New names for fungi of medical importance: can we have our cake and eat it too?

Re: Borman AM, Johnson EM. Name changes for fungi of medical importance, 2018-2019. *Journal of Clinical Microbiology* Oct 2020, JCM.01811-20 **DOI:** 10.1128/JCM.01811-20

Sarah E. Kidd[1,6], Catriona L. Halliday[2], Brendan McMullan,[3,4] Sharon C-A. Chen,[2] Juliet Elvy[5,6]

[1] National Mycology Reference Centre, Microbiology & Infectious Diseases, SA Pathology, Adelaide, South Australia, Australia.

[2] Clinical Mycology Reference Laboratory, Centre for Infectious Diseases and Microbiology Laboratory Services, ICPMR, NSW Health Pathology, Westmead Hospital, The University of Sydney, Westmead, New South Wales, Australia.

[3] Department of Immunology and Infectious Diseases, Sydney Children's Hospital, Randwick, New South Wales, Australia

[4] School of Women's and Children's Health, University of New South Wales, Kensington, New South Wales, Australia

[5] Department of Microbiology, Wellington Southern Community Laboratories, Wellington Regional Hospital, Newtown, Wellington, New Zealand

[6] Royal College of Pathologists of Australasia Quality Assurance Programs (RCPAQAP), Microbiology Section, St. Leonards, Sydney, New South Wales, Australia

Corresponding author: Dr Sarah E. Kidd

National Mycology Reference Centre, Microbiology and Infectious Diseases, SA Pathology, PO Box 14, Rundle Mall, Adelaide, SA, 5000, Australia.

Phone: +61 8 8222 3544

Fax: +61 8 8222 3543

Email: sarah.kidd@sa.gov.au

The recently published update of fungal nomenclature[1] generated heated debate on social media with predictions of patient harm and disruption of mycological literature, one example being the following Tweets from the Twitter exchange at [https://twitter.com/ABsteward/status/1313985253405536264] (accession date, 23 October 2020).

> LeonardH (@OSheaLaos): "Why the change? Do they no longer belong to the Candida family?" (8 October 2020, 10:20 a.m.)
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> S. Kidd (@thefunguskidd): '"Candida" is an artificial construct for white yeasts - It has no taxonomic value. The 'new' names represent the phylogenetic basis for these genera/species.' (8 October 2020, 8:50 p.m.)
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> B. Spellberg (@BradSpellberg): "I'm sure the families of patients who are harmed due to wrong treatment being given caused by name change will take comfort in the knowledge that their loved one's sacrifice helped advance taxonomic science." (9 October 2020, 9:37 p.m.)"

Nomenclature changes are not new and have been increasing in mycology, for reasons well explained by the authors. For example, re-assignment of various species out of the 'genus' *Candida* is apt because '*Candida*' is an artificial grouping of white budding yeasts with little reflection of the evolution of species which were placed within this genus.

Arguments that taxonomic changes have clinical repercussions, however valid, can be mitigated. As the authors state, laboratories can support the transition by including in the report the more familiar species name, e.g. "*Pichia kudriavzevii* (formerly referred to as *Candida krusei*)". If repeated consistently, over time the new genera/species names will

become associated with the clinical knowledge attributed to the previous names. Not many clinicians today will recall that *Cryptococcus neoformans* was previously *Torula histolytica*, among other names, with similar resistance encountered to the change. There are also potential clinical benefits which should not be overlooked; renaming *Candida krusei* (*Pichia kudriavzeveii*), and *Candida glabrata* (*Nakaseomyces glabrata*), for example, emphasises fluconazole non-susceptibility in keeping with traits of genera *Pichia* and *Nakaseomyces,* but in contrast to other *Candida* species.

Current nomenclature changes include those of common pathogenic fungi and to achieve change safely, communication between the clinical microbiology laboratory and clinicians is key, but such practice is already a requirement. Additionally, commercial fungal identification databases are slow in update implementation and education of laboratory staff on detecting and reporting identifications with obsolete nomenclature is essential. We note however, that the recently updated Clinical Laboratory Standards Institute documents M27-Ed4, M59-Ed3 and M60-Ed2 continue to refer to *Candida* species by their previous names;[2-4] this requires urgent discussion.

Concerns about disruptions to mycology literature are likely overstated. NCBI databases for journal articles and molecular data are underpinned by a standardised taxonomy database, which ensures that searches for a particular organism retrieves all relevant material, regardless of the species name they were originally submitted under.[5]

The Royal College of Pathologists of Australasia Quality Assurance Programs (RCPAQAP) Mycology external quality assurance (EQA) module has taken a progressive approach to fungal nomenclature changes with the goal of promoting consistent reporting among Australasian laboratories. A list of clinically important fungal species is updated and

distributed annually, indicating nomenclature changes with explanation where appropriate. Commentary is provided in survey reports and superseded taxonomy is removed from the dropdown list of species for EQA result submission. To further reinforce nomenclature changes within clinical laboratories, since 2018 EQA participants reporting species names that have been communicated as obsolete for >1 year are scored with a minor discordance. Initially, 43% of participants were penalized for reporting an obsolete species, but this reduced to <1% over only two years.

In conclusion, we acknowledge that fungal nomenclature change will take time to embed but support the advice of Borman and Johnson,[1] that with clear guidance to support clinicians and laboratories we can move forward with taxonomic progress whilst minimising risk to patients.

References

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5. Federhen S. 2012. The NCBI Taxonomy database. *Nucleic Acids Res.*; **40**(Database issue):D136-43.

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