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Efficient Utilization of Korean Medical Fungal Pathogen Resource Bank for Clinical Research

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A "pathogen resource" contains information about pathogens (e.g., bacteria, fungi, viruses, and protozoa) and microbial derivatives (e.g., DNA, RNA, plasmid, clone, and cDNA). Pathogen resources are important for their potential use in healthcare research because they contain clinical and epidemiological information that is different from microbial resources. In October 2014, the "Nagoya Protocol" on access and benefit-sharing with the Convention on Biological Diversity was enacted to restrict the movement of transboundary pathogens and protect the natural pathogen resources of each country. On July 2017, the Korean Medical Fungal Pathogen Resource Bank (KMFRB) was established to secure, discover, and develop biological resources focused on medical fungi. KMFRB has since been operating under the National Culture Collection for Pathogens of the National Institute of Health based on the Act No. 13992. This report aims to provide general information regarding KMFRB and suggest efficient ways to utilize human fungal pathogen resources for clinical research.

Key Words: Human pathogen resource, Korean Medical Fungal Pathogen Resource Bank (KMFRB), Medical fungi

INTRODUCTION

Recently, fungal infections have been causing considerable clinical and economic burdens due to the increased number of immunocompromised patients from numerous cases, such as severe cancer, various organ transplants, and bone

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marrow transplantation. Mucosal candidiasis has become the most common fungal infection, and more than 150 million people are suffering from invasive fungal infections[1,2]. In Korea, nearly 2.1% of the total population is affected by fungal infections annually[1]. According to the National Health Insurance data, the prevalence of total fungal infections has increased from 6.9% in 2009 to 7.4% in 2013[3]. The mortality rate from invasive fungal infections is reportedly 22.4%[4]. For patients with hematologic cancer, the mortality rate is 50%, and for patients who received allogeneic hematopoietic stem cell transplantation, the rate is as high as 87%[1,3]. In cases of opportunistic infections, physicians need to accurately identify the human fungal pathogen involved along with the corresponding clinical information[1,3].

In October 2014, the "Nagoya Protocol" on access and benefit-sharing was enacted to restrict the movement of transboundary pathogens and to protect the natural resources of each country. This protocol is intended to implement the Convention on Biological Diversity[6]. However, such protocol is based on the concept of biological diversity, which is relatively difficult to apply for microorganisms. Considering this incongruence, this protocol is an obstacle in conducting microbial research. Countries with appropriate regulations should be able to promote their science and economy through international collaboration[5]. Accurate identification of the human fungal pathogen and its preservation are an important foundation for research in medical and healthcare environments.

However, many practical difficulties are encountered when using human fungal pathogen resources for clinical research. First of all, clinical and epidemiological information of a patient is needed to utilize the clinically relevant fungal pathogen resource for research. Second, compared with bacterial infection, human fungal infection is still poorly explored. Third, filamentous and dimorphic fungi generally depend on morphological identification. Thus, accurate identification of human fungal pathogens has limitations. Fourth, given the lack of awareness on the need for adequate national health insurance coverage for antifungal susceptibility testing[7], performing such test is difficult in routine clinical laboratories.

On June 26 2017, based on Act No. 13992, that is, the "Act on the Promotion of Collection, Management, and Utilization of Pathogen Resources", the National Culture Collection for Pathogens (NCCP) under the National Institute of Health designated a specialized fungal pathogen resource bank focused on medical fungi. Since July 1, 2017, the Korean Medical Fungal Pathogen Resource Bank (KMFRB), which is located at the International St. Mary's Hospital College of Medicine in Catholic Kwandong University, has specialized in collecting, analyzing, and preserving human fungal pathogens in Korea.

The present review aims to introduce general information on KMFRB and to promote efficient utilization of human fungal pathogen resources for clinical research.

SCOPE OF KMFRB

Recently, the importance of biological resources has been recognized, leading to a marketed increase in the establishment and expansion of microbial resource centers. A biological resource center (BRC) is defined as "a center that secures different types of adequate quantities of biological resources and provides the secured resources and bio-related information to researchers and developers"[7]. Culture collection plays a crucial role in long-term stable preservation of these microbes and provides authentic reference materials for scientists and industries. The culture collection centers for fugal resource are the American Type Culture Collection, Fungal Genetics Stock Center in the USA, Centraalbureau voor Schimmelcultures in the Netherlands, Leibniz Institute DSMZ-German Collection of Microorganisms and Cell Cultures, Belgian Coordinated Collections of Microorganisms, National Collection of Pathogenic Fungi in the UK, and Japan Collection of Microorganisms[8]. In Korea, around 20 major BRCs are funded by the national government, and more than 200 hospitals/laboratories function as registration and preservation institutions for the deposit of microbial resources. The institutions that preserve and distribute fungal resources are the Korean Collection for Type Culture, the Korean Culture Center of Microorganism, and the Korean Collection of Medical Fungi (KCMF), but they do not collect clinical information[8,9]. However, the KCMF is no longer in operation for collecting human pathogens. Collecting human fungal pathogen resources with clinical information has been relatively neglected, and the use of these resources for clinical research is still limited to meet the demand for medical research.

Unlike other fungal resources, human fungal pathogen resources are highly important because they include clinical and epidemiological information. The term "pathogen resource" based on Act No. 13992 is defined as any of the following resources with actual or potential value for healthcare study or the healthcare industry:

1. Pathogenic organisms (e.g., bacteria, fungi, viruses, and protozoa) that can cause infectious diseases in humans, and their related information.
2. Pathogen-derived materials (e.g., cytological materials, antigens, and antibodies) that exist naturally, and their related information.

The most important feature of KMFRB is that it collects

and distributes clinically important human fungal pathogen resources with their related clinical information. Since 2008, the NCCP in Korea has been operating three regional pathogen banks located in provinces, namely, Kyungpook, Gyeongsang, and Chongbuk. The need to establish a national collection bank for managing specific pathogens, such as human fungal, bacterial, or viral pathogens, had been gradually increasing[10]. Considering that fungal culture collections preserve a broad diversity of species and strains within a species, they can make discoveries in many other areas as well, such as biotechnology; functional, comparative, and evolution genomics; bioprocesses; and novel products[8,9]. As a result, KMFRB was established as a human fungal resource bank based on the "Act on the Acquisition, Management, and Utilization of Biological Research Resources" (Act No. 14079) and "Act on the Promotion of Collection, Management, and Utilization of Pathogen Resources (Act No. 13992, established on February 3, 2016)".

Major duties in KMFRB are as follows:

1. Collection of various fungal resource strains from clinical patients along with clinical and epidemiological information using a nationwide network
2. Characterization and standardization of human fungal pathogen resources and their information
3. Distribution and utilization for various R and D activities in the healthcare and medical fields

CHARACTERIZATION AND STANDARDIZATION OF HUMAN FUNGAL PATHOGEN RESOURCES

KMFRB has been making an effort to construct highly valuable medical fungal pathogen resources required for research in hospitals, universities, research institutes, and industries. KMFRB has operated a nationwide cooperation system composed of nationally distributed hospitals to continuously collect clinical information in wide-ranging clinical situations. The human fungal pathogen resources are transported from a nationwide network of hospitals to KMFRB and are stored using various preservation methods, such as overlay storage, freeze-drying, and ultra-low-temperature freezing storage[9,11].

Fungi are morphologically, ecologically, metabolically, and phylogenetically diverse. The most advanced approach for an accurate fungal identification is using a molecular technique that considers housekeeping genes in addition to the conventionally used Internal Transcribed Spacer (ITS) region and nuclear ribosomal DNA of small and large subunits[12,13]. For this molecular technique, the polyphasic taxonomic approach is more preferable in laboratory practice than any approach because it simultaneously exploits both conventional and molecular identification techniques. To correctly identify medical fungi, KMFRB employs a polyphasic approach that includes the morphologic identification of macroscopic and microscopic characteristics, DNA sequencing, and matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS) as part of a routine protocol for fungal identification[12]. Nomenclatures of fungi are regulated by the International Code of Nomenclature for algae, fungi, and plants, and the relevant websites for the fungal nomenclature database are found in Mycobank (http://www.mycobank.org) and Index Fungorum (http://www.indexfungorum.org).

Accurate identification through the polyphasic approach is important because human fungal pathogens have different antifungal susceptibility and virulence characteristics. Nowadays, MALDI-TOF MS has been gradually employed in laboratory practice to rapidly identify human fungal pathogens. MALDI designates a matrix that assists in desorption and ionization of highly abundant bacterial or fungal proteins through laser energy[14]. Similar to bacteria, yeast is normally tested by a "direct transfer" to a MALDI-TOF MS target plate, either with or without the addition of an on-plate formic acid treatment. Meanwhile, filamentous fungi need a more formal off-plate protein extraction step[15,16]. Recently, MALDI-TOF MS has rapidly become a standard method for yeast identification, outperforming the historical phenotypic systems. It is also used to identify filamentous and dimorphic fungi. Korea has three commercially available MALDI-TOF MS systems, namely, the Microflex Biotyper (Bruker Daltonics, Bremen, Germany), VITEK MS (bioMérieux, Marcy l'Etoile, France), and MicroIDSys (ASTA Corp, Suwon, Korea). Yeasts and filamentous fungi claimed by FDA have cleared/approved versions of at least one commercial MALDI-TOF MS system[16-18]. In 2017, the CLSI released an official document, that is, CLSI M58, which suggests a method for the identification of cultured microorganisms using MADLI-TOF MS15. In 2018, the CLSI updated the approved document, that is, CLSI MM18, which suggests an interpretive criterion for the identification of bacteria and fungi by DNA target sequencing[19].

The strains selected for their inclusion in the KMFRB were subcultured on Sabouraud dextrose agar for yeast and potato dextrose agar (PDA) for filamentous fungi. A single colony was picked from every culture, and subsequent propagations were kept to a minimum. After DNA extraction, ITS and D1/D2 regions of ribosomal DNA (rDNA) were amplified for yeasts. For filamentous fungi, the ITS region is amplified for species identification, considering that it is a barcoding region of fungi with additional genes (e.g., D1/D2 regions, calmo-

Table 1. Sequencing primers for several fungi of medical importance based on CLSI MM18

Organisms	Appropriateness of ITS	Comments for ITS	Alternative targets	Alternative methods by MALDI-TOF MS
Yeast and yeast-like fungi				
Ascomycetous yeasts, Basidiomycetous yeast	Resolution to genus and species	N/A	D1/D2 region	Aid
Candida spp.	Resolution to genus and species	ITS-2 alone can be sufficient for discriminating many *Candida* spp.	D1/D2 region	Can differentiate *C. auris* from other *Candida* spp.
Galactomyces (Geotrichum) candidum	Resolution to genus, with limited resolution to species	ITS alone is not recommended	N/A	N/A
Saccharomyces spp. *Saprochaete capitata Sporobolomyces* spp.	Resolution to genus and species	N/A	D1/D2 region	N/A
Cryptococcus spp.	Resolution to genus and species	ITS separates *C. neoformans* from *C. gattii* Poor ability to distinguish between *C. neoformans* var. *grubii* and *C. neoformans* var. *neoformans*.	D1/D2 region	Can also differentiate *C. neoformans* and *C. gattii*
Malassezia spp.	Resolution to genus and species	Provides 12% to 20% interspecies variability	D1/D2 region	N/A
Rhodotorula spp.	Resolution to genus and species	N/A	D1/D2 region mitochondrial cytochrome B	N/A
Trichosporon spp.	Resolution to genus and species	For the 6 most common patient species, intraspecies variability of 1% is observed.	D1/D2 region IGS sequencing	N/A
Filamentous fungi				
Aspergillus	Resolution to genus and complex	ITS-2 is highly conserved, ITS-1 is more divergent.	β-tubulin, actin, or calmodulin	May be useful (some molds)
Chrysosporium spp.	Resolution to genus and species	Most of 57 species can be distinguished in 9 clades. Distinction between *Chrysosporium* and *Malbranchea* is unclear.	D1/D2 region	May be useful (some molds)
Dimorphic fungi and other onygenales	Resolution to genus and species	N/A	Partial D1/D2 may be useful	May be useful (some molds)
Filamentous basidiomycetes	Resolution to genus and species.	Taxonomy is still in ompletely resolved.	28s rDNA may provide	May be useful (some molds)
Fusarium spp.	Poor resolution to genus and species	Not a useful target.	EF-lα, 28Sr DNA, *mtSSU*, *RPB2*, tublin	May be useful (some molds)

Table 1. Sequencing primers for several fungi of medical importance based on CLSI MM18 (Continued)

Organisms	Appropriateness of ITS	Comments for ITS	Alternative targets	Alternative methods by MALDI-TOF MS
Purpureocillium lilacinum, *Rasamsonia argillacea* spp., complex *Sarocladium*, and *Acremonium*	Resolution to genus and species	N/A	D1/D2 sequencing may not be sufficiently	May be useful (some molds)
Talaromyces (formerly *Penicillium*) *marneffe*[7]	Resolution to genus and species	*T. marneffei* may share high sequence identity with *Penicillium verrucosum*	Tubulin	May be useful (some molds)
Mucorales	Resolution to genus and usually to species	Good differentiation between genera, with interspecies variation of 0% to 40% and intraspecies differences of 0% to 2%. *Lichtheimia* taxonomy is incompletely resolved.	D1/D2 region may provide resolution to species	May be useful (some molds) *Lichtheimia* taxonomy: MLST or MALDI-TOF MS
Phialemonium spp. *Trichoderma* spp. Entomophthoromycetes	Resolution to genus and (usually) to species	N/A	N/A	May be useful (some molds)
Dermatophytes				
Common dermatophytes	Resolution to genus and species	ITS-1 region has greater value than the ITS-2 region. LR1 and SR6R primers have been recommended.	28S rDNA D2 region (≈312~314 bp)	May be useful (some molds)
Microsporum canis complex	Resolution to genus and species	Minimum interspecies variation ≈ 1.4%	28S rDNA D2 region (≈312 bp)	N/A
Trichophyton rubrum complex	Resolution to genus and species	2 well-separated species complexes, *T. rubrum* and *T. violaceum*	28S rDNA D2 region (≈312 bp)	N/A
Trichophyton mentagrophytes complex (taxonomy is still unresolved)	Resolution to genus and species	ITS does not resolve several closely related species.	28S rDNA D2 region (≈312 bp)	N/A

Abbreviations: bp, base pair(s); DNA, deoxyribonucleic acid; IGS, intergenic spacer; ITS, internal transcribed spacer; EF, elongation factor; MALDI-TOF MS, matrix-assisted laser desorption/ionization time-of-flight mass spectrometry; MLST, multilocus sequence typing; rDNA, ribosomal DNA; N/A, not available

dulin, and ∝-tubulin) for generating multigene phylogeny. Furthermore, a detailed information for fungal identification is described in CLSI MM18, with the guidelines of primer selection, quality controls, and reference databases. Especially, these guidelines contain reporting strategies, such as revising tables, with regard to how the MALDI-TOF MS may be used to complement sequencing for identification. Table 1 summarizes the major target sequence primers for the fungal identification in KMFRB and includes information about the alternative method MALDI-TOF MS[19].

Considering the increasing number of invasive fungal infections and the expanded use of new and established antifungal agents, antifungal drug resistance is recognized as an important clinical problem[20]. Susceptibility to antifungal agents varies depending on the species of fungi. In addition, sensitivity varies depending on whether the fungi are in yeast or mold form. Therefore, the antifungal susceptibility test is important for selecting an appropriate antifungal drug and detecting developed resistance. Both organizations, namely, the CLSI and the Subcommittee on Antifungal Susceptibility Testing

and European Committee on Antimicrobial Susceptibility Testing Subcommittee on Antifungal Susceptibility Testing (EUCAST-AFST), have generated consensus documents that describe standardized methods for antifungal susceptibility testing[21-27]. These guidelines include the selection of isolated fungal colonies from other microorganisms, the preparation of a standardized inoculum, and the validation of testing procedures. The antifungal susceptibility test plays an increasingly important role in treating a patient with fungal infection and in monitoring the development antifungal resistance in epidemiologic studies[21-27]. Several commercial methods, such as E-test (bioMerieux, Marcy l'Etoile, France), the Sensititre

Table 2. Clinical breakpoints for common *Candida* species using CLSI M60 broth microdilution method

Organisms	Antifungal agent	MIC (μg/mL)			
		Susceptible	Susceptible dose-dependent	Intermediate	Resistant
C. albicans	Anidulafungin	≤0.25	–	0.5	≥1
	Caspofungin	≤0.25	–	0.5	≥1
	Voriconazole	≤0.12	–	0.25~0.5	≥1
	Micafungin	≤0.25	–	0.5	≥1
	Fluconazole	≤2.0	4.0	–	≥8
C. glabrata	Anidulafungin	≤0.12	–	0.25	≥0.5
	Caspofungin	≤0.12	–	0.25	≥0.5
	Micafungin	≤0.06	–	0.12	≥0.25
	Fluconazole	–	≤32	–	≥64
C. guilliermondii	Anidulafungin	≤2	–	4	≥8
	Caspofungin	≤2	–	4	≥8
	Micafungin	≤2	–	4	≥8
C. krusei	Anidulafungin	≤0.25	–	0.5	≥1
	Caspofungin	≤0.25	–	0.5	≥1
	Micafungin	≤0.25	–	0.5	≥1
	Voriconazole	≤0.5	–	1	≥2
	Fluconazole	–	–	–	–
C. parapsilosis	Anidulafungin	≤2	–	4	≥8
	Caspofungin	≤2	–	4	≥8
	Micafungin	≤2	–	4	≥8
	Voriconazole	≤0.12	–	0.25~0.5	≥1
	Fluconazole	≤2	4.0	–	≥8
C. tropicalis	Anidulafungin	≤0.25	–	0.5	≥1
	Caspofungin	≤0.25	–	0.5	≥1
	Micafungin	≤0.25	–	0.5	≥1
	Voriconazole	≤0.12	–	0.25~0.5	≥1
	Fluconazole	≤2.0	4.0	–	≥8

YeastOne colorimetric plate (TREK Diagnostic Systems, Inc., Cleveland, OH), and the VITEK 2 yeast susceptibility test (bioMerieux), are available for the antifungal susceptibility test. For yeast, these methods are reproducible, accurate, and available for the use in clinical laboratories. The CLSI guidelines developed a standardized method for filamentous fungi, including *Aspergillus* spp., *Fusarium* spp., *Paecilomyces* spp., *Scedosporium* spp., *Trichoderma* spp., several dematiaceous (brown-black) molds, and Mucorales[23,24]. Broth microdilution method is generally used for these filamentous fungi based on the CLSI 38 guideline. Filamentous fungi were inoculated on PDA and incubated at 35℃ for 7 days. The fungal spores were suspended in saline buffer with 0.1% Tween 20. Inoculum concentration was adjusted using a spectrophotometer for the final concentration within 0.2×10^4 and 2.5×10^4 CFU/mL. The detailed information for broth microdilution method was described in the CLSI M38 guideline for filamentous fungi and the CLSI M27 guideline for yeast. The updated minimum inhibitory concentration (MIC) breakpoints and *in vitro* antifungal activities in the guidelines are summarized in Tables 2, 3, and 4[21,23-25,28-30]. Currently, KMFRB provides a range of the associated services, including the construction of various antibiograms for antifungal drugs, such as amphotericin B, flucytosine, fluconazole, posaconazole, itraconazole, voriconazole, ketoconazole, anidulafungin, micafungin, casopofungin, and terbinafine.

In KMFRB, human fungal pathogens are collected along with a wide range of information on well-characterized species' identification, and antimicrobial susceptibility data. Clinical and epidemiological information, such as age, sex, admission ward, immunosuppressive drug history, underlying disease, major diagnosis, associated infectious disease, overseas travel experience, and race, are also collected. This information in KMFRB is expected to be valuably used in improving the treatment standard of future infectious diseases, studying antifungal drug resistant mechanism, and developing novel therapeutic agents.

Table 3. *In vitro* antifungal activities of posaconazole, fluconazole, itraconazole, voriconazole, and amphotericin B against all fungi, molds, and yeasts

Organism	Antifungal agent	Number tested	MIC (μg/mL)	
			50%	90%
All fungi	Amphotericin B	16567	1	1
	Itraconazole	18877	0.125	1
	Posaconazole	22850	0.063	1
	Voriconazole	9598	0.031	0.5
	Fluconazole	17884	0.5	128
All molds	Amphotericin B	89	1	2
	Itraconazole	3204	0.5	4
	Posaconazole	4499	0.125	1
	Voriconazole	1.826	0.25	2
	Fluconazole	1779	256	256
All yeasts	Amphotericin B	101	0.12	1
	Itraconazole	15673	0.125	1
	Posaconazole	18351	0.063	1
	Voriconazole	7772	0.031	0.5
	Fluconazole	16105	0.5	16
Dermatophytes	Posaconazole	180	0.031	0.25
	Itraconazole	180	0.063	0.25
	Fluconazole	180	4	64

Table 4. *In vitro* antifungal activities of new antifungal drugs against common onychomycosis-causing fungi

Organism	Antifungal agent	Number tested	MIC (μg/mL)	
			50%	90%
T. rubrum	Efinaconazole	130	0.002	0.008
	Terbinafine		0.008	0.015
	Ciclopirox		0.125	0.25
	Itraconazole		0.03	0.06
	Amorolfine		0.008	0.015
T. mentagrophytes	Efinaconazole	129	0.004	0.015
	Terbinafine		0.008	0.03
	Ciclopirox		0.06	0.25
	Itraconazole		0.06	0.125
	Amorolfine		0.008	0.015
*C. albicans**	Efinaconazole	105	0.001	0.06
	Terbinafine		1	4
	Ciclopirox		0.125	0.25
	Itraconazole		0.008	0.125
	Amorolfine		0.03	0.125

*MIC endpoint determined at 24 h in *Candida albicans*

UTILIZATION OF KMFRB

KMFRB has currently collected over 2800 strains of mold and yeast isolates, with clinical significance and tested for antifungal susceptibility for over 980 strains against major antifungal drugs from 11 laboratories located in 9 cities or provinces. Of them, 600 strains were selected and deposited in the NCCP from 2017 to 2018. The bank includes yeast strains of species from numerous genera, such as *Candida* (including *C. auris*), *Cyberlindnera*, *Saccharomyces*, *Trichosporon*, and *Cryptococcus*. Meanwhile, mold strains included species from several genera, such as *Aspergillus*, *Trichophyton*, *Penicillium*, *Fusarium*, *Microsporum*, *Alternaria*, *Purpureocillium*, *Schizophyllum*, *Byssochlamys*, *Rasamsonia*, *Sporotrix*, *Irpex*, *Paecilomyces*, *Porostereum*, *Trichoderma*, and *Verruconis*. KMFRB contains 321 (53.5%) antifungal drug-resistant strains with low and high levels of resistance determined by the MIC of the following major antifungal drugs for yeast: amphotericin B, flucytosine, fluconazole, posaconazole, itraconazole, voriconazole, anidulafungin, micafungin, and casopofungin for yeasts; for molds, terbinafine, ketoconazole, amphotericin B, flucytosine, fluconazole, posaconazole, itraconazole, voriconazole, anidulafungin, micafungin, and casopofungin were used[21,23-26,28].

The collection of human fungal pathogens includes original mold strains from cutaneous, subcutaneous, and deep-seated human infection; pathogenic yeast strains; and dimorphic fungal pathogen strains. KMFRB has also collected human fungal pathogens with clinical and epidemiological information through general deposit from research communities. General deposit is free of charge, and the deposited isolates are handled in biosafety levels 1 and 2. Isolates must be submitted in pure culture on a slant or any medium that supports the growth of the human fungal pathogen. To protect the depositor's rights and promote the utilization of fungal pathogen resources in the field of medical research and development, both the depositor and KMFRB should settle a material deposit agreement (MDA). The distribution of human fungal pathogen resources preserved in the NCCP can be requested through online sites (http://nccp.cdc.go.kr or http://is.cdc.go.kr).

In clinical research, human fungal pathogen resources in KMFRB are beneficial for research communities. First, common fungal pathogen resources with various geometric distribution could be used in the case studies of fungal infection because

they contain information on the frequency of infections in Korea and epidemiological dynamics. Therefore, human fungal pathogen resources have a significant potential in future infection control studies as well as fungal epidemiological research for the prevention of the spread of antifungal resistance. Second, collecting strains from numerous human specimens would contribute to the development of medically useful antifungal agents, and the data could also be used in industrial research for natural preservatives. Third, the antifungal susceptibility data from numerous fungal species allow the investigation of fungal epidemiology in a medical environment. The data about antifungal susceptibility could be eventually used as a foundation for the development of new antifungal drugs or *in vitro* medical devices. Fourth, the diversity and taxonomy of rare human fungal pathogen strains could serve as a new resource for the research community. Fifth, establishing an online/offline system for collecting, depositing, and distributing human fungal pathogen resources from KMFRB would provide researchers with a useful nationwide network in sharing their discoveries and allow sustained research on human fungal infection. Finally, KMFRB allows the continuous exploration of extreme and unexplored human pathogens, the isolation of new strains and species, and their long-term preservation.

CONCLUSION

KMFRB has collected well-characterized human fungal pathogen resources that contain clinical and epidemiological information. In KMFRB, the polyphasic approach is used as a routine process for the accurate detection of fungi and effective characterization from clinical isolates. In addition, *in vitro* antifungal susceptibility data play an important role in treating a patient with fungal infection by guiding therapeutic decisions and in tracking the development of antifungal resistance in epidemiological study. The collected human fungal pathogen resources will be utilized for a broad spectrum of researches and significantly contribute to not only the advancement of basic and clinical science of medical microbiology but also the development of antifungal agents in the industry.

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CONFLICT OF INTEREST

In relation to this article, we declare that there is no conflict of interest.

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