Occurrence and genetic variability of *Candida parapsilosis sensu lato* in Hungary

Sándor Kocsubé,1 Mónika Tóth,1 Csaba Vágvölgyi,1 Ilona Dóczi,2 Miklós Pesti,3 István Pócsi,4 Judit Szabó5 and János Varga1,6

1Department of Microbiology, Faculty of Sciences, University of Szeged, PO Box 533, H-6701 Szeged, Hungary
2Department of Clinical Microbiology, Faculty of Medicine, University of Szeged, PO Box 427, H-6701 Szeged, Hungary
3Department of General and Environmental Microbiology, University of Pécs, H-7601 Pécs, Hungary
4Department of Microbiology and Biotechnology, Medical and Health Science Center, University of Debrecen, PO Box 63, H-4010, Debrecen, Hungary
5Institute of Medical Microbiology, Faculty of Sciences, University of Debrecen, PO Box 63, H-4010, Debrecen, Hungary
6CBS Fungal Biodiversity Centre, Uppsalaalen 8, 3584 CT Utrecht, The Netherlands

The occurrence and genetic variability of *Candida parapsilosis* isolates in two Hungarian hospitals, located in Debrecen and Pécs, were examined. Among the 209 *Candida* isolates examined, 20 were found to belong to *C. parapsilosis sensu lato*, based on morphological, physiological and molecular data. The frequency of occurrence of *C. parapsilosis* isolates (9.6 %) was lower than that observed in Europe but higher than that observed previously in Hungary. The genetic variability of *C. parapsilosis sensu lato* isolates was also examined using random amplified polymorphic DNA (RAPD) analysis and sequence analysis of the intergenic transcribed spacer (ITS) region of the rRNA gene cluster. The genetic variability of the isolates was relatively high, as revealed by RAPD analysis. Two isolates were found to belong to the recently described *Candida metapsilosis* species (*C. parapsilosis* group III), based on ITS sequence data, RAPD analysis and phenotypic data. These two isolates could also be distinguished from *C. parapsilosis sensu stricto* isolates using a primer pair developed for the detection of *C. parapsilosis* group I isolates. To the best of the authors’ knowledge, this is the first report on the identification of *C. metapsilosis* from bloodstream infection.

INTRODUCTION

Infections caused by *Candida* species are widespread throughout the world. Although *Candida albicans* is the most common *Candida* species encountered as a cause of human infection, other *Candida* species have been increasingly associated with disseminated disease since the 1990s. Among them, *C. parapsilosis* has been the second most common yeast species isolated from bloodstream infections in several surveys (Safdar *et al.*, 2002; Messer *et al.*, 2006; Bassetti *et al.*, 2006). This species has emerged as an important nosocomial pathogen, with clinical manifestations that include fungaemia, endocarditis, endophthalmatitis, septic arthritis and peritonitis, and infection usually occurs in association with invasive procedures or prosthetic devices (Weems, 1992). In some children’s hospitals, *C. parapsilosis* has become the predominant species causing candidaemia (Levy *et al.*, 1998). This species is more frequent in bloodstream infections of neonates, in transplant recipients and in patients who have received parenteral nutrition or previous antifungal therapy (Almirante *et al.*, 2006). This species is also frequently associated with catheter-associated candidaemia and intravenous hyperalimentation (Kremery & Barnes, 2002).

Previous studies have clarified that *C. parapsilosis sensu lato* isolates can be divided into three groups that can be
distinguished based on several criteria, including randomly amplified polymorphic DNA (RAPD) analysis (Lehmann et al., 1992), isoenzyme electrophoresis (Lin et al., 1995), sequences of the internal transcribed spacer (ITS) region of the rRNA gene cluster (Lin et al., 1995; Pryce et al., 2006), hybridization to a fingerprinting probe (Enger et al., 2001), DNA relatedness (Roy & Meyer, 1998), morphotyping (Cassone et al., 1995), electrophoretic karyotypes (Lott et al., 1993), single nucleotide polymorphisms (Fundiya et al., 2004), mitochondrial DNA sequence differences (Nosek et al., 2002; Kosa et al., 2006) and biofilm-producing abilities (Song et al., 2005). Recently, Tavanti et al. (2005) have recognized C. parapsilosis groups II and III as separate species, Candida orthopsilosis and Candida metapsilosis, respectively, based on multilocus sequence typing studies. Accordingly, C. parapsilosis sensu lato includes C. parapsilosis sensu stricto and the two newly described species. The two latter species are recovered relatively rarely in clinical samples (Tavanti et al., 2005). In addition, C. parapsilosis group IV has also been recognized recently among Brazilian clinical Candida isolates by Iida et al. (2005).

In this study, we examined the occurrence of C. parapsilosis among Candida isolates collected in Hungarian hospitals, and examined the genetic variability of these isolates using sequence analysis of the ITS region and the RAPD technique.

METHODS

Clinical samples. Altogether, 209 Candida isolates from blood samples from two Hungarian hospitals, located in Debrecen and Pécs, were examined. All examined isolates came from different patients. C. parapsilosis isolates were identified by standard morphological and physiological methods within the hospitals (Barnett et al., 2000).

Phenotyping. The API 20C AUX version 3.0 kit (bioMérieux) was used to type the species. Isolates from stored slants were streaked onto nutrient agar and incubated at 30 °C for 24 and 48 h. Samples were then analysed according to the manufacturer’s prescribed methods. The antifungal susceptibilities of isolates were determined by the Etest method (AB Biodisk). The Etest was performed in accordance with the manufacturer’s instructions, with the use of Etest strips were 0.016–256 mg l⁻¹ for amphotericin B. The incubation time was 24–48 h at 30 °C, depending on the growth characteristics. The MICs for amphotericin B were taken as the drug concentrations causing 100% inhibition. MICs for azoles were read at the visually selected end point of 80% inhibition of growth. Interpretative susceptibility criteria for these antifungal agents were used as published by the Clinical and Laboratory Standards Institute (CLSI) and in the literature (National Committee for Clinical Laboratory Standards, 2002; de Hoog et al., 2000).

Genotyping. Isolates were cultivated in YPD medium (0.5% Bacto yeast extract, 1% glucose, 0.5% Bacto peptone) and centrifuged, and DNA was extracted from the cells using the Masterpure yeast DNA purification kit (Epitect Biotechnologies) according to the instructions of the manufacturer. For confirmation of the species assignment of the isolates, the species-specific primer pair developed for C. parapsilosis by Luo & Mitchell (2002) was used. For the identification of C. parapsilosis sensu stricto (group I) isolates, the primer pair developed by Pontieri et al. (2001) was applied. The ITS region of the isolates was amplified using primers ITS1 and ITS4 (White et al., 1990). DNA fragments were purified from the excised agarose blocks using Genelute spin columns (Sigma-Aldrich). Direct sequencing of the fragments was performed on an ABI 373A DNA sequencer (Applied Biosystems) using deoxy terminator reaction chemistry. Sequences were determined from both strands using ITS1 and ITS4 as primers. The GenBank accession numbers for the ITS sequences of C. metapsilosis 12821 and Bp57 are DQ786952 and DQ786953, respectively.

RAPD analysis of the isolates was carried out according to the literature (Williams et al., 1990). Fungal DNA sequences were amplified by using the following decamer primers of the Operon random primer kit (Operon Technology): OPC-02 (5'-GTGAGGCGTC-3'), OPC-05 (5'-GATGACGCC-3'), OPC-07 (5'-GCCTCCCGCA-3'), OPC-09 (5'-CTCACCGTCC-3'), OPC-12 (5'-GTGATCGTCC-3'), OPC-14 (5'-TGCGTGTGTC-3'), OPC-16 (5'-CACACTCCAG-3'), OPC-18 (5'-TGTAAGTGGGTG-3'), OPC-20 (5'-ACTTCCGGGAC-3'), OPD-12 (5'-ACCCGATCCT-3'), OPE-17 (5'-CTACTGCGGT-3'), OPG-07 (5'-GAACCTGCCG-3'), OPG-19 (5'-GATCGCCAAA-3'), OPG-17 (5'-GAATCCTGCG-3'), OPR-15 (5'-GACAACGAG-3') and OPW-17 (5'-ACCGCGCTGT-3'), and UBC (University of British Columbia) primers UBC 8 (5'-CTGGCCGTGA-3'), UBC 18 (5'-GGCGCGTATTA-3') and UBC 66 (5'-GGACGGGGGTA-3').

Data analysis. Sequence alignments were performed by using CLUSTAL_X (Thompson et al., 1997) and improved manually. Evolutionary distances between the sequences were calculated by Kimura’s formula (Kimura, 1980) using the program DNADIST. Phylogenetic trees were prepared by the neighbour-joining method (Saitou & Nei, 1987) using the program NEIGHBOR of the PHYLIP package. Bootstrap values were calculated from 1000 replications of the bootstrap procedure using programs SEQBOOT, DNADIST, NEIGHBOR and CONSENSE of the package (Felsenstein, 1995).

RAPD bands were scored visually. Only those bands were taken into account which were amplified in all three separate RAPD reactions. The binary matrices of RAPD data were converted to distance matrices using PhyTools (Bunje, 1997). RAPD data were analysed by the neighbour-joining method using the program NEIGHBOR of the PHYLIP package (Saitou & Nei, 1987; Felsenstein, 1995).

RESULTS AND DISCUSSION

Occurrence of C. parapsilosis in Hungarian hospitals

Altogether, 103 and 106 Candida isolates were collected in two Hungarian hospitals located in Debrecen and Pécs, respectively, during 2004–2005. Among these, 10 and 16 isolates, respectively, were recovered to belong to C. parapsilosis sensu lato, based on morphological and physiological criteria (Table 1). The C. parapsilosis species-specific primer pair (Luo & Mitchell, 2002) was successfully used to confirm the identity of eight and 12 isolates as C. parapsilosis sensu lato. API 20C AUX tests also confirmed that these isolates belonged to C. parapsilosis sensu lato. Overall, 9.6% of the collected isolates were found to belong to C. parapsilosis sensu lato, while the remaining isolates were found to belong to C. albicans, Candida lusitaniae (teleomorph Clavispora lusitaniae; Kurtzman & Fell, 1998) or Candida krusei.
Table 1. Origin and species assignment of the Candida isolates examined in this study

<table>
<thead>
<tr>
<th>Strain number</th>
<th>Origin</th>
<th>Species assignment based on ITS sequences</th>
</tr>
</thead>
<tbody>
<tr>
<td>12821</td>
<td>Blood, Debrecen</td>
<td>C. metapsilosis</td>
</tr>
<tr>
<td>3929</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>1188/1</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>6761</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>11811</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>5312</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>5308</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>25329</td>
<td>Blood, Debrecen</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp57</td>
<td>Throat, Pécs</td>
<td>C. metapsilosis</td>
</tr>
<tr>
<td>Bp73</td>
<td>Stomach, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp42</td>
<td>Blood, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp101</td>
<td>Blood, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp113</td>
<td>Blood, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp75</td>
<td>Nail, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp46</td>
<td>Blood, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp54</td>
<td>Fingernail, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp3</td>
<td>Nail, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp90</td>
<td>Sputum, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>Bp94</td>
<td>Blood, Pécs</td>
<td>C. parapsilosis</td>
</tr>
<tr>
<td>5311</td>
<td>Blood, Debrecen</td>
<td>C. lusitaniae</td>
</tr>
<tr>
<td>5068/1</td>
<td>Blood, Debrecen</td>
<td>C. lusitaniae</td>
</tr>
<tr>
<td>Bp47</td>
<td>Blood, Pécs</td>
<td>C. krusei</td>
</tr>
<tr>
<td>Bp39</td>
<td>Clinical sample, Pécs</td>
<td>C. albicans</td>
</tr>
<tr>
<td>Bp63</td>
<td>Blood, Pécs</td>
<td>C. krusei</td>
</tr>
<tr>
<td>Bp86</td>
<td>Blood, Pécs</td>
<td>C. krusei</td>
</tr>
</tbody>
</table>

(teleomorph Issatchenkia orientalis; Kurtzman & Fell, 1998) (Table 1). This observation could have been caused by misidentifications or, more probably, by contamination of some of the cultures during storage of the isolates after morphological identification.

Previously, C. parapsilosis has been found to be responsible for about 19% of bloodstream Candida infections in Europe (Pfaller et al., 2001). More recent surveys have revealed that C. parapsilosis is responsible for more than 20% of candidaemias in Italy (Bassetti et al., 2006; Bedini et al., 2006), Spain (Almirante et al., 2006; Rodriguez et al., 2006; San Miguel et al., 2006) and South American countries (Brito et al., 2006; Rodero et al., 2005), while this species is encountered less frequently in Turkey (12.5%; Yapar et al., 2006) and Norway (6%; Sandven et al., 2006). In a worldwide survey, Messer et al. (2006) have found C. parapsilosis to be responsible for candidaemias in 16.36% of the 336 cases examined from Europe. In another survey, Tortorano et al. (2004, 2006) have found that C. parapsilosis is responsible for 6.9–30% (mean 13.54%) of candidaemias in different European countries, with the highest incidence found in Spain. In a previous study, Dóczi et al. (2002) found that C. parapsilosis was responsible for 4.9% of bloodstream infections caused by Candida species in a university hospital in Hungary. These data indicate that the frequency of C. parapsilosis infections varies widely among different institutions and countries (Pfaller et al., 2001). The 9.6% incidence of this species found in this survey is higher than that observed previously in Hungary, but lower than the mean observed in European countries.

Genetic variability of C. parapsilosis isolates

RAPD analysis of the isolates was carried out by using 21 random decamer primers. The genetic variability observed among the isolates was low: most isolates exhibited very similar or the same RAPD patterns with most primers tested (Fig. 1). Similarly low genetic variability has been observed among C. parapsilosis sensu stricto isolates by Zeng et al. (1996), Lehmann et al. (1992) and Enger et al. (2001). For preparation of the similarity matrix, the presence or absence of 72 DNA bands was taken into account. The dendrogram based on RAPD data indicates that the C. parapsilosis isolates form two main clusters which are supported by high bootstrap values (Fig. 2). One of these includes two isolates, 12821 and Bp57, which could also be distinguished from other C. parapsilosis isolates using the C. parapsilosis group I-specific primer pair developed by Pontieri et al. (2001). This primer pair did not amplify the expected product from isolates 12821 and Bp57 (data not shown).

Sequences of the ITS region of the isolates were also determined. Phylogenetic analysis of sequence data indicated
that two of the isolates that belonged to *C. parapsilosis sensu lato* were members of the *C. metapsilosis* species (see Supplementary Fig. S1). In other studies, *C. metapsilosis* has been identified in the USA, Japan, Brazil, Norway and Belgium (Enger et al., 2001; Rycovska et al., 2004; Iida et al., 2005; Tavanti et al., 2005). To the best of our knowledge, the present study is the first report on the occurrence of this species in Central Europe. In addition, in this study, *C. metapsilosis* was isolated from a bloodstream infection for the first time. The results of the API 20C AUX tests also indicated that these two isolates belonged to the *C. metapsilosis* species, since in a similar manner to the results of Lin et al. (1995), the two isolates could grow on D-xylitol, in contrast to the *C. parapsilosis sensu stricto* isolates (data not shown).

**Antifungal susceptibility tests**

All isolates were susceptible to the antifungal drugs tested, with MICs \(< 1\) mg l\(^{-1}\) for amphotericin B and voriconazole, \(< 8\) mg l\(^{-1}\) for fluconazole and \(< 0.125\) mg l\(^{-1}\) for itraconazole. The lowest MIC values were obtained for itraconazole and voriconazole. According to earlier studies, the amphotericin B, fluconazole, itraconazole and voriconazole susceptibilities of *C. parapsilosis* isolates range from 0.03 to 2 mg l\(^{-1}\), 0.06 to 16 mg l\(^{-1}\), 0.03 to 2 mg l\(^{-1}\) and 0.02 to 1 mg l\(^{-1}\), respectively (Lin et al., 1995; Rex et al., 1995; Pfaffer et al., 2001; Lu et al., 2004; St-Germain et al., 2001; Tortorano et al., 2004, 2006; de Hoog et al., 2000). The MIC values obtained for *C. metapsilosis* isolates fell within the range of MICs of *C. parapsilosis* isolates (data not shown). *C. metapsilosis* isolates exhibited lower mean MIC values for voriconazole and amphotericin B than *C. parapsilosis* isolates. Similarly, lower MIC values have been observed for amphotericin B in *C. metapsilosis* than in *C. parapsilosis* in earlier studies (Lin et al., 1995).

However, further isolates should be examined to draw definite conclusions.

In conclusion, 9.6% of *Candida* infections were found to be caused by *C. parapsilosis sensu lato* in our survey of two Hungarian hospitals. Two of these isolates were found to belong to the recently described *C. metapsilosis* species. This is believed to be the first report on the identification of *C. metapsilosis* from bloodstream infection. Further studies are in progress to identify the rest of the *Candida* isolates using molecular and phenotypic data, and to survey other Hungarian hospitals for the presence of *C. metapsilosis*.

**ACKNOWLEDGEMENTS**

This work was financially supported by grant GVOP-3.1.1-2004-05-0471/3.0. The technical assistance of Judit Deák and Mária Lele is gratefully acknowledged.

**REFERENCES**


