

A 9-Year Experience of *Aspergillus* Infections from Isfahan, Iran

This article was published in the following Dove Press journal:
Infection and Drug Resistance

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Purpose: Aspergillosis is an important fungal disease affecting millions of individuals worldwide. The genus of *Aspergillus* consist of various complexes, causing a wide spectrum of diseases from superficial infections in immunocompetent hosts to life-threatening disseminated infections among immunocompromised patients. This study aimed to identify *Aspergillus* species by phenotypic (total isolates) and molecular tests (35 isolates), obtained from patients in Isfahan (the third-largest city of Iran) between 2010 and 2018, and determine the susceptibility of 35 clinical isolates to itraconazole (ITR), amphotericin-B (AMB), and voriconazole (VOR).

Patients and Methods: Based on clinical signs, a total of 2385 suspected cases were included in this retrospective study from January 2010 to December 2018. Direct microscopic examination with potassium hydroxide, sabouraud dextrose agar with chloramphenicol, and czapekdox agar media was applied to identify etiologic agents. Thirty-five *Aspergillus* species collected from January 2016 to December 2018 were identified by PCR-sequencing of ITS1-5.8SrDNA-ITS2 region, and their susceptibility to ITR, AMB, and VOR was determined using E-test.

Results: Based on direct microscopy and positive culture, 132 out of 2385 suspected cases had *Aspergillus* infection (5.5%). Fifty-four patients were male, and 78 patients were female. Patients in the age groups of 41–50 and 21–30 years had the highest and lowest frequencies, respectively. *Aspergillus flavus/oryzae* (n=54), *A. fumigatus* (n=24), *A. niger* (n=15), and *A. terreus* (n=12) were the most prevalent *Aspergillus* species, respectively. Among 35 *Aspergillus* species, the MIC ranges of AMB, ITR, and VOR for *A. flavus/oryzae*, *A. niger*, and *A. terreus* were (0.5–4 µg/mL; 0.5–16 µg/mL; 0.25–8 µg/mL), (1 µg/mL, 1 µg/mL, 1 µg/mL), and (4–4 µg/mL, 0.5–1 µg/mL, 0.5–1 µg/mL), respectively.

Conclusion: *Aspergillus* infections have a wide spectrum of clinical manifestations and often occur in immunocompromised patients. Accurate identification at the species level is essential since the emergence of cryptic species is connected to different patterns of AFST that affect patient treatment outcomes. Azole-resistant *Aspergillus* spp. is a global concern, and the detection of the route of resistance is pivotal to prevent and control infection.

Keywords: *Aspergillus*, causative agents, E-test, itraconazole, amphotericin-B, voriconazole

Introduction

Aspergillosis is a wide-spectrum fungal disease affecting millions of people worldwide. It ranges from mycotoxicosis, onychomycosis, and allergic syndromes in immunocompetent hosts to life-threatening invasive or systemic infections among immunosuppressed patients, such as those undergoing a solid organ transplant, hematopoietic stem cell transplant (HSCT), chemotherapy, besides those taking corticosteroids.^{1,2} Approximately 1.6 million people die due to Invasive fungal diseases (IFDs), such as systemic aspergillosis, annually.³ The European Organization for Research and Treatment of Cancer and the Mycoses Study Group Education and

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Research Consortium (EORTC/MSGERC) consensus definitions of “proven,” “probable,” and “possible” IFDs have been updated in 2019.⁴ These classifications have been of great value to researchers, who manage diagnostic tests, perform clinical trials of antifungal agents, and undertake epidemiologic investigations. *Aspergillus* species are ubiquitous saprophytic molds with four subgenera, which are subdivided into several sections.⁵ They can be found in hospital surroundings, such as ventilation equipment, surfaces, water, food, trees, and decaying vegetation. Among the hyaline filamentous fungi, *Aspergillus* is one the most important genus, generating enormous airborne conidia that when inhaled, it could cause nosocomial outbreaks.^{5,6} The genus *Aspergillus* is a large and important genus mainly connected to medical relevance as fungal pathogens (*A. niger*, *A. terreus*, *A. fumigatus*), biotechnologic and industrial applications (*A. oryzae*, *A. niger*), and food spoilage and mycotoxin production (*A. parasiticus*, *A. flavus*). The most routinely occurring human pathogenic *Aspergillus* species is *Aspergillus fumigatus* (67–73%), followed by *A. flavus* (10–16%), *A. niger* (5–9%), *A. terreus* (3–4%), and the others.^{7–9} In clinical mycology laboratories, the identification of *Aspergillus* species relies principally on morphological criteria, including microscopic traits (eg, the shape of conidigenous cells, conidiophore, conidial germination, and mycelial structures) and macroscopic features (eg, color, surface topography, and texture of colonies).⁶ Species identification based on morphological features is controversial, being now challenged versus molecular techniques. Identification of fungal species on the basis of phylogenetic relationships has unveiled “cryptic” species within morphologically indiscernible microorganisms such as in *A. flavus*.¹⁰ Molecular data progressively indicate that some known single “species” of fungi unambiguously consist of disparate species. Further, phylogenetics has uncovered cryptic species in the genus of *Aspergillus* containing *A. flavus*, *A. bombycis*, and *A. niger*.^{10,11} The significance of the cryptic species lies in differences in antifungal susceptibility. In recent years, molecular diagnosis in clinical laboratories has been applied for the precise identification of causal agents.^{12,13} The impressive antifungal treatment has become exclusively significant as the number of immunosuppressed patients has been increased in parallel with life-threatening invasive fungal infections (IFIs). It is indeed challenging to treat fungal infections due to the growing emergence of drug-resistant isolate and also immune system status of patients. Over the last decades, in vitro antifungal susceptibility testing for some antifungal drugs, such as echinocandins and azoles,

have been developed to modify the treatment of aspergillosis.¹⁴ Due to the extensive use of antifungals and emerging azole-resistant *Aspergillus* species, the in vitro susceptibility testing of clinical isolates is essential both for the global surveillance of *Aspergillus* susceptibility to antifungal agents and appropriate treatment of patients.¹⁵ The Clinical and Laboratory Standards Institute (CLSI) has introduced a reference broth microdilution (BMD) method for antifungal susceptibility testing (AFST) of molds; however, this method is labor intensive. Commercialized E-test strips comprising defined gradients of antifungal agents are a more easy and favorable approach for AFST; however, the ability of E-test to detect azole-resistant strains has not yet proven.¹⁶ This retrospective study aims to identify *Aspergillus* clinical isolates obtained from patients referred to mycology reference laboratory in Isfahan (the third-largest city of Iran) by phenotypic (all isolates) and molecular tests (35 isolates), between 2010 and 2018, and determine the susceptibility of 35 clinical isolates to itraconazole (ITR), amphotericin-B (AMB), and voriconazole (VOR).

Patients and Methods

Patients

A total of 2385 suspected cases (1386 males versus 999 females) were included in this retrospective study from January 2010 to December 2018. The study protocol was reviewed and approved by the Ethics Committee of Isfahan University of Medical Sciences (IR.MUI.MED.REC.1398.012). Demographic and clinical data, including age, sex, job, and clinical signs, were documented for each subject. These cases were housekeepers (n=691), farmers (n=471), freelancers (n=382), employees (n=308), students (n=193), unemployed (n=106), retirees (n=98), children (69), and unknown (n=67). Patients who had taken antifungal drugs for the past 7 days were excluded from the study.

Phenotypic Tests

Direct microscopic examination (DME) was performed for each sample using potassium hydroxide (KOH) 10%-20%, according to the type of clinical samples. Sabouraud dextrose agar (SDA) with chloramphenicol (0.04 g/L) and cycloheximide free (Difco, Detroit, MI, USA), together with czapekdox agar (QUELAB, Quebec, Canada) media, were applied for culture. The specimens obtained from superficial lesions and deep tissues were incubated at 30°C and 37°C, respectively, and then were checked for the fungal growth up to 21 days.¹⁷ Morphological

characters for identification of *Aspergillus* species are colony growth rate, sporulation degree, cleistothecia or sclerotia production, colony texture, hypha color pigmentation, and colony reverses.¹⁸ Discriminating features of conidiphore and conidial heads among various *Aspergillus* species are dimension, shape, texture, besides the color of stipes, the shape and size of vesicles, phialides (uniseriate or biseriate), the absence or presence of metulae between phialides and vesicle, conidia formation, and Hülle-cells (if present).

Molecular Species Identification

From January 2016 to December 2018, all clinical isolates (no, 35) were identified using the polymerase chain reaction (PCR)-sequencing technique.

PCR

Genomic DNA from the clinical sample was extracted using phenol/chloroform technique¹⁹ and the amplified ITS1-5.8SrDNA-ITS2 region was sent for sequence analysis. Briefly, PCR mixture, including 2.5 μ L of 10 \times reaction buffer, 1.5 mM MgCl₂, 0.4 mM dNTPs, 1.25 U of Taq polymerase, 30 pmol of ITS1 primer (5'-TCC GTA GGT GAA CCT GCG G-3'), 30 pmol of ITS4 primer (5'-TCC TCC GCT TAT TGA TAT GC-3'), and 3 μ L of extracted DNA, was applied in a final volume of 25 μ L. The PCR cycling conditions were an initial denaturation phase at 94°C for 5 min, followed by 35 cycles of denaturation at 94°C for 30 s, annealing at 55°C for 45 s, extension at 72°C for 1 min, and a final extension phase at 72°C for 7 min. Six microliters of PCR products were loaded on 1.5% agarose gel, stained with 0.5 μ g/mL ethidium bromide, visualized by gel documentation system (UVITEC, UK), and then photographed.

Sequencing

Amplicons were purified with GenCatch™ PCR Cleanup Kit (Epoch Life Science, USA), and cycle sequencing reactions were performed in the forward direction (Bioneer, South Korea). Ultimately, the products were analyzed with Chromas 2.6.6 (<https://technelysium.com.au/wp/chromas/>) and evaluated using NCBI BLAST searches against fungal sequences existing in DNA databases (<http://blast.ncbi.nlm.nih.gov/Blast.cgi>).

Antifungal Susceptibility Testing (AFST)

The antifungal susceptibility of *Aspergillus* species obtained from January 2016 to December 2018 (35

isolates) was determined by using the agar diffusion E-test (bioMérieux, France) with RPMI medium (Sigma Chemical Co., St. Louis, MO, USA), according to the supplier's recommendations. Conidial suspensions were calibrated to an optical density yielded 10⁶ CFU/mL.²⁰ The suspension was applied to spread fungi onto the surface of RPMI 1640 agar supplemented with 2% glucose and morpholinepropanesulfonic acid (MOPS) via direct inoculation with a sterile cotton swab. The minimum inhibitory concentration (MIC) was assessed at 100% inhibition for all antifungal agents, including ITR, AMB, and VOR, after incubation at 35°C for 48 hours. The lowest antifungal concentration was considered, at which the border of the elliptical inhibition separated the scale of the strip.^{21,22}

Data Analysis

The association between the clinical samples type and *Aspergillus* species was analyzed by chi-square (χ^2) and Fisher's exact tests in SPSS version 23. Further, MIC ranges, MIC50, MIC90, and geometric mean (GM) of antifungal agents were calculated for clinical isolates in the section of AFST.

Results

One hundred and thirty-two out of 2385 suspected cases had *Aspergillus* infection (5.5%). Fifty-four patients were male, and 78 patients were female. The age range of the patients was 21–76 years, with the mean age of 51.4 years. Patients in the age groups of 41–50 and 21–30 years had the highest and lowest frequencies, respectively. *Aspergillus flavus/oryzae* (n=54), *A. fumigatus* (n=24), *A. niger* (n=21), *A. terreus* (n=12), *A. nidulans* (n=6), and *A. clavatus* (n=3) were the most prevalent *Aspergillus* species (Table 1). Twelve isolates remained unidentified and reported as *Aspergillus* spp. All sequences related to molecular identified species were deposited in GenBank, and accession numbers were obtained for them (MT582514 and MT584269-MT584302). The most *Aspergillus* species were obtained from bronchoalveolar lavage (BAL) (38.6%), toenail (21.2%), sinus (15.9%), ear (9.1%), fingernail (9.1%), eye (5.3%), and skin (0.7%). Figure 1 shows the frequency of different clinical types of *Aspergillus* infections from 2010 to 2018. According to EORTC/MSGERC criteria, there was no proven invasive aspergillosis; however, based on host factors, clinical features, and mycological evidence, 35 and 38 patients were recorded as probable and possible IFDs, respectively.

Table 1 *Aspergillus* Species Obtained from Different Clinical Samples

<i>Aspergillus</i> spp.	Clinical Symptoms	Male/ Female	Total Number	Identification Methods	Accession Numbers
<i>A. flavus/oryzae</i>	RTI (n=31), Onychomycosis (n=16), Sinusitis (n=5), Keratomycosis (n=2)	13/41	54	Phenotypic (n=22) PCR-sequencing (n=32)	N/A MT584269, MT584271- MT584290, MT584292- MT584302
<i>A. fumigatus</i>	RTI (n=10), Onychomycosis (n=7), Sinusitis (n=5), Otomycosis (n=2)	14/10	24	Phenotypic (n=24)	N/A
<i>A. niger</i>	Otomycosis (n=10), Sinusitis (n=6), Onychomycosis (n=2), Keratomycosis (n=1), RTI (n=1), Skin Lesion (n=1)	11/10	21	Phenotypic (n=20) PCR-sequencing (n=1)	N/A MT584291
<i>A. terreus</i>	Onychomycosis (n=7), RTI (n=4), Keratomycosis (n=1)	3/9	12	Phenotypic (n=10) PCR-sequencing (n=2)	N/A MT584270, MT582514
<i>A. nidulans</i>	Onychomycosis (n=4), RTI (n=1), Keratomycosis (n=1)	4/2	6	Phenotypic (n=6)	N/A
<i>A. clavatus</i>	RTI (n=1), Keratomycosis (n=1), Sinusitis (n=1)	1/2	3	Phenotypic (n=3)	N/A
<i>Aspergillus</i> spp.	Sinusitis (n=4), Onychomycosis (n=4), RTI (n=3), Keratomycosis (n=1)	8/4	12	Phenotypic (n=12)	N/A

Abbreviation: RTI, respiratory tract infection.

Statistical Analysis

Fisher's exact test showed that the association between the clinical samples type and *Aspergillus* species was not statistically significant ($p = 0.86$). The MIC₅₀ and MIC₉₀ values were calculated as the minimum concentrations of agents being able to inhibit 50-90% of the clinical isolates, respectively. The high and low off-scale MICs were included in the analysis by conversion to the next higher and lower antifungal agent concentrations.

AFST

The MIC ranges of antifungal agents were as follows: *A. flavus*: (AMB, 0.5–4 µg/mL), (ITR, 0.5–16 µg/mL), (VOR, 0.25–8 µg/mL); *A. niger*: (AMB, 1 µg/mL), (ITR, 1 µg/mL), (VOR, 1 µg/mL); *A. terreus*: (AMB, 4–4 µg/mL), (ITR, 0.5–1 µg/mL), (VOR, 0.5–1 µg/mL). Figure 2 shows an amphotericin B E-test strip on RPMI medium, demonstrating an MIC of 1 µg/mL in a susceptible *A. flavus/oryzae*. MIC ranges, MIC₅₀ (concentrations inhibiting ≥50% of growth), MIC₉₀ (concentrations inhibiting ≥90% of growth), and GM values for the 35 clinical isolates are presented in Table 2.

Discussion

Aspergillus species, as the most important opportunistic fungi, extensively are found in nature. They can cause a wide

spectrum of diseases in individuals with compromised immune systems.²³ Changes in epidemiological aspects have occurred due to the increase in the number of immunosuppressed patients, advances in recognition, speciation of clinical and environmental isolates, and extensive use of broad-spectrum antifungal drugs.^{7,24} The genus *Aspergillus* comprises various complexes, such as *A. flavus* complex, *A. fumigatus* complex, *A. nidulans* complex, *A. terreus* complex, and *A. ustus* complex. After *A. fumigatus* complex, *A. flavus* is considered as the second most prevalent *Aspergillus* species in medical laboratories and hospitals of Europe,²⁵ the United States,²⁶ Brazil²⁷ and arid regions of the Middle East.²⁸ *A. niger* and *A. terreus* are ranked second in Korea, and Austria, respectively.²⁹ Contrary to these findings, *A. flavus* is the most common *Aspergillus* species in the present investigation. Often, people are infected with this fungal disease by daily inhalation of hundreds of spores, as well as colonization of a fungus in the respiratory tract if the immune system is suppressed. In line with this concept, the most *Aspergillus* species were obtained from BAL samples in the present study. The fungal cell wall component galactomannans (GM) are polysaccharides, including a mannose backbone with galactose as side groups released during the hyphal growth.³⁰ It is a biologic marker and used as a noninvasive method for detecting aspergillosis in blood or BAL. One of the

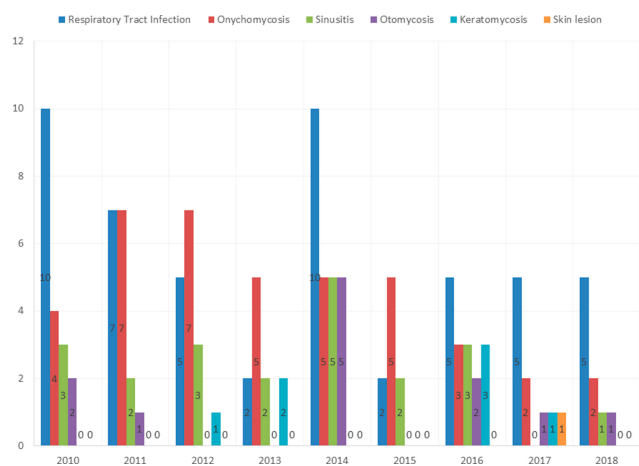


Figure 1 The frequency of different clinical types of *Aspergillus* infections from 2010 to 2018.

major limitations of this study was the lack of information about this test among patients. Some investigations reported that *A. fumigatus* is more common in the Western countries, whereas *A. flavus* is more prevalent in the Asia and Middle East.^{31,32} In the present work, 33.3% of cases with onychomycosis were recognized; while, Veer et al,³³ and Wijesuriya et al,³⁴ reported 48.885% of onychomycosis from India and Sri Lanka, respectively. Naghibzadeh et al,³⁵ detected 1.2% of *Aspergillus* sinusitis in Tehran, Iran, from 2007 to 2009, whereas 15.9% of *Aspergillus* sinusitis was reported in the present research. This significant difference could be related to the climatic conditions of the two regions or the duration of investigations. Ebadollahi-Natanzi et al,³⁶ detected 32 patients (26.4%) with fungal keratitis due to the *Aspergillus* spp. from Tehran, Iran, between 2011 and 2013,



Figure 2 Amphotericin B E-test strip on RPMI medium showed a MIC of 1 µg/mL (susceptible to amphotericin B).

while we isolated only 7 *Aspergillus* spp. (5.3%) from keratomycosis. Otitis (swimmer's ear) is an acute or chronic superficial fungal infection of the external auditory canal, occasionally involving middle parts of the ears. Gharaghani et al,³⁷ reported 5.7% to 81% of otitis (with a mean value of 51.3%) in different areas of Iran. The incidence of otitis externa in our study was 9.1%. Determination of antifungal susceptibility patterns for clinical strains is crucial step to develop an effective strategy for infection management. The first choice for treatment of human Aspergillosis is azole drugs, such as VOR, ITR, and isavuconazole (ICZ).³⁸ In the present study, 35 *Aspergillus* spp. containing *A. flavus/oryzae*, *A. terreus*, and *A. niger* were tested using E-test against three antifungal drugs, including ITR, VOR, and AMB. Some investigations have compared the CLSI BMD methods with E-test for susceptibility testing of molds; however, they have been confined to selected antifungal agents or a limited subcategory of fungal species.³⁹⁻⁴¹ Lamoth et al showed good agreement between the two methods, depending on the fungus and antifungal tested.¹⁶ Nevertheless, some *Aspergillus* species, such as *A. terreus*, demonstrated higher MICs in the E-test method, possibly reflecting the innate resistance of these species to amphotericin B.⁴² Triazole MIC values for *Aspergillus* species are usually lower with the E-test compared to the CLSI BMD method; thus, the use of the E-test strip for antifungal susceptibility testing of posaconazole among *Aspergillus* species are not recommended.⁴³ The E-test reveals to be comparable to the CLSI BMD method for in vitro antifungal testing of voriconazole among *Aspergillus* species, and it can detect triazole-resistant isolates.¹⁶ Another limitation of our research was the lack of AFST data for other species, such as *fumigatus*, *nidulans*, and *clavatus*. Resistance to azole drugs would develop in response to the continued exposure of fungus to azolic agents and transmission of gene mutations to the new conidia.⁴⁴ In the absence of clinical breakpoints, the concept of epidemiological cut-off values (ECV) has been described by CLSI. The MIC separates wild and non-wild strains, considering the latter as those with possible mutational or acquired resistance based on their phenotypic MIC values. The ECV can predict possible resistance to an antifungal drug, for which there is not adequate information to establish breakpoints.^{45,46} According to CLSI M59 document,⁴⁶ ECV of AMB, ITR, and VOR for *A. flavus/oryzae*, *A. terreus*, and *A. niger* is (4, 1, 2 µg/mL), (4, 2, 2 µg/mL), and (2, 4, 2 µg/mL), respectively. Although Alborzi et al,⁴⁷ showed that 36.1% of *Aspergillus* species were resistant to AMB, in the present study, it was seen in 12.5% of clinical isolates. Johnson et al,⁴⁸ reported that clinical

Table 2 MIC Range, MIC₅₀, MIC₉₀, Geometric Mean (GM) and MIC Values Distribution of the Three Antifungals

Aspergillus Species (No.)	MIC Range (µg/mL)	MIC ₅₀ (µg/mL)	MIC ₉₀ (µg/mL)	GM	MIC Values (µg/mL)						
					0.25	0.5	1	2	4	8	16
<i>A. flavus/oryzae</i> (32)	AMB (0.5–4)	1	4	0.94	0	15	9	4	4	0	0
	ITR (0.5–16)	2	4	1.57	0	7	7	12	3	2	1
	VOR (0.25–8)	0.5	2	0.82	5	12	6	6	2	1	0
<i>A. terreus</i> (2)	AMB (4–4)	N/A	N/A	4	0	0	0	0	2	0	0
	ITR (0.5–1)			0.7	0	1	1	0	0	0	0
	VOR (0.5–1)			0.7	0	1	1	0	0	0	0
<i>A. niger</i> (1)	AMB (1)	N/A	N/A	N/A	0	0	1	0	0	0	0
	ITR (1)				0	0	1	0	0	0	0
	VOR (1)				0	0	1	0	0	0	0

outcomes could not be totally predictable for AMB due to the host conditions, such as cellular immune functions, antibody titers, underlying disease, and pharmacokinetic properties, playing pivotal roles to determine treatment outcomes. Considering intrinsic resistance or variable susceptibility of *flavus/oryzae* and *A. terreus* to AMB,^{38,49} treatment with this antifungal may not be a wise choice. Many investigations have reported resistance to azole agents, especially ITC, with high rates showed in European countries, such as the United Kingdom and the Netherlands, where azole-resistance rates reached 38%.^{50,51} This high rate of resistance to azoles may be attributed to cross-resistance with agricultural triazoles and long-term azole therapy among patients with chronic aspergillosis.⁵² In the present study, a 78% rate of ITC resistance was shown in *A. flavus/oryzae* isolates, implicating wide use of triazoles for the aspergillus infection treatment and azole fungicides for Iranian agriculture.^{53,54} Isolates with decreased susceptibility to ITC are regularly cross-resistant to other triazoles, such as VOR.⁵⁵ In agreement, 28% of *A. flavus/oryzae* isolates were resistant to VOR in the current investigation. Azoles and 14 α -demethylase inhibitors (DMIs) are abundantly used for material preservation and crop protection against phytopathogenic molds.^{56,57} It is likely that breathing in the resistant spores of these environmental strains leads to clinical infections.⁵⁶ The relation between the use of the triazoles and cross-resistance to medical triazoles, such as voriconazole, has major signals for the evaluation of health risks associated with the use of DMIs; however, further studies are needed to understand the environmental route of resistance development. The role of mutations in *cyp51A* and *cyp51C* genes, besides overexpression of ATP-binding cassette (ABC) transporter genes (*atrF*, *mdr1*, *mdr2*, and *mdr4*), has been

shown among VOR-resistant of *A. flavus* earlier.^{58–60} Our study was limited by the fact that we were unable to detect resistance mechanism analysis for *A. flavus/oryzae* with high voriconazole and itraconazole MICs.

Conclusion

Aspergillus infections have a broad spectrum of clinical manifestations and often occur in immunocompromised patients. Since people with immunodeficiency disorders are on the rise, opportunistic fungi have been noticed as one of the main concerns of morbidity and mortality in such patients. Accurate identification at the species level is essential as the emergence of cryptic species is connected to specific patterns of AFST that affect patient treatment outcomes. In the present study, 12.5%, 78%, and 28% of *A. flavus/oryzae* isolates were resistant to AMB, ITR, and VOR, respectively. Azole-resistant *Aspergillus* spp. is a global issue. Understanding the route of resistance is essential to perform executable prevention and control measures. When the prevalence of environmental resistant isolates to azoles is above 10%, empirical therapy should not include voriconazole monotherapy.^{61,62}

Abbreviations

IFDs, invasive fungal diseases; EORTC/MSGERC, The European Organization for Research and Treatment of Cancer and the Mycoses Study Group Education and Research Consortium; HSCT, haematopoietic stem cell transplant; DME, direct microscopic examination; KOH, potassium hydroxide; SDA, sabouraud dextrose agar; PCR, polymerase chain reaction; MOPS, morpholinepropanesulfonic acid; ITR, itraconazole, AMB, amphotericin

B; VOR, voriconazole; AFST, antifungal susceptibility testing; GM, galactomannan; ICZ, isavuconazole; CLSI, Clinical and Laboratory Standards Institute; DMIs, demethylase inhibitors; ABC, ATP-binding cassette.

Data Availability

All sequences were deposited in the GenBank database, and accession numbers were obtained for them, and inserted into the manuscript (MT582514, and MT584269 – MT584302).

Ethics Approval and Informed Consent

Participants gave their consent for publication of the study. This investigation was approved by the Ethics Committee of Isfahan University of Medical Sciences. The code number is IR.MUI.MED.REC.1398.012.

Consent for Publication

All participants (patients) gave their consent for publication of the present investigation.

Informed Consent

Informed consent from all patients and parents/Legally authorized representatives of minor patients was obtained at the pint of data collection.

Acknowledgments

The authors appreciate Shefa Laboratory personnel for data collection of patients, and also we are grateful to Dr. Hamid Badali for his support regarding antifungal susceptibility testing.

Author Contributions

All authors contributed to data analysis, drafting or revising the article, gave final approval of the version to be published, and agree to be accountable for all aspects of the work.

Funding

This study was supported by Isfahan University of Medical Sciences, Isfahan, Iran, and number: 297163. The role of the funding body was in the design of the investigation.

Disclosure

The authors declare that there is no conflict of interest.

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