Molecular differentiation and antifungal susceptibilities of Candida parapsilosis isolated from patients with bloodstream infections

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The genetic heterogeneity and antifungal susceptibility patterns of Candida parapsilosis isolated from blood cultures of patients were investigated in this study. Randomly amplified polymorphic DNA (RAPD) analysis generated 5 unique profiles from 42 isolates. Based on the major DNA fragments of the RAPD profiles, the isolates were identified as RAPD type P1 (29 isolates), P2 (6 isolates), P3 (4 isolates), P4 (2 isolates) and P5 (1 isolate). Sequence analysis of the internal transcribed spacer (ITS) gene of the isolates identified RAPD type P1 as C. parapsilosis, P2 and P3 as Candida orthopsilosis, P4 as Candida metapsilosis, and P5 as Lodderomyces elongisporus. Nucleotide variations in ITS gene sequences of C. orthopsilosis and C. metapsilosis were detected. Antifungal susceptibility testing using Etests showed that all isolates tested in this study were susceptible to amphotericin B, fluconazole, ketoconazole, itraconazole and voriconazole. C. parapsilosis isolates exhibited higher MIC50 values than those of C. orthopsilosis for all of the drugs tested in this study; however, no significant difference in the MICs for these two Candida species was observed. The fact that C. orthopsilosis and C. metapsilosis were responsible for 23.8 and 4.8 % of the cases attributed to C. parapsilosis bloodstream infections, respectively, indicates the clinical relevance of these newly described yeasts. Further investigations of the ecological niche, mode of transmission and virulence of these species are thus essential.

INTRODUCTION

The incidence of candidiasis among hospitalized patients has increased generally in recent years, with a larger proportion of bloodstream infections being caused by non-albicans Candida spp. (Pfaller & Diekema, 2007). Among the Candida spp., Candida parapsilosis has been described as the second or third most common yeast species isolated from patients with bloodstream infections in Europe, Canada, Asia and Latin America (Almirante et al., 2006; Messer et al., 2006; Pfaffer et al., 2005). This yeast is believed to be of low virulence, but is well adapted to the human commensal environment, and occurrence of infection among hospitalized patients is particularly associated with carriage by the hands of health-care workers (Almirante et al., 2006; Bonassoli et al., 2005; Lin et al., 1995; Lupetti et al., 2002; Messer et al., 2006). C. parapsilosis bloodstream infections have been reported in association with catheter colonization and intravenous hyperalimentation in neonates (Sarvikivi et al., 2005), due to the capability of the yeast to form a biofilm on plastic intravascular devices (Branchini et al., 1994; Pfaffer et al., 1995). Catheter removal has been shown to be effective in clearance of fungaemia (Levy et al., 1998; Rex, 1996).

C. parapsilosis has been considered a clonal organism in the past. However, this yeast is now differentiated into three species using molecular typing techniques (Lin et al., 1995; Roy & Meyer, 1998; Tavanti et al., 2005). Whilst the species C. parapsilosis is retained for genotype I isolates, genotypes II and III have been proposed as the separate species Candida orthopsilosis and Candida metapsilosis (Tavanti et al., 2005). These two newly described species are phenotypically identical, but genotypically distinct from C. parapsilosis (Kocsbue et al., 2007; Lin et al., 1995; Tavanti et al., 2005).

Both C. orthopsilosis and C. metapsilosis have been reported from bloodstream infections and infections at other anatomical sites (Gomez-Lopez et al., 2008; Kocsbue et al., 2007; Tavanti et al., 2007). C. orthopsilosis was found to be responsible for 4.5 % of infections/colonization attributed to C. parapsilosis (Tavanti et al., 2007), and the organism was isolated from the blood samples of 2 out of 13 patients examined in their study. Kocsbue et al. (2007) reported the identification of 1 C. metapsilosis isolate from a total of 209 C. parapsilosis blood isolates (0.5 %). The

Abbreviation: RAPD, randomly amplified polymorphic DNA.
prevalence of *C. orthopsilosis* and *C. metapsilosis* was 1.4 and 1.7 %, respectively, in a study conducted in Spain (Gomez-Lopez et al., 2008).

*Lodderomyces elongisporus* has been recognized as a third yeast species that is found to be closely related to *C. parapsilosis*. Data on small-subunit rRNA gene sequencing show that it is a distinct species that is closely related to *C. parapsilosis* (James et al., 1994). This species has been reported in bloodstream infections of patients from Asia and Mexico (Lockhart et al., 2008).

In this study, *C. parapsilosis* isolates from patients with fungaemia in our hospital were differentiated by randomly amplified polymorphic DNA (RAPD) analysis. The identities of isolates with unique RAPD profiles were determined by sequence analysis of the ITS1–5.8S rRNA gene–ITS2 region of the yeasts. As there were no data on the antifungal susceptibility of our *C. parapsilosis* isolates, Etests were performed to determine the MIC values against amphotericin B, fluconazole, itraconazole, ketoconazole and voriconazole.

### METHODS

#### Clinical isolates
A total of 42 isolates of *C. parapsilosis* obtained from different patients with bloodstream infections, randomly collected from 2004 to 2007, were used in this study. The ages of the patients ranged from 1 month to 83 years, with a mean age of 36.7 years. Twelve individuals (28.6 %) were paediatric patients with ages ranging from 1 month to 13 years. All isolates were identified as *C. parapsilosis* using the API 20C AUX system (bioMérieux).

#### DNA extraction
Yeast genomic DNA was extracted as described by Makimura et al. (1994) with slight modifications. Briefly, yeast cells were boiled for 15 min in lysis buffer containing 100 mM Tris/HCl (pH 8), 0.5 % SDS and 30 mM EDTA. The lysate was then added to 2.5 M potassium acetate solution and incubated on ice for 1 h before centrifuging at 13,226 g for 5 min. The yeast DNA in the supernatant was precipitated with isopropanol, washed twice with ethanol, air dried and resuspended in 50 μl distilled water prior to use in the PCR.

#### RAPD analysis
Amplification was performed using the single primer M13 (5′-GAGGGTGGCGGTTCT-3′) or (GTG)₅ sequence repeats, as described by Meyer et al. (1997). The PCR master mix (25 μl) contained 10 mM Tris/HCl (pH 8.3), 50 mM KCl, 1.5 mM MgCl₂, 0.2 mM dNTPs, 0.15 mM primer, 2.5 U Taq DNA polymerase (MBI Fermentas) and 25 ng yeast DNA. PCR conditions were 35 cycles of denaturation at 94 °C for 20 s, annealing at 52 °C for 1 min and extension at 72 °C for 2 min. A 10 μl aliquot of the amplification products was separated by electrophoresis on a 2.0 % agarose gel. The RAPD profiles were visualized under UV light and photographed. Isolates were assigned to their respective RAPD types based on the presence or absence of DNA fragments generated from the PCR.

#### ITS sequence analysis
Amplification of the ITS1–5.8S rRNA gene–ITS2 fragment was performed with primer ITS1 (5′-TGGTA-GGTAACCTGCAG-3′) and ITS4 (5′-TCCCTCCGCTATTGATATGC-3′) (White et al., 1990). The amplicon was purified using a GeneAll PCR SV kit (General Biosystem) and the subsequent sequencing reaction was performed with a BigDye terminator cycle sequencing kit (Applied Biosystems) on an ABI-3730 Genetic Analyzer (Applied Biosystems) using ITS1 and ITS4 as primers. Sequences were imported into the BioEdit sequence alignment program and inspected manually (Hall, 1999). The neighbour-joining method of MEGA software (version 4.0) was employed to determine the phylogenetic status of the isolates (Kumar et al., 2004). The reliability of different phylogenetic groupings was evaluated using bootstrap tests (1000 bootstrap replicates). Type strains included for analysis were: *C. parapsilosis* CBS 604T (GenBank accession no. AJ63531), *C. orthopsilosis* ATCC 96130T (AJ698048), *C. metapsilosis* ATCC 96144T (AJ698049) and *L. elongisporus* CBS 2606 (AY391845).

#### Antifungal susceptibility tests
Etests were performed according to the manufacturer’s instructions (AB Biodisk). The antifungal agents used were amphotericin B, fluconazole, itraconazole, ketoconazole and voriconazole (in strips provided in the Etest kit). Comparisons of proportions were performed using the Mann–Whitney test of the SPSS statistical package (version 13.0). A P value of <0.05 was considered statistically significant.

### RESULTS

#### RAPD analysis
Based on the major DNA fragments (ranging from 200 bp to approximately 2 kb) generated by primer M13 (Fig. 1a), five RAPD profiles (designated P1–P5) were obtained. RAPD types P1, P4 and P5 could easily be recognized based on their unique profiles. RAPD types P2 and P3 were differentiated based on several faintly stained DNA fragments of <1 kb generated in the profiles. Similar typing results were obtained using (GTG)₅ sequence repeats (Fig. 1b). A total of 29 (69.0 %) of the isolates were identified as RAPD type P1, 6 (14.3 %) as P2, 4 (9.5 %) as P3, 2 (4.8 %) as P4 and 1 (2.4 %) as P5.

#### ITS sequence analysis
A total of 461–504 nt of the ITS1–5.8S rRNA gene–ITS2 regions of 18 RAPD type P1 isolates and all RAPD type P2–P5 isolates were determined. Fig. 2 shows the multiple alignment of the ITS sequences of *C. parapsilosis* and its closely related species. Fig. 3 is a dendrogram illustrating the genetic relationships of *C. parapsilosis* and its related species based on their ITS sequences. *C. parapsilosis, C. orthopsilosis* and *C. metapsilosis* isolates were grouped in the same cluster as their respective type strains. *L. elongisporus* was distinctly differentiated from the *Candida* spp.

Table 1 shows the percentages of sequence similarity of the yeasts when compared with their respective type strains. The ITS gene sequences of RAPD type P1 isolates showed 100 % sequence similarity with *C. parapsilosis* type strain CBS 604T. All six RAPD type P4 isolates demonstrated 100 % sequence similarity with *C. orthopsilosis* type strain (ATCC 96130T). Three RAPD type P3 isolates exhibited 99.3 % sequence similarities (3 nt differences) with the *C. orthopsilosis* type strain, whilst the remaining one exhibited 99.1 % sequence similarity (4 nt differences) with the type strain.

The two RAPD type P4 isolates in this study exhibited 99.3 and 98.3 % (3 and 8 nt differences, respectively) sequence
similarity with *C. metapsilosis* type strain ATCC 96144T. The only RAPD type P5 isolate in this study showed 100% sequence similarity with the *L. elongisporus* type strain CBS 2606 (Table 1).

*C. parapsilosis* accounted for 69.0% of the isolates in this study. This was followed by *C. orthopsilosis* (23.8%) and *C. metapsilosis* (4.8%). The distribution of *C. parapsilosis*, *C. orthopsilosis* and *C. metapsilosis* among the paediatric patients were seven (58.3%), three (25.0%) and two (16.7%) isolates. The distribution of *C. parapsilosis* and *C. orthopsilosis* in the adult patients were 22 (73.3%) and 7 (23.3%) isolates, respectively. No. *C. metapsilosis* was isolated from adult patients in this study.

**Antifungal susceptibility tests**

The isolates were susceptible to all of the antifungal drugs tested, with MICs \(<1\ \mu g\ \text{ml}^{-1}\) for amphotericin B, ketoconazole, itraconazole, and voriconazole and \(<6\ \mu g\ \text{ml}^{-1}\) for fluconazole (Table 2). The lowest MIC values were obtained for ketoconazole. Although *C. parapsilosis* isolates exhibited higher MIC<sub>50</sub> values than those of *C. orthopsilosis* for all of the drugs tested in this study, no significant difference in the MIC<sub>50</sub> values for these two *Candida* species was observed (Table 2). The MIC range of *C. metapsilosis* and *L. elongisporus* isolates fell within the MIC range of *C. parapsilosis* (Table 2). Overall, the MICs of our isolates were well below the plasma levels normally achieved for these drugs.

**DISCUSSION**

Identification of *Candida* spp. from clinical specimens, particularly blood culture, is important to facilitate optimal antifungal therapy and patient management (Edwards et al., 1997; Rex et al., 2000). Molecular techniques are excellent tools for identification and strain typing of yeasts. Analysis of new species that are closely related to *C. parapsilosis* has been performed using various molecular techniques including RAPD analysis (Kocsuè et al., 2007; Lehmann et al., 1992; Lin et al., 1995; Tavanti et al., 2007; Zancope´-Oliveira et al., 2000), nucleotide sequence analysis (Iida et al., 2005; Kato et al., 2001; Lin et al., 1995; Lockhart et al., 2008; Nosek et al., 2002; Pryce et al., 2006), DNA–DNA hybridization (Roy & Meyer, 1998), probe hybridization (Enger et al., 2001), analysis of mitochondrial DNA (Rycovska et al., 2004), multilocus sequence typing (Tavanti et al., 2005), microsatellite analysis (Lasker et al., 2006), amplification fragment length polymorphism analysis (Tavanti et al., 2007) and RFLP analysis of genomic DNA (Van Asbeck et al., 2008). In this study, the occurrence and susceptibility profiles of our isolates were investigated by RAPD and sequence analysis of ITS genes.

RAPD analysis using a single primer, M13, was used initially in this study to provide a quick screening of the genetic heterogeneity of the yeasts. The RAPD profiles generated were stable, especially with the major DNA fragments. The typing results were reproducible using another primer, (GTG)<sub>5</sub> sequence repeats, in the RAPD analysis (Fig. 1). The genomic homogeneity among *C. parapsilosis* isolates as observed by RAPD analysis and sequence analysis of ITS genes in this study has been demonstrated previously by various molecular techniques (Kocsuè et al., 2007; Lehmann et al., 1992; Tavanti et al., 2005, 2007). However, a recent investigation of the size polymorphisms in loci harbouring microsatellite repeat sequences of *C. parapsilosis* group I isolates (Lasker et al., 2006) demonstrated 30 different microsatellite genotypes
from 42 isolates. Due to the high discriminatory power of microsatellite analysis, this technique has been proposed for *C. parapsilosis* outbreak and epidemiological investigations (Lasker et al., 2006).

In a recent study to analyse the distribution of the subtypes of *C. parapsilosis* from various geographical localities, Van Asbeck et al. (2008) divided their isolates into two groups: VII-1 (dominant subtype showing RAPD profiles consistent with *C. parapsilosis sensu stricto*) and non-VII-1 (all remaining subtypes). Approximately 82% VII-1 isolates were reported for the USA, Europe, Brazil and Israel strains; however, there was diversity in the genotypic groups of *C. parapsilosis* isolated from different geograph-

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**Fig. 2.** Multiple alignment of ITS gene sequences of *C. parapsilosis* and related species.
ical areas, with isolates from Mexico showing a significantly lower proportion of VII-1 isolates. The findings in this study also showed that there was a low frequency (69.0 %) of *C. parapsilosis* in the Malaysian isolates. Whether the difference observed in yeast distribution has any association with treatment and management of the infections will require further investigation.

The genetic heterogeneity of *C. orthopsilosis* and *C. metapsilosis*, as reflected by RAPD analysis and detection of nucleotide variations in the ITS gene in this study, has been demonstrated by other investigators (Iida et al., 2005; Lasker et al., 2006; Rycovska et al., 2004; Tavanti et al., 2005, 2007; Van Asbeck et al., 2008). The greater genetic variability of these newly described yeasts compared with *C. parapsilosis* has caused difficulties in the development of molecular techniques for the subtyping of these yeasts (Lasker et al., 2006; Tavanti et al., 2005).

The identification of *C. orthopsilosis* and/or *C. metapsilosis* from clinical isolates has been reported in Europe and the USA (Enger et al., 2001; Gomez-Lopez et al., 2008; Kocsübę et al., 2007; Tavanti et al., 2005, 2007). It is thought that the low frequencies of these newly described species in clinical specimens have prevented further analysis of these yeasts. There is also little information on the frequency of *C. orthopsilosis* and *C. metapsilosis* isolated from cases of *C. parapsilosis* bloodstream infections. The occurrences of *C. orthopsilosis* and *C. metapsilosis* (23.8 and 4.8 % of the cases, respectively) attributed to *C. parapsilosis* bloodstream infections in this study were found to be higher than those reported by others (Gomez-Lopez et al., 2008; Kocsübę et al., 2007; Tavanti et al., 2007). Isolation of both *C. orthopsilosis* and *C. metapsilosis* from the blood cultures of paediatric patients was also documented in this study for what is believed to be the first time. In fact, a higher frequency of *C. orthopsilosis* was noted in the blood cultures of paediatric patients compared with those of

![Fig. 3. Dendrogram based on ITS gene sequences of *C. parapsilosis* and related species.](http://jmm.sgmjournals.org)

### Table 1. Percentage sequence similarity and nucleotide differences of blood isolates compared with the type strains of *C. parapsilosis*, *C. orthopsilosis*, *C. metapsilosis* and *L. elongisporus*

<table>
<thead>
<tr>
<th>Strain</th>
<th>Percentage nucleotide similarity / no. of nucleotide differences</th>
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<tbody>
<tr>
<td></td>
<td><em>C. parapsilosis</em> CBS 604&lt;sup&gt;T&lt;/sup&gt;</td>
</tr>
<tr>
<td><em>C. parapsilosis</em></td>
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<tr>
<td>CBS 604&lt;sup&gt;T&lt;/sup&gt;</td>
<td>100/0</td>
</tr>
<tr>
<td>RAPD type P1 (n=18)</td>
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</tr>
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<td><em>C. orthopsilosis</em></td>
<td></td>
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<tr>
<td>ATCC 96139&lt;sup&gt;T&lt;/sup&gt;</td>
<td>94.5/26</td>
</tr>
<tr>
<td>RAPD type P2 (n=6)</td>
<td>94.5/26</td>
</tr>
<tr>
<td>RAPD type P3 (n=3)</td>
<td>94.3/27</td>
</tr>
<tr>
<td>RAPD type P3 (n=1)</td>
<td>94.1/28</td>
</tr>
<tr>
<td><em>C. metapsilosis</em></td>
<td></td>
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<tr>
<td>ATCC 96144&lt;sup&gt;T&lt;/sup&gt;</td>
<td>91.8/40</td>
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<tr>
<td>RAPD type P4 (n=1)</td>
<td>92/39</td>
</tr>
<tr>
<td>RAPD type P4 (n=1)</td>
<td>91/44</td>
</tr>
<tr>
<td><em>L. elongisporus</em></td>
<td></td>
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<tr>
<td>CBS 2606&lt;sup&gt;T&lt;/sup&gt;</td>
<td>81.1/95</td>
</tr>
<tr>
<td>RAPD type P5 (n=1)</td>
<td>81.1/95</td>
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Table 2. *In vitro* antifungal susceptibilities of *C. parapsilosis* and related species in this study

<table>
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<th>Clinical isolate</th>
<th>Antifungal drug</th>
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<tr>
<td></td>
<td>Amphotericin B</td>
</tr>
<tr>
<td><em>C. parapsilosis</em> (n=21)</td>
<td></td>
</tr>
<tr>
<td>MIC range (µg ml⁻¹)</td>
<td>&lt;0.002–0.75</td>
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<tr>
<td>MIC₅₀ (µg ml⁻¹)</td>
<td>0.047</td>
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<tr>
<td>MIC₉₀ (µg ml⁻¹)</td>
<td>0.75</td>
</tr>
<tr>
<td><em>C. orthopsilosis</em> (n=8)</td>
<td></td>
</tr>
<tr>
<td>MIC range (µg ml⁻¹)</td>
<td>0.006–0.125</td>
</tr>
<tr>
<td>MIC₅₀ (µg ml⁻¹)</td>
<td>0.023</td>
</tr>
<tr>
<td>MIC₉₀ (µg ml⁻¹)</td>
<td>0.125</td>
</tr>
<tr>
<td><em>C. metapsilosis</em> (n=2)</td>
<td></td>
</tr>
<tr>
<td>3516</td>
<td>0.023</td>
</tr>
<tr>
<td>3506</td>
<td>0.016</td>
</tr>
<tr>
<td><em>L. elongisporus</em> (n=1)</td>
<td></td>
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<tr>
<td>3179</td>
<td>0.012</td>
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</tbody>
</table>

In conclusion, this study presented the identification of newly described yeast species that are closely related to *C. parapsilosis* from the blood cultures of our patients. Although the blood isolates in this study were identified initially by conventional biochemical tests as *C. parapsilosis*, these organisms could be differentiated further into *C. parapsilosis*, *C. orthopsilosis*, *C. metapsilosis* and *L. elongisporus* using RAPD and sequence analysis of ITS genes. The fact that *C. orthopsilosis* and *C. metapsilosis* were responsible for 23.8 and 4.8% of these cases attributed to *C. parapsilosis* bloodstream infections, respectively, indicates the clinical relevance of these yeast species. Further investigations of the ecological niche, mode of transmission and virulence of these newly described species are thus essential.

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