Molecular identification and in-vitro antifungal susceptibility testing of Candida species isolated from patients with onychomycosis

Pakshir K1*, Zomorodian K1, Zakaei A2, Motamedi M2, Rahimi Ghiasi M2, Karamitalab M2

1 Basic Sciences in Infectious Diseases Research Center, Department of Parasitology and Mycology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran
2 Department of Parasitology and Mycology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran

*Corresponding author: Keyvan Pakshir, Basic Sciences in Infectious Diseases Research Center, Department of Parasitology and Mycology, School of Medicine, Shiraz University of Medical Sciences, Shiraz, Iran. Email: pakshir@sums.ac.ir

(Received: 25 November 2015; Revised: 12 December 2015; Accepted: 27 December 2015)

Abstract

Background and Purpose: Candida species are the most opportunistic fungi affecting the nails and resulting in onychomycosis. In this study, we identified and evaluated in-vitro susceptibility of the recovered isolates against fluconazole (FLC), voriconazole (VRC), and clotrimazole (CLT) using the Clinical and Laboratory Standards Institute (CLSI) M27-A3 document.

Materials and Methods: From patients with either clinically or mycologically proven onychomycosis, 97 isolates comprising of seven Candida species were isolated, which were identified by both conventional and molecular techniques such as polymerase chain reaction-restriction fragment length polymorphism. In addition, Candida dubliniensis was confirmed by restriction endonuclease analysis. Antifungal susceptibility of each isolate against the three azoles applied in this study was determined using the CLSI microdilution reference method M27-A3.

Results: Candida parapsilosis (C. parapsilosis) was the most frequently isolated species (n=44), followed by C. albicans (n=23), C. tropicalis (n=13), C. glabrata (n=7), C. krusei (n=6), C. guilliermondii (n=3), and C. dubliniensis (n=1). All the isolates were susceptible to CLT. VRC had lower minimum inhibitory concentration (MIC) values for the isolates compared to FLC. Geometric mean MIC values of VRC, FLC, and CLT for C. parapsilosis isolates were 0.07 μg/ml, 0.8 μg/ml, and 0.35 μg/ml, respectively. Collectively, all species exhibited greater susceptibility to VRC in comparison to C. albicans (P<0.001).

Conclusion: This study showed that non-albicans Candida species were the most common etiologic agents of non-dermatophyte onychomycosis. The major antifungal agents used in clinics to empirically treat yeast onychomycosis are FLC and CLT. Our data suggested that CLT is a better choice for the treatment of Candida onychomycosis, especially in drug resistant cases.

Keywords: Candida albicans, Candidiasis/microbiology, Candidiasis/pathogenicity, Clotrimazole, Fluconazole, Onychomycosis, Voriconazole

How to cite this paper:

Introduction

The genus Candida includes approximately 200 different species, of which only a few were adequately documented as human opportunistic pathogens. Candida infections, which may be superficial or invasive (or a combination of both), usually occur in immunocompromised patients [1]. Superficial infections that can be managed successfully with topical antifungal agents usually involve the skin, nails, or mucous membranes [2].

The azoles are the most effective antifungal agents for the management of yeast infections, which inhibit lanosterol biosynthesis from disrupting the function of the yeast cell membrane. They include imidazoles (e.g., miconazole, econazole, ketoconazole, and clotrimazole [CLT]) and triazoles (e.g., fluconazole [FLC], itraconazole, and voriconazole [VRC]), which were used successfully to treat yeast infections [2, 3].

Even though there may be some controversy regarding the correlation between in-vitro susceptibility testing data and clinical outcomes, in-vitro antifungal data can be beneficial for predicting potential outcomes and drawbacks such as resistance [3]. The
Identification and antifungal susceptibility of Candida species

CLSInternational microdilution reference method is a testing platform used across the globe to obtain standardized results that can be compared with other studies. 

Candida onychomycosis should be distinguished from onychomycoses caused by either dermatophytes or a number of different filamentous fungi [4-9], as choosing the appropriate treatment without culture can result in non-responsive cases. Owing to the fact that onychomycoses may require months to resolve, providing the appropriate treatment during the early treatment phases seems to be imperative. Several groundbreaking studies, performed in Iran, identified the etiologic agents of onychomycosis, and then based upon in-vitro susceptibility studies evaluated the potential outcomes using different antifungal agents [9-13].

With the advent of molecular tools allowing for rapid genomic studies, determination of phylogenetic relationships as a way to identify yeast taxa was accentuated. This approach has resulted in several yeast taxa being redefined and reclassified. The separation of C. dubliniensis from C. albicans based on differences in their phylogeny is but an example. Owing to the revision of many yeast species, especially in the Candida genus, the application of molecular methods has become mandatory for their accurate identification. Among the more novel molecular tools, polymerase chain reaction-restriction fragment length polymorphism (PCR-RFLP) is one of the most accurate methods for the identification of Candida species [14, 15].

Material and Methods

Isolates

Patients with clinically or mycologically confirmed onychomycosis were enrolled in this study. A total of 97 Candida isolates were isolated from fingernail specimens, collected using the standard aseptic techniques, and were placed on Sabouraud dextrose agar (Merck, Germany) and incubated at 30°C. The yeast colonies were purified using the standard methods to insure only one yeast, which is devoid of potential contaminating bacteria, was present.

The new subcultures were transferred to Sabouraud dextrose agar after which small portions of the purified colonies were added to microtubes containing distilled water and were maintained at -20°C. For the evaluation of conventional and molecular methods, both were applied for the identification of each isolate.

The conventional method

The isolates were initially identified according to the results of chlamydoconidia formation in Corn Meal Agar with Tween 80 (Merck, Germany) incubated at 30°C, germ tube formation in fresh serum incubated for up to three hours at 37°C, and colony color on the chromogenic medium of CHROMagar Candida (Biomerieux, France) incubated at 30°C. CHROMagar is used for presumptive identification of some yeasts and differentiation of C. albicans, C. tropicalis, and C. krusei.

The molecular method (PCR-RFLP)

We used a PCR-RFLP technique as described before [14, 15]. DNA extraction was performed using phenol-chloroform method [16]. A loop full of fresh yeast was harvested and suspended in 300 μl of lysis buffer (10 mM Tris, 1 mM ethylenediaminetetraacetic acid [EDTA] pH 8, 1% sodium dodecyl sulfate [SDS], 100 mM NaCl, and 2% Triton X-100) with phenol-chloroform and glass beads, and then was vortexed. Total DNA was precipitated with 2-propanol, washed with 70% ethanol, air-dried, and suspended in 50 μl of Tris–EDTA buffer (10 mM Tris, 1 mM EDTA), and was kept at -20°C before use.

Internal transcribe spacer (ITS) region of ITS1-5.8S-ITS2 segment of the ribosomal DNA gene was amplified [14]. A set of universal primers (ITS1, 5-TCCGTAGGGTGAACCTGCGG and ITS4, 5-TCCTCCGCTATTGATATGC) (Metabion International, Martinsried, Germany) were employed for amplification. PCR amplification was carried out in a final volume of 50 μl. Each reaction contained 1 μl of template DNA, 0.5 μM of each primer, and 0.20 mM of each deoxynucleoside triphosphate (dNTP), 5 μl of 10× PCR buffer, and 1.25 U of Taq polymerase (Roche Molecular Biochemicals, Mannheim,
An initial denaturation step at 94°C for five minutes was followed by 30 cycles of denaturation at 94°C for 30 seconds, annealing at 56°C for 45 seconds, and extended at 72°C for one minute, with a final extension step at 72°C for seven minutes. The PCR product was electrophoresed on 1.2% agarose gel and stained with ethidium bromide.

For differentiation between Candida species, amplified PCR products were digested with MspI restriction endonuclease to achieve the best species-specific pattern, and additional enzyme of BlnI (AvrII) was applied to differentiate C. dubliniensis from C. albicans. Restriction fragments were separated by 1.8% agarose gel electrophoresis in Tris-Borate-EDTA (TBE) buffer for approximately one hour at 100 V and visualized by staining with ethidium bromide.

Antifungal susceptibility testing

Antifungal susceptibility testing of FLC, VRC, and CLT was performed according to the Clinical and Laboratory Standards Institute (CLSI) using micro-dilution method with minor modification. RPMI 1640 (with L-glutamine and phenol red, without bicarbonate; Sigma, USA) was prepared and buffered at pH 7.0 with 0.165 mol of 3-N-morpholino propanesulfonic acid (MOPS) (Sigma-Aldrich, Germany).

Serial dilutions of the drugs were prepared in 96-well microtiter trays using RPMI 1640 media buffered with MOPS (Sigma, St. Louis, USA). Stock inocula were prepared by suspending three colonies of each isolate in 5 ml sterile 0.85% NaCl and adjusting the turbidity to a 0.5 McFarland standard at 530 nm wavelength to achieve 1–5×10⁶ cells/ml density.

Working suspensions were prepared by making a 1/1000 dilution with RPMI of the stock suspension for each Candida species. The trays were incubated at 35°C for 24-48 hours in humid atmosphere. The growth in each well was compared with control wells. Minimum inhibitory concentrations (MICs) were visually determined and defined as the lowest concentration of the drugs that produced no visible growth. Each experiment was performed in duplicate.

Candida albicans (ATCC10261) and C. parapsilosis (ATCC 4344) were used as controls. For FLC, MIC for susceptible, susceptible dose dependent, and resistant were ≤8 μg/ml, 16-32 μg/ml, and ≥64 μg/ml, respectively. For VRC, MIC for susceptible, susceptible dose dependent, and resistant were ≤1 μg/ml, 2 μg/ml, and ≥4 μg/ml, respectively.

Statistical analysis

To analyze the data, Chi-square test was performed, using SPSS version 15. Geometric mean of MICs was calculated, as well.

Results

The number of Candida species, as identified by the conventional and molecular methods, is summarized in Table 1. PCR-RFLP using MspI restriction endonuclease enzyme was able to distinguish seven Candida species as shown in Table 2 and Figure 1.

<table>
<thead>
<tr>
<th>Candida species</th>
<th>Germ tube</th>
<th>Chlamidoconidia</th>
<th>Colony color on CHROMagar</th>
<th>Polymerase chain reaction-restriction fragment length polymorphism</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. parapsilosis (44)</td>
<td>1</td>
<td>0</td>
<td>White-pink (38)</td>
<td>44</td>
</tr>
<tr>
<td>C. albicans (23)</td>
<td>21</td>
<td>22</td>
<td>Green (23)</td>
<td>23</td>
</tr>
<tr>
<td>C. tropicalis (13)</td>
<td>4</td>
<td>1</td>
<td>Blue (13)</td>
<td>13</td>
</tr>
<tr>
<td>C. glabrata (7)</td>
<td>0</td>
<td>0</td>
<td>Pink-purple (5)</td>
<td>7</td>
</tr>
<tr>
<td>C. krusei (6)</td>
<td>0</td>
<td>0</td>
<td>Pink-purple (6)</td>
<td>6</td>
</tr>
<tr>
<td>C. guilliermondii (3)</td>
<td>0</td>
<td>0</td>
<td>Blue-purple (3)</td>
<td>3</td>
</tr>
<tr>
<td>C. dubliniensis</td>
<td>1</td>
<td>1</td>
<td>Green (1)</td>
<td>1</td>
</tr>
<tr>
<td>Total</td>
<td></td>
<td></td>
<td></td>
<td>97</td>
</tr>
</tbody>
</table>
Identification and antifungal susceptibility of Candida species

C. parapsilosis was the most predominant species among the isolates (45.3%), whereas C. albicans was the second (23.7%) most common taxon. When B1nI (AvrII) restriction endonuclease enzyme was employed, one of the C. albicans isolates was re-identified as C. dubliniensis.

The results of antifungal activity of VRC, FLC, and CLT against the Candida species are presented in Table 3. CLT had potent activity against the isolates tested with MIC ranging from 0.03 µg/ml to 16 µg/ml. MIC50 and MIC90 of the isolates for CLT, VRC, and FLC were 0.5 mg/L and 0.06 mg/L, 0.5 mg/L and 5.6mg/L , as well as 8 mg/L and 16 mg/L, respectively.

Geometric mean MICs for CLT were 0.25 µg/ml for C. albicans, 0.35 µg/ml for C. parapsilosis, 1.8 µg/ml for C. tropicalis, 2 µg/ml for C. glabrata, 0.35 µg/ml for C. krusei, 0.14 µg/ml for C. guilliermondii, and 2 µg/ml for C. dubliniensis.

Furthermore, 19.5% and 7.2% of the isolates had low susceptibility to VRC and FLC, respectively. VRC was active against 79.3% of the isolates with geometric mean MIC values of 0.57 µg/ml for C. albicans, 0.07 µg/ml for C. parapsilosis, 1.06 µg/ml for C. tropicalis, 0.14 µg/ml for C. glabrata, 0.06 µg/ml for C. krusei, 0.5 µg/ml for C. guilliermondii, and 0.5 µg/ml for C. dubliniensis.

FLC geometric mean MIC values for Candida species are exhibited in Table 3. FLC was more effective compared to VRC (P≤0.001). There was a significant difference between C. albicans and non-C. albicans regarding sensitivity to VRC (P=0.001).

Table 2. Frequency of Candida species isolated from onychomycosis

<table>
<thead>
<tr>
<th>Candida species</th>
<th>No.</th>
<th>Percent</th>
</tr>
</thead>
<tbody>
<tr>
<td>C. parapsilosis</td>
<td>44</td>
<td>45.3</td>
</tr>
<tr>
<td>C. albicans</td>
<td>23</td>
<td>23.7</td>
</tr>
<tr>
<td>C. tropicalis</td>
<td>13</td>
<td>13.4</td>
</tr>
<tr>
<td>C. glabrata</td>
<td>7</td>
<td>7.2</td>
</tr>
<tr>
<td>C. krusei</td>
<td>6</td>
<td>6.1</td>
</tr>
<tr>
<td>C. guilliermondii</td>
<td>3</td>
<td>3.09</td>
</tr>
<tr>
<td>C. dubliniensis</td>
<td>1</td>
<td>1.03</td>
</tr>
<tr>
<td>Total</td>
<td>97</td>
<td>100</td>
</tr>
</tbody>
</table>

Figure 1. Polymerase chain reaction- restriction fragment length polymorphism profile of some isolates: C. parapsilosis (up 1-3, 6 and down 2, 5-9), C. albicans (up 4, 9 and down 3, 4, 10, 12, 13), C.tropicalis (up 5, 7) and C. krusei (up 8 and down 11)

Table 3. Antifungal susceptibility of Candida species isolated from onychomycosis, S (Susceptible), SDD (Susceptible Dose Dependent), and R (resistant), GM (Geometric mean)

<table>
<thead>
<tr>
<th>Species</th>
<th>Voriconazole</th>
<th>Fluconazole</th>
<th>Clotrimazole</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td>S</td>
<td>SDD</td>
<td>R</td>
</tr>
<tr>
<td>C. parapsilosis</td>
<td>42</td>
<td>0</td>
<td>2</td>
</tr>
<tr>
<td>C. albicans</td>
<td>13</td>
<td>0</td>
<td>10</td>
</tr>
<tr>
<td>C. tropicalis</td>
<td>6</td>
<td>0</td>
<td>7</td>
</tr>
<tr>
<td>C. glabrata</td>
<td>3</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>C. krusei</td>
<td>6</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>C. guilliermondii</td>
<td>7</td>
<td>0</td>
<td>0</td>
</tr>
<tr>
<td>C. dubliniensis</td>
<td>0</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>Total (%)</td>
<td>77 (79.3%)</td>
<td>1 (1%)</td>
<td>19 (19.5%)</td>
</tr>
</tbody>
</table>
Discussion

Candida species are the principal non-dermatophytic etiologic agents of onychomycosis in patients living in Shiraz, Iran. Identification of Candida spp. isolated from patients with onychomycosis using molecular tools was an important contribution to understanding their epidemiology in the city of Shiraz, southern Iran. PCR-RFLP is an ideal method for distinguishing Candida species from each other, especially C. dubliniensis [14, 15].

Using B1nl restriction enzymes, we were able to distinguish C. dubliniensis from among the C. albicans isolates. This is the first instance in which C. dubliniensis was demonstrated to be an etiologic agent of onychomycosis in Iran. Typical for this taxon and C. albicans, it produced germ tubes and chlamydoconidia, and developed green colored colonies on CHROMagar. C. dubliniensis was sensitive to CLT and VRC at 2 μg/ml and 0.5 μg/ml concentrations, respectively, but had a low MIC of 16 μg/ml to FLU.

Zomorodian et al. [19] recovered 16 isolates of C. dubliniensis from denture-related stomatitis from Iranian patients, whereas Ghahri et al. [20] used PCR-RFLP with MboI endonuclease restriction enzyme and could not distinguish C. dubliniensis from among 67 isolates of C. albicans recovered from onychomycosis in Tehran, Iran. This discrepancy in results might be pertinent to the type of restricted enzyme they used.

In the current study, C. parapsilosis was the most common isolate recovered from our patients. Our results are not congruent with the findings of other Iranian studies [21, 22]. Hashemi et al. identified C. albicans (41%) as the main etiologic agent of onychomycosis in Tehran, Iran [10]. Chadeganipur et al. reported C. albicans as the most prevalent yeast causing onychomycosis in Isfahan, Iran [11].

Moreover, Farasat et al., using an ITS sequencing method, identified C. pulcherrima as the causative agent of nail lesions [12]. Our findings are in line with those of the study by Segal et al. [23] and other studies performed in Spain and Hong Kong, which reported C. parapsilosis as the predominant species [24, 25]. The inconsistency among the results may be associated with the use of different identification tools and demographic groups as well as the fact that C. parapsilosis is a complex of closely related species, which require further studies. We purposefully chose our identification methods to avoid such problems.

The CLSI broth microdilution method is recommended for evaluation of antifungal activity of Candida species [17, 18]. In our former study, we assessed antifungal activity among clinical Candida isolates and reported 96.6% susceptibility to FLC [19]. Khosravi et al. in a study conducted in Tehran, Iran, reported that 85.7% of onychomycosis isolates belonged to Candida species and that the isolates were susceptible to FLC [13].

In our study, MICs of non-albicans isolates were significantly lower than the C. albicans isolates (P=0.001). All the isolates had diverse geometric mean MICs to CLT; 19.5% of the isolates were resistant to VRC, and C. albicans were the most resistant isolates. VRC was employed for the treatment of disseminated candidiasis; however, it is not commonly used for the treatment of onychomycosis [26-34]. In Iran, VRC is used for highly resistant cases when the imidazoles are ineffective due to resistance or possible non-compliance. FLC is the most common drug of choice, used for the treatment of onychomycosis, primarily in combination with other antifungal agents [3, 26]. In our study, 87.6% of the isolates were sensitive to FLC; thus, it could be the best choice for combination therapy with CLT.

Conclusion

In summary, this study showed that PCR-RFLP is an efficient method for identification of Candida species and that FLC is more effective than the other agents tested against the isolates. We were unable to correlate in vitro antifungal data to in vivo response according to 90/60 rule [32] and it was not in the scope of this study to attempt to correlate in-vitro antifungal data to in-vivo response. The data can aid physicians to choose an effective potential drug for treating onychomycosis patients.
Acknowledgments
This study was extracted from an MD thesis by Alireza Zakaei and was funded by Deputy of Research and Technology of Shiraz University of Medical Sciences, Shiraz, Iran (Grant No. 6000). Our special thanks go to professor Emeritus Michael R. McGinnis from Medical University of Texas for his editorial comments.

Authors’ Contributions
K. Pakshir contributed to study concept and design, drafted and revised the manuscript, and analyzed and interpreted the data. K. Zomorodian contributed to study concept and design, drafted and revised the manuscript, and interpreted the data. A. Zakaei contributed to sample collection and laboratory examination. M. Motamedi cooperated with sample collection and laboratory examination, interpreted the data, revised the manuscript, and performed statistical analysis. M. Rahimi Ghiasi and M. Karamitalab contributed to sample collection and laboratory examination. P. Jafari performed statistical analysis.

Conflicts of Interest
The authors declare no conflicts of interest.

Financial Disclosure
Dr Keyvan Pakshir reported receiving research grants from Shiraz University of Medical Sciences for this research (grant number 6000).

Authors have no financial interests related to the material in the manuscript.

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