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MINIREVIEW

Name Changes for Fungi of Medical Importance, 2018 to 2019

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ABSTRACT The current article summarizes recent changes in nomenclature for fungi of medical importance published in the years 2018 to 2019, including new species and revised names for existing ones. Many of the revised names have been widely adopted without further discussion. However, those that concern common pathogens of humans may take longer to achieve general usage, with new and current names reported together to engender increasing familiarity with the correct taxonomic classification.

KEYWORDS taxonomy, classification, revisions, *Candida*

Conventional methods of fungal identification, which are based on examination of morphological and phenotypic features, are complicated by the astonishing diversity of organisms capable of causing human infections, especially in immunocompromised hosts. The recent adoption of molecular approaches to fungal identification has led to profound changes in fungal nomenclature and taxonomy as correct taxonomic relationships and affiliations are recognized. Many phyla have been shown to be polyphyletic and have been disbanded or substantially revised, multiple cryptic species have been described in numerous well-known morphospecies, long-recognized species have been moved to new genera on the basis of genotypic comparisons, and new genera and species have been erected to accommodate novel organisms delineated by detailed phylogenetic analyses.

In addition to the upheavals driven by these modern polyphasic approaches to the delineation of taxonomic boundaries, implementation of the dictates of the Amsterdam Declaration (1) has driven further widespread nomenclatural changes. From 1 January 2013, the practice of employing separate names to the teleomorph (sexual) and anamorph (asexual) states of fungi was prohibited, with the result that mycologists must choose a single name (sometimes from numerous existing ones) for many thousands of extant species. This new code of nomenclature also abandoned the practice of assigning precedence to the teleomorph name over its anamorph alternative(s) by allowing any of the multiple published legitimate names for a given species to be chosen as the correct name. In an attempt to lessen unnecessary and transient nomenclatural instability, working groups and committees established under the auspices of the International Commission on the Taxonomy of Fungi (ICTF) and the Nomenclature Committee for Fungi (NCF) will propose lists of retained (protected) and rejected names for key species/genera, with only definitive changes being ratified.

Currently, there is no single source that clinicians, microbiologists, and mycologists can consult that captures all nomenclatural changes proposed for fungi of medical importance; novel fungal taxa and proposals to reassign or rename existing taxa are published continually in a wide range of scientific journals. However, for new names and combinations to be accepted as validly published, the International Code of Nomenclature for algae, fungi, and plants (ICN) requires that all such taxa are registered in recognized online repositories. The principal repositories, MycoBank (http://www.mycobank.org/) and Index Fungorum (http://www.indexfungorum.org), are invaluable

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TABLE 1 List of new fungal taxa from human clinical material from the period from 2018 to 2019

Species	Order	Source(s)	Clinical relevance	Reference no.	MB accession no.[a]
Alternaria anthropophila	*Pleosporales*	Tissue	Subcutaneous infection	11	MB 829636
Alternaria atrobrunnea	*Pleosporales*	Exudate	Ulcerative lesions	11	MB 829637
Alternaria guarroi	*Pleosporales*	Biopsy	Ulcerative lesions	11	MB 829638
Arthroderma chilionensis	*Onygenales*	Skin scrapings	Not established	8	MB 825172
Aspergillus dobrogensis	*Eurotiales*	Toe nail	Not established	31	MB 821313
Aspergillus microperforatus	*Eurotiales*	Toe nail, lymph node	Not established	32	MB 820080
Aspergillus suttoniae	*Eurotiales*	Sputum	Not established	33	MB 823689
Blastomyces emzantsi	*Onygenales*	Various clinical sites	Blastomycosis	5	MB 828102
Curvularia coimbatorensis	*Pleosporales*	Corneal scrapings	Keratitis	16	MB 833656
Curvularia tamilnaduensis	*Pleosporales*	Corneal scrapings	Keratitis	16	MB 833657
Diaporthe oculi	*Diaporthales*	Cornea	Keratitis	17	MB 825540
Diaporthe pseudooculi	*Diaporthales*	Cornea	Keratitis	17	MB 825541
Fusarium riograndense	*Hypocreales*	Nasal cavity	Rhinosinusitis	34	MB 814515
Gambiomyces profunda	*Pleosporales*	Various tissues	Superficial/subcutaneous	15	MB 835156
Gloniopsis percutanea	*Hysteriales*	Various tissues	Subcutaneous	12	MB 830898
Gloniopsis pneumoniae	*Hysteriales*	Lung tissue	Not established	12	MB 830899
Knoxdaviesia dimorphospora	*Ophiostomatales*	Fluid	Bursitis	13	MB 821526
Microascus ennothomasiorum	*Microascales*	Biopsy of thumb nodule	Subcutaneous infection	14	MB 826957
Nannizzia perplicata	*Onygenales*	Skin scrapings	Tinea corporis	9	MB 826930
Trichophyton indotineae	*Onygenales*	Skin scrapings	Tinea corporis	10	MB 833488
Wickerhamiella verensis	*Saccharomycetales*	Blood culture	Fungemia	35	MB 833012

[a]MB, MycoBank.

sources of up-to-date taxonomic information. However, given the speed of change, even they are not complete/correct across all genera of medically important fungi. The present article represents an update to two previous ones (2, 3) which provided lists of novel taxa and revised names for existing taxa for fungi of medical importance published between 2012 and 2015 (2) and 2016 and 2017 (3).

METHODS

To capture new fungal taxa and nomenclatural revisions described between 2018 and 2019, systematic literature searches were conducted in the PubMed database (https://pubmed.ncbi.nlm.nih.gov/) using a variety of search terms, including "fungal sp. nov.," fungal gen. nov.," "fungal new species," "fungal new genus," "novel fungus," "ascomycete sp. nov.," "basidiomycete sp. nov," "mucorales sp. nov," "fungal taxonomic revision," and "fungal comb. nov." In addition, MycoBank and Index Fungorum were extensively searched to find taxonomic changes and additions to the most common fungal genera associated with human disease. The last date of access to all of these resources was 7 August 2020.

The novel taxa retained for inclusion here were those that had been recovered from human specimens. In some cases, a proven etiological role in human infection has been established; in others, the clinical significance of the organism remains unknown. New species/genera from veterinary sources were excluded, regardless of whether they were proven agents of infection, as were extant species which had been recognized as agents of human disease for the first time. The names listed in Tables 1 and 2 of the current article are those that fulfill the ICN rules for valid publication in that they (i) are in Latin binomial form, (ii) are accompanied by a description in Latin or English, (iii) have a holotype deposited in a recognized culture collection, and (iv) have been registered in MycoBank and published with a MycoBank accession number.

Here, we have also chosen to address the issue of the heterogeneous and clearly polyphyletic nature of the genus *Candida*, which contains in excess of 200 species encompassing at least 13 teleomorph genera (4). Although a number of the taxonomic revisions discussed here for *Candida* and related pathogenic yeast species have been proposed prior to the period from 2018 to 2019, previous updates in this series have largely not addressed this issue. With only 3 exceptions (discussed below), all revised yeast names listed in Table 3 also fulfill the ICN requirements for valid publication.

TABLE 2 List of revised fungal taxa from 2018 through 2019

Previous species name	Revised species name	Order	Reference no.	MB accession no.[a]
Candida infanticola	*Wickerhamiella infanticola*	*Saccharomycetales*	22	MB 815725
Candida pararugosa	*Wickerhamiella pararugosa*	*Saccharomycetales*	22	MB 815736
Chaetomium atrobrunneum	*Amesia atrobrunnea*	*Sordariales*	36	MB 818 832
Diutina (*Candida*) *mesorugosa*	*Diutina rugosa*	*Saccharomycetales*	24	Not applicable
Fusarium solani species complex 6 (FSSC6)	*Fusarium metavorans*	*Hypocreales*	18	MB 821742
Fusarium metavorans	*Neocosmospora metavorans*	*Hypocreales*	20	MB 823607
Fusarium solani species complex 9 (FSSC9), *Cylindrocarpon tonkinense*/*Fusarium tonkinense*	*Neocosmospora tonkinensis*	*Hypocreales*	20	MB 822904
Fusarium solani species complex 7 (FSSC7)	*Neocosmospora gamsii*	*Hypocreales*	20	MB 822899
Fusarium solani species complex *20 (FSSC20)*	*Neocosmospora suttoniana*	*Hypocreales*	20	MB 822903
Fusarium solani species complex 43 (FSSC43)	*Neocosmospora catenata*	*Hypocreales*	20	MB 822898
Fusarium keratoplasticum	*Neocosmospora keratoplastica*	*Hypocreales*	20	MB 822901
Fusarium lichenicola	*Neocosmospora lichenicola*	*Hypocreales*	20	MB 822900
Fusarium petrophila	*Neocosmospora petroliphila*	*Hypocreales*	20	MB 822902
Emmonsia crescens	*Emergomyces crescens*	*Onygenales*	7	MB 330349
Emmonsia soli	*Emergomyces soli*	*Onygenales*	6, 7	MB 821087

[a]MB, MycoBank.

RESULTS AND DISCUSSION

The list of novel fungal taxa from human samples described between 2018 and 2019 is presented in Table 1 and includes new (often cryptic) species in several well-known human-pathogenic fungal genera, *Alternaria*, *Aspergillus*, *Curvularia*, and *Fusarium*. It is

TABLE 3 List of how taxonomic revisions affected basidiomycete and ascomycete yeasts of medical importance

Previous species name	Revised species name	Order	Reference no.	MB accession no.
Candida bracarensis	*Nakaseomyces bracarensisa*[a]	*Saccharomycetales*	37	NA[b]
Candida catenulata	*Diutina catenulata*	*Saccharomycetales*	23	MB 813778
Candida eremophila	*Pichia eremophila*	*Saccharomycetales*	38	MB 508435
Candida etchellsii	*Starmerella etchellsii*	*Saccharomycetales*	39	MB 823618
Candida fabianii	*Cyberlindnera fabianii*	*Saccharomycetales*	40	MB 534382
Candida famata	*Debaryomyces hansenii*	*Saccharomycetales*	41	MB 296478
Candida fermentati	*Meyerozyma caribbica*	*Saccharomycetales*	42	MB 513462
Candida glabrata	*Nakaseomyces glabrataa*[a]	*Saccharomycetales*	37	NA
Candida inconspicua	*Pichia cactophila*	*Saccharomycetales*	43	MB 320493
Candida kefyr	*Kluyveromyces marxianus*	*Saccharomycetales*	44	MB 316062
Candida krusei	*Pichia kudriavzevii*	*Saccharomycetales*	45	MB 337013
Candida guilliermondii	*Meyerozyma guilliermondii*	*Saccharomycetales*	42	MB 513463
Candida lambica	*Pichia fermentans*	*Saccharomycetales*	46	MB 252130
Candida lipolytica	*Yarrowia lipolytica*	*Saccharomycetales*	47	MB 108643
Candida lusitaniae	*Clavispora lusitaniae*	*Saccharomycetales*	48	MB 111257
Candida nivariensis	*Nakaseomyces nivariensisa*[a]	*Saccharomycetales*	49	NA
Candida norvegensis	*Pichia norvegensis*	*Saccharomycetales*	50	MB 320514
Candida pelliculosa	*Wickerhamomyces anomalus*	*Saccharomycetales*	38	MB 508390
Candida pintolopesii	*Kazachstania telluris*	*Saccharomycetales*	51	MB 487688
Candida pulcherrima	*Metschnikowia pulcherrima*	*Saccharomycetales*	52	MB 334124
Candida rugosa	*Diutina rugosa*	*Saccharomycetales*	23	MB 813768
Candida sorbosivorans	*Starmerella sorbosivorans*	*Saccharomycetales*	39	MB 823645
Candida utilis	*Cyberlindnera jadinii*	*Saccharomycetales*	40	MB 534383
Cryptococcus albidus	*Naganishia albida*	*Filobasidiales*	27	MB 813141
Cryptococcus curvatus	*Cutaneotrichosporon curvatum*	*Trichosporonales*	27	MB 818663
Cryptococcus diffluens	*Naganishia diffluens*	*Filobasidiales*	27	MB 813172
Cryptococcus laurentii	*Papiliotrema laurentii*	*Tremellales*	27	MB 813295
Pseudozyma antarctica	*Moesziomyces antarcticus*	*Ustilaginales*	53	MB 812714
Pseudozyma aphidis	*Moesziomyces aphidis*	*Ustilaginales*	53	MB 812715
Pseudozyma parantartica	*Moesziomyces parantarcticus*	*Ustilaginales*	53	MB 812717
Rhodotorula minuta	*Cystobasidium minutum*	*Cystobasidiales*	54	MB 809340
Rhodotorula slooffiae	*Cystobasidium slooffiae*	*Cystobasidiales*	54	MB 809341
Stephanoascus ciferrii	*Trichomonascus ciferrii*	*Saccharomycetales*	55	MB 530083
Trichosporon cutaneum	*Cutaneotrichosporon cutaneum*	*Trichosporonales*	27	MB 813398
Trichosporon loubieri	*Apiotrichum loubieri*	*Trichosporonales*	27	MB 813417
Trichosporon mucoides	*Cutaneotrichosporon mucoides*	*Trichosporonales*	27	MB 813402
Trichosporon mycotoxinivorans	*Apiotrichum mycotoxinivorans*	*Trichosporonales*	27	MB 813420

[a]Members of the *Nakaseomyces* clade that currently lack formal registration with MycoBank (MB).
[b]NA, not available.

also notable for the presence of another endemic dimorphic pathogen, *Blastomyces emzantsi* (5), described from a case series of *Blastomyces* infections in non-HIV-infected patients in South Africa. To date, this novel addition to the *Ajellomycetaceae* appears geographically restricted to this continent, where it was predominantly associated with extrapulmonary disease (skin and bone), although this likely followed hematogenous dissemination from a primary pulmonary infection. This continues the description of multiple novel dimorphic pathogens following the detailed molecular analyses of often historical cases that was observed in the previous two updates in this series (2, 3). An additional novel dimorphic pathogen, *Emmonsia soli* (6), was described in 2018 from a single isolate from soil. The fact that this species, together with the extant *Emmonsia crescens*, appears in Table 2 after a proposal to reassign both organisms to the genus *Emergomyces* (7) underscores the pace of taxonomic change among the *Ajellomycetaceae* and follows the previous decision to move the type species of *Emmonsia* (*E. parva*) to *Blastomyces* (6). Novel additions to the wider *Onygenales* include three new dermatophyte relatives, *Arthroderma chilionensis* (8), *Nannizzia perplicata* (9), and *Trichophyton indotineae* (10). While human infection with *N. perplicata* was proven in a single case of tinea corporis, the clinical significance of *A. chilionensis* remains to be established. *T. indotineae* is of clear clinical significance, as this novel taxon was erected to encompass the highly terbinafine-resistant *Trichophyton interdigitale*-like strains circulating on the Indian subcontinent that possess missense mutations in the squalene epoxidase gene and differ from tradition strains of *T. interdigitale* by their negativity on Christensen urease agar (10).

The presence of several novel dermatophyte relatives in Table 1 of this article and the equivalent table of the previous incarnation (3) again reflects the fact that fungi isolated from visible superficial fungal infections are overrepresented compared to ubiquitous environmental saprobes that might be associated with pulmonary manifestations or colonization. The same is true for rarer agents of deeper, subcutaneous infection and ocular infections where diagnosis and isolation of the causative agents are less problematic. A third of the novel taxa (7/21) listed in Table 1 were isolated from various subcutaneous infections or ulcerative skin lesions and include novels species in *Alternaria* (11), *Gloniopsis* (12), *Knoxdaviesia* (13), and *Microascus* (14) and the only novel genus described during this period, with three isolates of *Gambiomyces profunda* from clinical specimens (15). Similarly, four of the species listed in Table 1 were associated with cases of keratitis and included two novel taxa in each of the genera *Curvularia* (16) and *Diaporthe* (17). While *Curvularia* spp. are well-known human pathogens previously associated with a wide range of superficial and deeper infections, including keratitis (16), *Diaporthe* spp. are extremely rare pathogens of humans and have not previously been reported from ocular infections.

The number of existing fungal taxa with proposed nomenclatural changes during the period from 2018 to 2019 (Table 2) is similar in length to the lists presented in previous updates. Previous lists were bolstered by genus- or family-wide taxonomic reappraisals of clinically important fungi, including the dermatophytes and several genera within *Ajellomycetaceae* and *Cryptococcus* spp. in the *neoformans* and *gattii* complexes (2, 3). Here, many of the proposed changes concern fungi of the *Fusarium solani* species complex and several additional members of the *Ajellomycetaceae* and several yeast species with *Candida* anamorphs. As discussed above, it has recently been proposed to move remaining members of the defunct genus *Emmonsia* (*E. crescens* and *E. soli*) into *Emergomyces* (7) on the basis that large yeast form intermediaries produced during thermal conversion by several *Emergomyces* and *Blastomyces* spp. are not dissimilar from the true adiaspore tissue forms of "*Emmonsia*." The principal arguments against this proposal include the relatively large genetic distances between "*Emmonsia*" species and *Emergomyces* and the fact that the large yeast form intermediaries are likely *in vitro* artifacts of the thermal dimorphic transition that are not seen during infection. It remains to be seen whether this proposal will gain widespread acceptance.

In 2018, *Fusarium metavorans* (18) was formally proposed as the name to replace *Fusarium solani* species complex clade 6 (FSSC6), one of the most common agents of

human opportunistic infections. While this appeared to be a significant (albeit small) step toward starting to formally name the hundreds of cryptic species in "*Fusarium*," it highlights another currently unresolved issue which also confronts many medically important genera, including *Candida* (see below) and *Aspergillus*, which are clearly polyphyletic if teleomorph divisions are emphasized in delineating generic boundaries. The type species of *Fusarium* is *Fusarium sambucinum*, which has a *Gibberella* teleomorph. Thus, based on teleomorph boundaries, all those current *Fusarium* species which have teleomorphs other than *Gibberella* should be removed, including *Fusarium solani* (teleomorph *Neocosmospora*). On this basis, *Neocosmospora solani* was recently epitypified (19), linking it to FSSC clade 5. As can be seen from Table 2, formal species names within *Neocosmospora* have now also been proposed for three further "*Fusarium solani*" lineages (FSSC7, FSSC20, and FSSC43) and an additional 4 "*Fusarium*" species, and *Fusarium metavorans* has been tentatively renamed *Neocosmospora metavorans* only 8 months after the former name was proposed (20). In general, we believe that moves to resolve nomenclature of polyphyletic genera should be applauded. However, this proposed fragmentation of the historical concept of genus "*Fusarium*" based on traditional teleomorph boundaries has received significant scientific opposition, based both upon molecular phylogenetic analyses that suggest that most "*Fusarium*" species can be accommodated in a robust monophyletic group (the "terminal *Fusarium* clade" [discussed in reference 21]) and arguments that fragmentation would negatively impact scientific communication and nomenclatural continuity. Given these conflicting viewpoints, we suggest that clinical laboratories continue to use the name *Fusarium* until such issues are definitively resolved in order to limit potential future confusion and instability.

The final three taxonomic revisions listed in Table 2 concern pathogenic yeast species with anamorph names previously in *Candida*. Phylogenetic and biochemical analyses of yeasts isolated from flowers resulted in the transfer of 18 species formerly assigned to *Candida* to the genus *Wickerhamiella*, including the human-pathogenic species formerly known as *Candida pararugosa* and *Candida infanticola* (22). In a separate study, *Diutina mesorugosa* (ex-*Candida mesorugosa*), a member of the *Diutina rugosa* complex (23), could not be meaningfully separated from *D. rugosa* either by multilocus sequence typing or based on phenotypic properties and is now considered synonymous (24). An increasing number of taxonomic reassignments of members of the polyphyletic genus *Candida*, which contains in excess of 200 species encompassing at least 13 teleomorph genera (4), have been proposed over recent years. Similar issues have also been highlighted for several genera of basidiomycete yeasts of clinical importance. Since these proposals went largely unreported in previous versions of this update, we have chosen to summarize the key changes here (despite the fact that many predate the 2018 to 2019 period) to provide a more complete update on the taxonomic status of clinically relevant "*Candida*" species. A list of clinically relevant basidiomycete and ascomycete yeast species with revised taxonomic affiliations is presented in Table 3. With the exception of the 3 species in the *Nakaseomyces* clade (*Candida bracarensis*, *Candida glabrata*, and *Candida nivariensis*) which have not undergone formal registration with MycoBank, all new species names fulfill the ICN rules for valid publication and are accompanied by unique MycoBank accession numbers. The phylogenetic rationales supporting these proposals are given in greater detail in references 4 and 25 to 27. In our laboratory, we have reported the identity of all clinical isolates using these revised names (including for the three species in the *Nakaseomyces* clade) since January 2019, together with a comment linking the novel names to the single most recent previous name listed in Table 3 (e.g., "isolate identified as *Nakaseomyces glabrata*, previously known as *Candida glabrata*"), without undue clinical confusion. We believe that this revised taxonomy that reflects phylogenetic relationships correlates better with unusual antifungal resistance profiles observed with many of the less common species of pathogenic yeasts (28, 29). For example, the innate resistance of isolates of *Pichia kudriavzevii* (ex-*Candida krusei*) to fluconazole and flucytosine appears unusual compared with most other pathogenic "*Candida*" species but is a

feature shared by many different *Pichia* species (28, 29). Thus, we believe that the practice of employing revised names for these pathogenic yeast species will be more informative to the clinician than persisting with the current misleading practice of using historical genera to group hundreds of genetically distantly related yeast species.

In conclusion, we hope that the current review has captured most, if not all, of the proposed new or revised species names and nomenclatural changes affecting fungi of medical importance during the period from 2018 to 2019. As in previous editions, the list of novel species includes newly recognized cryptic or sibling species in common well-established taxa, together with genuinely novel agents of superficial, subcutaneous, and disseminated human infections. Many of these novel species have been described around a single isolate. Understanding of their general prevalence, possible wider clinical relevance, and whether these initial isolates are representative of the species as a whole will await the isolation and examination of additional examples. Further work will also be required to fully understand the importance of new cryptic species reported during this period and to determine whether they possess clinically relevant differences in pathogenicity or antifungal susceptibility that justify their identification beyond the "species complex" level (30).

Historically, many nomenclatural changes in medically important fungi were met with considerable resistance and often took decades to gain complete acceptance (30). However, the rapidly increased pace of change over the last decade, driven both by advanced molecular phylogenetic approaches and the adoption of the revised rules governing the naming of fungi, has resulted in taxonomic changes to many fungi of medical importance. In the future, it is almost inevitable that many more medically important fungi will be similarly affected, with the result that ongoing clinical education will be essential. We believe that, with the exception of proposals to fragment the historical genus *Fusarium* as discussed above, the majority of the other taxonomic changes described in the current paper (including those affecting pathogenic yeast species listed in Tables 2 and 3) are reasonable and appropriate for immediate implementation. Inevitably, in the short term, this revised nomenclature is likely to cause some confusion for clinicians. This can be alleviated in part by reporting of novel names alongside their previous incarnation(s) until they have gained widespread recognition, together with regular reviews providing updates of the type presented here and elsewhere (4).

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