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Changes in the fungal nomenclature: why and how to manage?

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Fungal taxonomy is complex and evolutive. As a result, the nomenclature can itself be confused. Recently, several articles focused on the changes in naming medically important fungi and the level of acceptance and use by clinicians (1–5). This short paper revisits the reasons for such modifications.

Fungal taxonomy is complex because, for a long time, the dual naming of species according to the sexual stage varied. While human fungal pathogens mostly have lost their capacity for sexual reproduction, some persist and it is difficult to put aside older names used for decades by scientists from different fields of expertise (medical mycologists, botanists ...). In addition, the polyphyletic character of some species such as *Fusarium* species for which different teleomorph species do exist: *Neocosmospora*, *Gibberella*, *Nectria*, *Callonectria*... gives rise to another level of complexity. Thanks to the One Fungus One Name initiative adopted in 2011 (6), the use of a single name should be prioritized and the practice of assigning precedence to the teleomorph name over its anamorph alternative(s) is abandoned.

Fungal taxonomy is also an evolutive field of science. For example, Takashima and colleagues point out that approximately 70% of species names listed in the fifth edition of the reference textbook “The Yeasts” are expected to change (5). This is the result of the reassignment of some common taxa into new taxonomic entities: *Pichia kudriavzevii*, *Meyerozyma guilliermondii*, *Clavispora lusitaniae* ... or the creation of new

clades such as *Nakaseomyces* that includes 3 environmental species and 3 pathogenic species, namely *Nakaseomyces nivariensis*, *Nakaseomyces bracarensis* and *Nakaseomyces glabrata*, validating the genetic distance between this clade from other *Candida* species, notably those belonging to the «Serine clade» that gathers common pathogenic species such as *Candida albicans*, *Candida parapsilosis*, *Candida tropicalis* and the fact that *Candida* genus has been artificially constructed for yeasts responsible for candidiasis without any phylogenetic basis (7). In addition, easy access to amounts of nucleotide sequence data has disrupted the previously established morphological taxonomy. This led to the demonstration of cryptic (phylogenetic) species that have modified in depth the nomenclature (1). This is of particular importance for the *Aspergillus* genus, now subdivided into four subgenera containing complexes of species or sections, composed of multiple cryptic species (8). Previously restricted to medical centers having access to sequencing facilities, this level of discrimination became more widely available as MALDI-TOF mass spectrometry now offers the possibility of cryptic species identification (8, 9). The clinical impact of identifying isolates at the cryptic species is not yet fully determined but one can cite that some in the *A. fumigatus* species complex, such as *Aspergillus lentulus*, exhibit various antifungal susceptibility (10). One can however note that the adoption of such a level of species discrimination is a source of controversy, as shown in the literature on the genus *Cryptococcus* (11, 12). Finally, changes in the naming are sometimes rapid and difficult to follow for the non-expert: *Fusarium solani* clade 6 became *Fusarium metavorans* and then *Neocosmospora metavorans* within a few months (13). No so easy to follow !!!

Undoubtedly, these changes will arise difficulties in clinical-microbiology interactions. New names will inevitably conduct in some incomprehension between clinicians using the oldest names and microbiologists aware of the taxonomic updates and new nomenclature. Education and reinforced exchanges and highlighting the advantages of some changes (yes, they do exist) should be the rule. For example, Kidd et al recently underlined that “true” *Candida* species naturally exhibit susceptibility to fluconazole, whereas newly reassigned species such as *P. kudriavzevii* (formerly *Candida krusei*), *Nakaseomyces glabrata* (formerly, *Candida*

glabrata) ... do not (2). The future will tell us if epidemiological or clinical traits are associated with newly described taxa. The experience from Australian colleagues is encouraging, as the majority of clinical laboratories (93.5%) and clinicians (72.8%) are aware of those changes. Changes in the naming are effective in 72.8% of the labs with 68.7% of the clinicians that remember having received information about the updated nomenclature (3). Indeed, one possibility is to combine previous names alongside novel ones. This is exemplified in the recently released list of priority fungal pathogens of WHO that used the terminology *N. glabrata* (*C. glabrata*) (who still remembers *Torulopsis glabrata* ??), validating this new binomial determination (14). Kidd and colleagues thus encourage microbiologists to "take steps toward utilization of updated fungal nomenclature as soon as is practical". Surely, these new names will be progressively recognized in the future and, once widely used, the old names can be abandoned.

Readers can find lists of new or revised fungal taxa pathogens for humans in references (1, 4). MycoBank (www.mycobank.org) and Index Fungorum (<http://www.indexfungorum.org>) should serve as reference repositories for fungal taxonomy.

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