



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
<i>Alternaria anthropophila</i>	Pleosporales	Tissue	Subcutaneous infection	11	MB 829636
<i>Alternaria atrobrunnea</i>	Pleosporales	Exudate	Ulcerative lesions	11	MB 829637
<i>Alternaria guarroi</i>	Pleosporales	Biopsy	Ulcerative lesions	11	MB 829638
<i>Arthroderma chilionensis</i>	Onygenales	Skin scrapings	Not established	8	MB 825172
<i>Aspergillus dobrogensis</i>	Eurotiales	Toe nail	Not established	31	MB 821313
<i>Aspergillus microperforatus</i>	Eurotiales	Toe nail, lymph node	Not established	32	MB 820080
<i>Aspergillus suttoniae</i>	Eurotiales	Sputum	Not established	33	MB 823689
<i>Blastomyces emzantsi</i>	Onygenales	Various clinical sites	Blastomycosis	5	MB 828102
<i>Curvularia coimbatorensis</i>	Pleosporales	Corneal scrapings	Keratitis	16	MB 833656
<i>Curvularia tamilnaduensis</i>	Pleosporales	Corneal scrapings	Keratitis	16	MB 833657
<i>Diaporthe oculi</i>	Diaporthales	Cornea	Keratitis	17	MB 825540
<i>Diaporthe pseudooculi</i>	Diaporthales	Cornea	Keratitis	17	MB 825541
<i>Fusarium riograndense</i>	Hypocreales	Nasal cavity	Rhinosinusitis	34	MB 814515
<i>Gambiomycetes profunda</i>	Pleosporales	Various tissues	Superficial/subcutaneous	15	MB 835156
<i>Gloniopsis percutanea</i>	Hysteriales	Various tissues	Subcutaneous	12	MB 830898
<i>Gloniopsis pneumoniae</i>	Hysteriales	Lung tissue	Not established	12	MB 830899
<i>Knoxdaviesia dimorphospora</i>	Ophiostomatales	Fluid	Bursitis	13	MB 821526
<i>Microascus ennothomasiolum</i>	Microascales	Biopsy of thumb nodule	Subcutaneous infection	14	MB 826957
<i>Nannizzia perplicata</i>	Onygenales	Skin scrapings	Tinea corporis	9	MB 826930
<i>Trichophyton indotineae</i>	Onygenales	Skin scrapings	Tinea corporis	10	MB 833488
<i>Wickerhamiella verensis</i>	Saccharomycetales	Blood culture	Fungemia	35	MB 833012

^aMB, 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
<i>Candida infanticola</i>	<i>Wickerhamiella infanticola</i>	Saccharomycetales	22	MB 815725
<i>Candida pararugosa</i>	<i>Wickerhamiella pararugosa</i>	Saccharomycetales	22	MB 815736
<i>Chaetomium atrobrunneum</i>	<i>Amesia atrobrunnea</i>	Sordariales	36	MB 818 832
<i>Diutina (Candida) mesorugosa</i>	<i>Diutina rugosa</i>	Saccharomycetales	24	Not applicable
<i>Fusarium solani</i> species complex 6 (FSSC6)	<i>Fusarium metavorans</i>	Hypocreales	18	MB 821742
<i>Fusarium metavorans</i>	<i>Neocosmospora metavorans</i>	Hypocreales	20	MB 823607
<i>Fusarium solani</i> species complex 9 (FSSC9), <i>Cylindrocarpon tonkinense/Fusarium tonkinense</i>	<i>Neocosmospora tonkinensis</i>	Hypocreales	20	MB 822904
<i>Fusarium solani</i> species complex 7 (FSSC7)	<i>Neocosmospora gamsii</i>	Hypocreales	20	MB 822899
<i>Fusarium solani</i> species complex 20 (FSSC20)	<i>Neocosmospora suttoniana</i>	Hypocreales	20	MB 822903
<i>Fusarium solani</i> species complex 43 (FSSC43)	<i>Neocosmospora catenata</i>	Hypocreales	20	MB 822898
<i>Fusarium keratoplasticum</i>	<i>Neocosmospora keratoplastica</i>	Hypocreales	20	MB 822901
<i>Fusarium lichenicola</i>	<i>Neocosmospora lichenicola</i>	Hypocreales	20	MB 822900
<i>Fusarium petrophila</i>	<i>Neocosmospora petrophila</i>	Hypocreales	20	MB 822902
<i>Emmonsia crescens</i>	<i>Emergomycetes crescens</i>	Onygenales	7	MB 330349
<i>Emmonsia soli</i>	<i>Emergomycetes soli</i>	Onygenales	6, 7	MB 821087

^aMB, 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.
<i>Candida bracarensis</i>	<i>Nakaseomyces bracarensis</i> ^a	Saccharomycetales	37	NA ^b
<i>Candida catenulata</i>	<i>Diutina catenulata</i>	Saccharomycetales	23	MB 813778
<i>Candida eremophila</i>	<i>Pichia eremophila</i>	Saccharomycetales	38	MB 508435
<i>Candida etchellsii</i>	<i>Starmerella etchellsii</i>	Saccharomycetales	39	MB 823618
<i>Candida fabianii</i>	<i>Cyberlindnera fabianii</i>	Saccharomycetales	40	MB 534382
<i>Candida famata</i>	<i>Debaryomyces hansenii</i>	Saccharomycetales	41	MB 296478
<i>Candida fermentati</i>	<i>Meyerozyma caribbica</i>	Saccharomycetales	42	MB 513462
<i>Candida glabrata</i>	<i>Nakaseomyces glabrata</i> ^a	Saccharomycetales	37	NA
<i>Candida inconspicua</i>	<i>Pichia cactophila</i>	Saccharomycetales	43	MB 320493
<i>Candida kefyr</i>	<i>Kluyveromyces marxianus</i>	Saccharomycetales	44	MB 316062
<i>Candida krusei</i>	<i>Pichia kudriavzevii</i>	Saccharomycetales	45	MB 337013
<i>Candida guilliermondii</i>	<i>Meyerozyma guilliermondii</i>	Saccharomycetales	42	MB 513463
<i>Candida lambica</i>	<i>Pichia fermentans</i>	Saccharomycetales	46	MB 252130
<i>Candida lipolytica</i>	<i>Yarrowia lipolytica</i>	Saccharomycetales	47	MB 108643
<i>Candida lusitanae</i>	<i>Clavispora lusitanae</i>	Saccharomycetales	48	MB 111257
<i>Candida nivariensis</i>	<i>Nakaseomyces nivariensis</i> ^a	Saccharomycetales	49	NA
<i>Candida norvegensis</i>	<i>Pichia norvegensis</i>	Saccharomycetales	50	MB 320514
<i>Candida pelliculosa</i>	<i>Wickerhamomyces anomalus</i>	Saccharomycetales	38	MB 508390
<i>Candida pintolopesii</i>	<i>Kazachstania telluris</i>	Saccharomycetales	51	MB 487688
<i>Candida pulcherrima</i>	<i>Metschnikowia pulcherrima</i>	Saccharomycetales	52	MB 334124
<i>Candida rugosa</i>	<i>Diutina rugosa</i>	Saccharomycetales	23	MB 813768
<i>Candida sorbosivorans</i>	<i>Starmerella sorbosivorans</i>	Saccharomycetales	39	MB 823645
<i>Candida utilis</i>	<i>Cyberlindnera jadinii</i>	Saccharomycetales	40	MB 534383
<i>Cryptococcus albidus</i>	<i>Naganishia albidus</i>	Filobasidiales	27	MB 813141
<i>Cryptococcus curvatus</i>	<i>Cutaneotrichosporon curvatum</i>	Trichosporonales	27	MB 818663
<i>Cryptococcus diffluens</i>	<i>Naganishia diffluens</i>	Filobasidiales	27	MB 813172
<i>Cryptococcus laurentii</i>	<i>Papiliotrema laurentii</i>	Tremellales	27	MB 813295
<i>Pseudozyma antarctica</i>	<i>Moesziomyces antarcticus</i>	Ustilaginales	53	MB 812714
<i>Pseudozyma aphidis</i>	<i>Moesziomyces aphidis</i>	Ustilaginales	53	MB 812715
<i>Pseudozyma parantarctica</i>	<i>Moesziomyces parantarcticus</i>	Ustilaginales	53	MB 812717
<i>Rhodotorula minuta</i>	<i>Cystobasidium minutum</i>	Cystobasidiales	54	MB 809340
<i>Rhodotorula slooffiae</i>	<i>Cystobasidium slooffiae</i>	Cystobasidiales	54	MB 809341
<i>Stephanosascus ciferrii</i>	<i>Trichomonascus ciferrii</i>	Saccharomycetales	55	MB 530083
<i>Trichosporon cutaneum</i>	<i>Cutaneotrichosporon cutaneum</i>	Trichosporonales	27	MB 813398
<i>Trichosporon loubieri</i>	<i>Apiotrichum loubieri</i>	Trichosporonales	27	MB 813417
<i>Trichosporon mucoides</i>	<i>Cutaneotrichosporon mucoides</i>	Trichosporonales	27	MB 813402
<i>Trichosporon mycotoxinivorans</i>	<i>Apiotrichum mycotoxinivorans</i>	Trichosporonales	27	MB 813420

^aMembers of the *Nakaseomyces* clade that currently lack formal registration with MycoBank (MB).^bNA, 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 novel 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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