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Reclassification and Nomenclature of Common Pathogenic Fungi

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Abstract

The accurate identification of pathogenic fungi is crucial for diagnosing and treating fungal infections. Recent advancements in molecular biotechnology, phylogenetic analysis, and the requirements of the Melbourne Code have led to changes in the classification and naming of fungi. These changes have caused significant confusion for medical laboratories and clinical personnel. This article summarizes the classification and new names of common pathogenic fungi to enhance fungi identification skills and provide accurate information for clinical diagnosis and treatment.

Keywords

Fungi, Yeast, Nomenclature, 1 Species = 1 Name

1. Introduction

Invasive fungal infections (IFIs) pose a significant risk to human health, especially in immunocompromised individuals or those with severe underlying conditions. The incidence of IFIs has increased due to invasive procedures, widespread use of broad-spectrum antibiotics and corticosteroids, traumatic incidents, and multi-organ impairments [1] [2]. The International Code of Nomenclature for algae, fungi, and plants (Melbourne Code) asked for "one name per species," aiming to eliminate confusion arising from the dual nomenclature system of sexual and asexual types [3]. Furthermore, advancements in molecular biology and phylogenetic analysis have revealed that traditional morphology-based classification methods are inadequate for capturing evolutionary relationships. Consequently, many fungi have recently undergone taxonomic revisions based on molecular biological techniques. Despite the presence of temporary confusion, classifying fungi based on evolutionary analysis of key conserved

genes is more accurate than previous methods relying on morphological and biochemical characteristics. While some commercial fungal identification databases have updated species names, the 2022 CLSI M27 Mycodrug susceptibility Guidelines also include the new taxonomic names for some commonly encountered strains. However, data from fungal monitoring in Shandong Province over the last five years show that few clinical laboratories use these new species names in their reports. Therefore, adopting and recognizing this new classification system will be a lengthy process that requires significant effort from medical laboratories.

The classification and naming of fungi based on molecular biology more accurately reflects their phylogenetic relationships and species characteristics. For instance, although the genus Pneumocystis was once considered a protozoan, genetic sequence analysis has shown that it is more closely related to fungi. Consequently, the reclassification of the human pathogen *Pneumocystis jirovecii* in 1999 is now widely accepted.

Penicillium marneffei, initially classified under the Penicillium species, is not closely related to most Penicillium species and has been reclassified into the Talaromyces genus as *Talaromyces marneffei* due to sharing the same virulence factor. Before 2005, it was referred to as part of the *C. parapsilosis* groups I, II, and III, which exhibited significant differences in drug sensitivity [4]. **Table 1** summarizes recent naming changes of common pathogenic fungi, mainly including *Candida*, Cryptococcus, and *Trichosporon*.

2. Cryptococcus

The species complex of *C. gattii/C. neoformans*, the primary pathogen in Cryptococcus, has been divided into 7 species based on 11 gene loci [5]. *C. neoformans var. grubii* and *C. neoformans var. neoformans* have been renamed *C. neoformans* and *C. deneoformans*, respectively, with *C. neoformans* being serotype A. This renaming helps clarify the link between the pathogen and cryptococcal meningitis, which it frequently causes. Unlike *C. neoformans*, which primarily infects HIV patients or others with compromised immune systems, *C. gattii* typically infects individuals with normal immune function and is more resistant to antifungal treatment [6]. The species include *C. gattii* (Serotype B/molecular subtype VGI), *C. bacillisporus* (VGIII), *C. deuterogattii* (VGII), *C. tetragatii*, and *C. degattii* (VGIV/VGIII). Despite their varied biochemical characteristics and clinical pathogenicity, these species can be distinguished using the MALDI-TOF assay in clinical laboratories. Additionally, *C. albidus* and *C. diffluens*, which occasionally infect humans, have been reclassified to the genus *Naganishia*.

3. Candida

Based on molecular biology, the primary pathogenic bacteria in Candida are divided into several groups, mainly including the Candida albicans complex (comprising *C. albicans s.s.*, *C. dubliniensis*, *C. africanain*), the Candida parapsilosis

Table 1. Comparison of old and new names of common pathogenic fungi.

Former Name	Revised Name	Order	Former Name	Revised Name	Order
Phialemonium curvatum	***Phialemoniopsis curvata***	*Sordariales*	*Candida famata*	***Debaryomyces hansenii***	*Saccharomycetales*
Microsporum cookei	***Paraphyton cookei***	*Onygenales*	***Candida krusei***	***Pichia kudriavzevii***	*Saccharomycetales*
Microsporum gypseum	***Nannizzia gypsea***	*Onygenales*	*Candida lambica*	***Pichia fermentans***	*Saccharomycetales*
Microsporum persicolor	***Nannizzia persicolor***	*Onygenales*	*Candida inconspicua*	***Pichia cactophila***	*Saccharomycetales*
Cryptococcus albidus	***Naganishia albida***	*Filobasidiales*	*Candida norvegensis*	***Pichia norvegensis***	*Saccharomycetales*
Cryptococcus diffluens	***Naganishia diffluens***	*Filobasidiales*	*Candida pelliculosa*	***Wickerhamomyces anomalus***	*Saccharomycetales*
Cryptococcus neoformans var. grubii (serotype A, molecular types VNI and VNII)	***Cryptococcus neoformans***	*Filobasidiales*	***Candida guilliermondii***	***Meyerozyma guilliermondii***	*Saccharomycetales*
Cryptococcus neoformans var. neoformans (serotype D, molecular type VNIV)	***Cryptococcus deneoformans***	*Filobasidiales*	*Candida lipolytica*	***Yarrowia lipolytica***	*Saccharomycetales*
Cryptococcus Gattii (serotype B, molecular type VGI)	***Cryptococcus gattii***	*Filobasidiales*	*Candida lusitaniae*	***Clavispora lusitaniae***	*Saccharomycetales*
Cryptococcus laurentii	***Papiliotrema laurentii***	*Tremellales*	*Candida pintolopesii*	***Kazachstania telluris***	*Saccharomycetales*
Pseudozyma aphidis	***Moesziomyces aphidis***	*Ustilaginales*	*Candida pulcherrima*	***Metschnikowia pulcherrima***	*Saccharomycetales*
Rhodotorula minuta	***Cystobasidium minutum***	*Cystobasidiales*	*Candida utilis*	***Cyberlindnera jadinii***	*Saccharomycetales*
Candida bracarensis	***Nakaseomyces bracarensis***	*Saccharomycetales*	*Candida fabianii*	***Cyberlindnera fabianii***	*Saccharomycetales*
Candida glabrata	***Nakaseomyces glabratus***	*Saccharomycetales*	*Stephanoascus ciferrii*	***Trichomonascus ciferrii***	*Saccharomycetales*
Candida haemulonii group II	***Candida duobushaemulonii***	*Saccharomycetales*	*Cryptococcus curvatus*	***Cutaneotrichosporon curvatum***	*Trichosporonales*
Candida infanticola	***Wickerhamiella infanticola***	*Saccharomycetales*	*Trichosporon cutaneum*	***Cutaneotrichosporon cutaneum***	*Trichosporonales*
Candida pararugosa	***Wickerhamiella pararugosa***	*Saccharomycetales*	*Trichosporon mucoides*	***Cutaneotrichosporon mucoides***	*Trichosporonales*

Continued

Candida kefyr	***Kluyveromyces marxianus***	*Saccharomycetales*	*Trichosporon loubieri*	***Apiotrichum loubieri***	*Trichosporonales*
Candida mesorugosa	***Diutina rugosa***	*Saccharomycetales*	*Trichosporon mycotoxinivorans*	***Apiotrichum mycotoxinivorans***	*Trichosporonales*
Candida catenulata	***Diutina catenulata***	*Saccharomycetales*			

complex, and the Candida himalayana complex (which includes *C. haemulonii s.s.*, *C. haemulonii var. vulnera*, and *C. duobushaemulonii*) [7]. The species within these groups cannot be distinguished based on phenotypic characteristics. Due to significant heterogeneity and divergent evolutionary traits, many species within the genus Candida have been reclassified. For example, phylogenetic analysis of yeasts isolated from flowers reclassified 18 species originally grouped under Candida into *Wickerhamiella* [8]. Similarly, *C. guilliermondii* has been reclassified to *Meyerozyma guilliermondii*, *C. kefyr* to *Kluyveromyces marxianus*, and *C. lusitaniae* to *Clavispora lusitaniae* [9].

C. krusei and *C. glabrata* are closely related to clinical classification changes. *C. krusei* was renamed *Pichia kudriavzevii*, reflecting its natural resistance to fluconazole and fluorocytosine, which aligns more closely with Pichia than with other common pathogenic Candida species [10]. Thus, it may be more appropriate for laboratories to report it under the name *Pichia kudriavzevii*. The Candida glabrata complex, including *C. glabrata S.*, *C. bracarensis*, and *C. nivariensis*, has garnered attention due to the difficulty of predicting therapeutic outcomes based on in vitro drug sensitivity tests, with some strains showing resistance to echinocandins. Phylogenetic analysis indicates that this complex is distantly related to Candida albicans, leading to its classification in the newly named genus *Nakaseomyces*. Although this reclassification has been officially published, it has yet to be updated in various commercial databases. The reclassification of Candida genus members is ongoing. For instance, the complex group including Candida auricularia and Candida shimulon, known for multidrug resistance, may be reclassified into Clavispora [11]. Laboratory personnel should stay informed about these changes for accurate reporting.

4. Trichosporon

Trichosporon is among the largest genera in basidiomycetes, notable for producing articular spores and showing resistance to echinocandins. Apart from *T. asahii* infections, other strains can cause various infections in immunocompromised patients. Studies have identified *T. cutaneum* as a heterogeneous species due to its coenzyme Q molecular type, cell wall structure, G + C content, and serological characteristics. Recent phylogenetic analysis has led to the reclassification of spore fungi into five genera: *Apiotrichum*, *Cutaneotrichosporon*, *Effuseotrichosporon*, *Haglerozyma*, and *Trichosporon* [12]. The primary pathogen

T. asahii, along with rare strains *T. asteroides*, *T. inki*, and *T. ovoides*, remains in the *Trichosporon* genus. Meanwhile, *T. cutaneum* has been moved to the *Cutaneotrichosporon* genus. Additionally, *Cryptococcus curvatus*, often associated with non-new cryptococcosis, has been reclassified as *Cutaneotrichosporon curvatus*.

5. Dermatophyte

Based on morphological, biological characteristics, and phylogenetic analysis, dermatophytes have been reclassified into 9 genera. Most species were placed in the genera Trichophyton and Epidermophyton. Microsporum is now reserved for species related to animals, with only *M. canis* and some closely related species remaining in this genus. Species such as *M. cookei*, *M. gypseum*, and *M. persicolor*, which are clustered within the evolutionary branches of soil-dwelling species and rarely pathogenic to humans, have been reclassified based on phylogenetics of LSU, ITS, 60S L10, and TUB genes into the genera Paraphyton, Nannizzia, and Lophophyton [13].

6. Others

In addition, while the evolutionary analysis of certain fungal genera, like Aspergillus and Fusarium, reveals clear multi-lineages, reclassification remains a distant goal, and the strains lack distinctive clinical phenotypic features. To prevent confusion from changing fragmented names, these strains can temporarily continue to be reported using their current names or as complexes [9] [14].

7. Summary

The new taxonomic classifications and naming of species are aligned with fungal phylogeny. Furthermore, certain novel classifications are more closely related to the clinical characteristics of species, such as pathogenicity and resistance. The renaming of pathogenic fungi necessitates higher standards for medical laboratory personnel. It's essential to deepen our knowledge of fungal naming and taxonomy advancements and report detected pathogenic fungi names as accurately as possible. For instance, when reporting using the new taxonomic name, including previously used species names and providing explanations to clinicians will foster mutual progress between clinicians and laboratory staff.

Conflicts of Interest

The authors declare no conflicts of interest regarding the publication of this paper.

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