phase) will simply enable the smooth transition and connection of knowledge affiliated with the old and new names. Furthermore, the statement "given that some of the article's authors (and us) are affiliated with the International Mycological Association Nomenclature Committee for Fungi" is not accurate. The Nomenclature Committee for Fungi is not part of the International Mycology Association (IMA).

Our proposed global consensus guideline for fungal name changes is endorsed by 11 professional societies that are involved in medical mycology, laboratory diagnosis, and fungal diseases. The endorsement was achieved through a rigorous review process by representatives from each society. The upcoming International Nomenclature Committee for Clinical Fungi (https://www.isham.org/working-groups/nomenclature-clinical-fungi) includes taxonomists, medical mycologists, clinical microbiologists, infectious disease physicians, pharmacists, pathologists, and veterinary mycologists, representing 18 professional societies as well as industry partners who provide fungal databases for identification through their commercial platforms. Therefore, this committee is thus far the most internationally inclusive committee representing global efforts to address name changes of clinical fungi. In fact, we note that several lead authors from the letter from Kidd et al. are already members of this committee, and thus we anticipate that the different viewpoints on fungal nomenclature and taxonomy will be robustly discussed within the committee. Moreover, the development of evidence-based multifactorial criteria to guide the discussion and determination of fungal name changes for clinical usage is in process and will be reviewed and commented on by all committee members.

In summary, we hope that different disciplines involved in medical mycology will come together in an atmosphere of open discussion. We remain aware that any recommendation made by the committee will continue to evolve as new data or viewpoints become available.

AUTHOR AFFILIATIONS

[1]Radboudumc-CWZ Centre of Expertise for Mycology, Nijmegen, the Netherlands
[2]Foundation Atlas of Clinical Fungi, Hilversum, the Netherlands
[3]Department of Dermatology and Venereology, Peking University First Hospital, Beijing, China
[4]Department of Basic Pathology, Federal University of Paraná, Curitiba, Brazil
[5]Research Center for Medical Mycology, Peking University, Beijing, China
[6]International Society for Human and Animal Mycology (ISHAM), Working Group Nomenclature, 's-Hertogenbosch, the Netherlands
[7]Center for Innovative Therapeutics and Diagnostics, Richmond, Virginia, USA
[8]University of Maryland School of Medicine, Baltimore, Maryland, USA
[9]Nomenclature Committee for Fungi, International Mycological Association (IMA), Exeter, United Kingdom
[10]Fungal Diagnostics Laboratory Consortium (FDLC), Baltimore, Maryland, USA

[11]Mycoses Study Group, Education and Research Consortium (MSG-ERC), Pittsburgh, Pennsylvania, USA
[12]European Confederation of Medical Mycology (ECMM), 's-Hertogenbosch, the Netherlands
[13]Clinical and Laboratory Standards Institute (CLSI), Pittsburgh, Pennsylvania, USA
[14]Medical Mycological Society of the Americas (MMSA)
[15]ISHAM Working Group on Diagnostics, Basel, Switzerland
[16]Mycology Reference Laboratory, Spanish National Centre for Microbiology, Madrid, Spain
[17]Fungal Infection Study Group, European Society of Clinical Microbiology and Infectious Diseases (EFISG/ESCMID), Basel, Switzerland
[18]Departments of Medicine and Pathology, Duke University, Durham, North Carolina, USA
[19]Department of Microbiology and Infection Control, Statens Serum Institut, Copenhagen, Denmark
[20]Department of Clinical Microbiology, Copenhagen University Hospital Rigshospitalet, Copenhagen, Denmark
[21]Antifungal Susceptibility Testing Subcommittee of European Committee of Antimicrobial Susceptibility Testing (EUCAST-AFST)
[22]Department of Pathology and Laboratory Medicine, Clinical Microbiology Service, Memorial Sloan Kettering Cancer Center, New York, New York, USA
[23]Mycology Committee of Chinese Society for Microbiology, Beijing, China
[24]Institute of Microbiology, State Key Laboratory of Mycology, Chinese Academy of Sciences, Beijing, China
[25]Medical Mycology Society of Chinese Medicine and Education Association
[26]Asia PacificSociety for Medical Mycology
[27]ISHAM Working Group Veterinary Mycology and One Health, 's-Hertogenbosch, the Netherlands
[28]Mycological Society of China (MSC)
[29]Clinical Microbiology at The Ohio State University Wexner Medical Center, Columbus, Ohio, USA
[30]National Mycology Reference Laboratory, Public Health England, Bristol, United Kingdom
[31]Department of Microbiology, National Reference Laboratory for Antimicrobial Resistance in Fungal Pathogens, Medical Mycology Unit, Vallabhbhai Patel Chest Institute, University of Delhi, Delhi, India
[32]University of Texas Southwestern Medical Center, Dallas, Texas, USA
[33]Division of Infectious Diseases, Mount Auburn Hospital, Cambridge, Massachusetts, USA
[34]Infectious Diseases Society of America (ISDA), Arlington, Virginia, USA
[35]University of Cologne, Faculty of Medicine, Institute of Translational Research, Cologne Excellence Cluster on Cellular Stress Responses in Aging-Associated Diseases, Cologne, Germany
[36]Department I of Internal Medicine, University of Cologne, Excellence Center for Medical Mycology, Cologne, Germany
[37]Alberta Precision Laboratories, Public Health Laboratory, Calgary, Alberta, Canada
[38]Department of Mycology, Laboratoire de Santé Publique du Québec, Institut National de Santé Publique du Québec (INSPQ), Sainte-Anne-de-Bellevue, Québec, Canada
[39]Department of Pathology and Laboratory Medicine, London Health Sciences Center, London, Ontario, Canada
[40]Department of Mycology, Centre Hospitalier Universitaire de Rennes, Rennes, France
[41]University of Texas Health Science Center, San Antonio, Texas, USA
[42]Department of Pathology, Clinical and Molecular Microbiology, St. Jude Children's Research Hospital, Memphis, Tennessee, USA
[43]Department of Parasitology (Charité), Institute of Microbiology and Hygiene, Humboldt University, Berlin, Germany

[44]Onoris, École Nationale Vétérinaire, Agroalimentaire et de l'Alimentation Nantes-Atlantique, Nantes, France
[45]Department of Pediatric Hematology and Oncology, Infectious Disease Research Program, Center for Bone Marrow Transplantation, University Children's Hospital, Münster, Germany
[46]Laboratory Diagnostic Center, RWTH Aachen University Hospital, Aachen, Germany
[47]University of Utah School of Medicine, Salt Lake City, Utah, USA
[48]Loyola University Health System, Loyola University Chicago, Maywood, Illinois, USA
[49]Royal Botanic Gardens, Kew, Richmond, Surrey, United Kingdom
[50]Natural History Museum, London, United Kingdom
[51]University of Southampton, Southampton, United Kingdom
[52]Jilin Agricultural University, Chanchung, China
[53]General Committee for Nomenclature, International Botanical Congress (IBC)
[54]Advisory Board of International Commission on the Taxonomy of Fungi (ICTF)
[55]Division of Infectious Diseases, Medical University of Graz, Graz, Austria
[56]Translational Medical Mycology Research Unit, ECMM Excellence Center for Medical Mycology, Medical University of Graz, Graz, Austria
[57]European Hematology Association, Specialized Working Group for Infections in Hematology, The Hague, the Netherlands
[58]Department of Botany, Charles University, Prague, Czechia
[59]Clinical Microbiology Laboratory, UMMC Laboratories of Pathology, University of Maryland School of Medicine, Baltimore, Maryland, USA
[60]Public Health Ontario, Toronto, Ontario, Canada
[61]Department of Laboratory Medicine and Pathobiology, Canada and University of Toronto, Toronto, Ontario, Canada
[62]Institute of Hygiene and Medical Microbiology, Medical University of Innsbruck, Innsbruck, Austria
[63]Institut Pasteur, Paris, France
[64]University of Alabama at Birmingham, Birmingham, Alabama, USA
[65]Centers for Disease Control and Prevention, Atlanta, Georgia, USA
[66]Dartmouth Health, Lebanon, New Hampshire, USA
[67]National Institute of Allergy and Infectious Diseases, National Institutes of Health, Bethesda, Maryland, USA
[68]Westerdijk Fungal Biodiversity Institute, Utrecht, the Netherlands
[69]University of Pittsburgh Medical Center, Pittsburgh, Pennsylvania, USA
[70]University of Texas Health Science Center at Houston, Houston, Texas, USA
[71]Clinical Microbiology Laboratory, Wake Forest Baptist Medical Center, Winston-Salem, North Carolina, USA
[72]The American Board of Pathology, Tampa, Florida, USA
[73]American Board of Pathology (ABP), Chicago, Illinois, USA
[74]National Mycological Herbarium, Ottawa Research and Development Centre, Science and Technology Branch, Agriculture & Agri-Food Canada, Ottawa, Ontario, Canada
[75]Cleveland Clinic Lerner College of Medicine, Case Western Reserve University, Cleveland, Ohio, USA
[76]Department of Laboratory Medicine, Cleveland Clinic, Cleveland, Ohio, USA
[77]Infection Biology Program, Lerner Research Institute, Cleveland Clinic, Cleveland, Ohio, USA
[78]Beth Israel Deaconess Medical Center, Boston, Massachusetts, USA
[79]Lewis Katz School of Medicine, Temple University, Philadelphia, Pennsylvania, USA
[80]Mayo Clinic, Rochester, Minnesota, USA
[81]Hippokration Hospital, Thessaloniki, Greece
[82]Department of Laboratory Medicine, Microbiology Service, Clinical Center, National Institutes of Health, Bethesda, Maryland, USA
[83]Vanderbilt University Medical Center, Nashville, Tennessee, USA

[84]Consejo Nacional de Investigaciones Científicasy Tecnológicas (CONICET), Buenos Aires, Argentina
[85]Unidad de Parasitología, Sector Micología, Hospital J.M. Ramos Mejía, Buenos Aires, Argentina
[86]Engineering Laboratory of Microbial Breeding and Preservation of Hebei Province, School of Life Sciences, Institute of Life Sciences and Green Development, Hebei University, Baoding, China
[87]Department of Pathology and Laboratory Medicine, Weill Cornell Medical College, New York, New York, USA
[88]Public Health Wales Microbiology, Cardiff, United Kingdom
[89]Department of Pathology and Laboratory Medicine, University of Vermont Medical Center, Burlington, Vermont, USA
[90]Johns Hopkins University School of Medicine, Baltimore, Maryland, USA

AUTHOR ORCIDs

Sybren de Hoog http://orcid.org/0000-0002-5344-257X
Thomas J. Walsh http://orcid.org/0000-0002-4142-8711
Ana Alastruey-Izquierdo http://orcid.org/0000-0001-8651-4405
Maiken Cavling Arendrup http://orcid.org/0000-0002-4747-0144
Esther Babady http://orcid.org/0000-0003-4399-1249
Andrew Borman http://orcid.org/0000-0003-0585-5721
Andreas H. Groll http://orcid.org/0000-0003-1188-393X
Kimberly Hanson http://orcid.org/0000-0001-9790-277X
Randall T. Hayden http://orcid.org/0000-0002-3073-4115
Martin Hoenigl http://orcid.org/0000-0002-1653-2824
Julianne V. Kus http://orcid.org/0000-0001-6033-7244
Jacques F. Meis http://orcid.org/0000-0003-3253-6080
Sixto M. Leal Jr. http://orcid.org/0000-0001-6939-9572
Shawn R. Lockhart http://orcid.org/0000-0002-4383-5994
Kyung J. Kwon-Chung http://orcid.org/0000-0001-6671-0994
M. Hong Nguyen http://orcid.org/0000-0003-2065-3239
Elizabeth Palavecino http://orcid.org/0000-0002-4525-6064
Preeti Pancholi http://orcid.org/0000-0001-9053-0264
Daniel D. Rhoads http://orcid.org/0000-0002-7636-5191
Stefan Riedel http://orcid.org/0000-0002-0573-4957
Paschalis Vergidis http://orcid.org/0000-0002-6581-3956
Emmanuel Roilides http://orcid.org/0000-0002-0202-364X
Nancy L. Wengenack http://orcid.org/0000-0003-2853-8219
Nathan Wiederhold http://orcid.org/0000-0002-2225-5122
Lewis White http://orcid.org/0000-0003-3056-4205
Christina M. Wojewoda http://orcid.org/0000-0002-7761-4612
Sean X. Zhang http://orcid.org/0000-0003-1166-2563

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