

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

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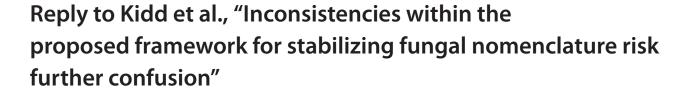
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Reply



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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* 

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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-clinicalfungi) 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.

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