Distribution of clinical yeasts in Taiwan

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ABSTRACT

To investigate the distribution of yeast pathogens in Taiwan, we have conducted Taiwan Surveillance of Antimicrobial Resistance of Yeasts (TSARY) in 2002. A total of 3926 yeast isolates were isolated from 24 hospitals between July and September in 2002. Candida albicans (69.1%) was the most common species, followed by Candida tropicalis (12.9%), Candida glabrata (8.3%), Candida parapsilosis (2.7%), Candida krusei (0.6%), and others (6.4%). To study the distribution of yeast pathogens according to the sources of isolation, we have collected and analyzed the clinical data of 945 isolates. Of those isolates, urine (39.6%) and sputum (22.3%) were the two most common sources for the yeast clinical isolates followed by blood (13.7%), central venous catheter (5.1%), wound (5.0%), and others (14.3%). Different species have different prevalence on different body sites. Urine was the most common source for C. glabrata (72.7%), Trichosporon species (60%), and C. tropicalis (45.9%). Sputum was the most common source for C. albicans (33.1%), whereas blood was the most common one for C. parapsilosis.

Key words: Candida species, sources of isolation, TSARY, Yeast.

Introduction

Yeast infections have been playing important role on nosocomial infections since two decades ago. For example, in the United States, yeast infections rank as the fourth most common cause of bloodstream infections (Pfaller et al., 1998). In Taiwan, the prevalence of hospital-acquired candidemia also increased significantly from 1981 through 1993 (Chen et al., 1997). The trend of increase in the prevalence of yeast infections is due to the prolonged chemotherapy for patients with cancers, viral and bacterial infections, and the improvement in intensive medical care. Among the yeast pathogens causing morbidity in seriously immunocompromised hosts, Candida albicans is the most frequently isolated species (Cheng et al., 2004; Pfaller et al., 2000; Yang et al., 2004). However, yeast infections caused by more treatment-resistant non-C. albicans Candida have been increasing during the past decade (Sanglard and Odds, 2002; Walsh et al., 2004; Yang et al., 2004).

The opportunistic yeast pathogens existing as part of the commensal microflora in humans

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are usually the etiological agents causing infections (Voss et al., 1994). Different species have various degrees of susceptibility to common antifungal agents (Hadfield et al., 1987; Orozco et al., 1998; Pfäffer et al., 2000). This phenomenon emphasizes the importance of nationwide surveillance. Thus, Taiwan Surveillance of Antimicrobial Resistance of Yeasts (TSARY) was initiated in 1999 (Lo et al., 2001; Yang et al., 2004) and the second round of TSARY was conducted in 2002 (Yang et al., 2005). Here we report the result of our investigation about the distribution of yeast pathogens collected in the TSARY 2002 according to type of hospitals and sources of isolation.

Materials and Methods

Organisms and media

All yeasts isolated from the 24 hospitals participating in the TSARY between July and September in 2002 were recorded. To further investigate the distribution of Candida species from different sources, every one of the participating hospitals was asked to submit all yeast isolates from blood and up to 50 clinically significant isolates from non-blood sources including the first 10 \( C. albicans \) and additional 40 isolates excluding \( C. albicans \). Duplicated isolates from same patients were excluded. All isolates were stored frozen at \(-70^\circ C\) in bead-containing Microbank cryovials (PRO-LAB Diagnostics, Austin, TX, U.S.A.). After their arrival at the laboratory at National Health Research Institutes (NHRI), the isolates were first subcultured on Sabouraud dextrose agar (SDA, BBL, Becton Dickinson, Cockeysville, MD, U.S.A.) to assess the purity and identifications. Pure isolates were labeled and stored in vials containing 50% glycerol at \(-70^\circ C\) for subsequent analysis.

Identification

The identification procedure for the yeast isolates was performed as previously described (Lo et al., 2001). In brief, isolates identified as \( C. albicans \) by the hospitals were first subjected to the germ tube test in brain heart infusion (BHI, BBL) medium containing 10% fetal bovine serum (JR12003, JRH Biosciences, Australia) at 37°C for 2–3 hours. To differentiate \( C. albicans \) from \( C. dubliniensis \), we have checked the cell growth of the germ tube positive isolates at 42°C (Sullivan and Coleman, 1998). Though all germ tube positive isolates were able to grow at 42°C, it is necessary to keep in mind that we cannot absolutely rule out the possibility that \( C. dubliniensis \) may be able to grow at 42°C as \( C. albicans \) does. The VITEK Yeast Biochemical Card (YBC, bioMerieux, St. Louis, MO, U.S.A.) was used to assess the identities of the germ tube negative isolates tested in the laboratory at NHRI, and the non-albicans Candida species isolates identified by hospitals. The API-32C (Marcy, L’ETOILE, France) was used to assess the results when the VITEK-YBC showed less than 90% confidence.

Database and analysis

The database contained the identifications of the collected isolates and the following characteristic information of each submitted isolate: hospital origin, location and type of the hospital, and the source of the isolate. The statistic significances of the differences in frequencies and proportions were determined by the chi-
square test with Mantel-Haenszel correction.

**Results**

A total of 24 hospitals consisting of 9 medical centers and 15 regional hospitals participated the TSARY 2002. There were 7 hospitals each located in North, Middle, and South of Taiwan and 3 hospitals located in East of Taiwan (Fig. 1). A total of 3926 yeasts were isolated from the patients of these hospitals between July and September in 2002. They consisted of 2711 *C. albicans* (69.1%), 507 *Candida tropicalis* (12.9%), 327 *Candida glabrata* (8.3%), 105 *Candida parapsilosis* (2.7%), 25 *Candida krusei* (0.6%), and 251 others (6.4%). Among the 251 isolates classified to others, the identifications for 155 of them were only to the

![Fig. 1](image-url)
To investigate the distribution of Candida species from different sources and patient ages, we have collected all yeast isolates from blood and up to the first 10 C. albicans with additional 40 yeasts from non-blood sites for further analysis. Of the 24 hospitals, 9 hospitals fulfilled the request and the remaining 15 hospitals provided less than 50 isolates. A total of 945 isolates was thus submitted from the hospitals to the laboratory at NHRI. The average number of isolates submitted per hospital was 39 (ranging from 11 to 87). By average, a medical center contributed more isolates than a regional hospital (56 vs. 29).

When classifying the isolates according to the sources, urine (39.6%) was the most common source followed by sputum (22.3%), blood (13.7%), central venous catheter (5.1%), wound (5.0 %), ascites (3.5%), pus (1.5%), and others (9.2%) (Table 1). According to the sources of isolation, the distribution of isolates is different in different types of hospitals. The isolates from regional hospitals had a higher percentage originated from urine (43.7% vs. 36%, p = 0.02) and sputum (29.7% vs. 17.5%, p = 0.0002) than that from medical centers. Whereas, the medical centers had a higher percentage of isolates from blood (16.5% vs. 10%, p = 0.008) than regional hospitals did. Among different regions, there was a significantly higher percentage of isolates from urine in the East region (55.7%, p = 0.003) and a parallel low from sputum (9.5%, p = 0.005). Interestingly, for those isolated from blood, there was a lower percentage from the North (8.7%, p = 0.05) and a higher percentage from the South (20.3%, p = 0.01).

The distribution of species from different sources is list on Table 2. Of 945 isolates, C. albicans was still the most common species (43%) and C. tropicalis was the most common non-albicans Candida species (25.8%), followed by C. glabrata (19.8%), C. parapsilosis (6.7%), Trichosporon species (1.1%), C. krusei (0.9%), Cryptococcus neoformans (0.8%), and 18 others (1.9%). Of the 130 isolates causing candidemia, there were 58 C. albicans (44.6%), 31 C. tropicalis (23.8%), 24 C. parapsilosis (18.5%), 13 C. glabrata (10%), 1 C. krusei (0.775%), 1 Trichosporon species (0.775%), 1 C. neoformans (0.775%), and 1 other (0.775%). Different species also had different prevalence regarding the sources of isolation. Urine was the most common source for C. glabrata (71.9%) and C. tropicalis (46.7%), sputum for C. albicans (30.9%) and blood for C. parapsilosis (36.2%).

Discussion

The morbidity and mortality rates associated with Candida infections have been increasing. This study provides a detailed analysis of the distribution of 945 isolated yeast pathogens according to types of hospital and sources. Candida glabrata isolates had the highest percentage (71.9%) for single source, urine, among all species. This observation is consistent with the previous reports that C. glabrata is second only to C. albicans for causing candiduria (Pfaller et al., 1999; Yang et al., 2004).

In the past, nearly 80% of candidemia could be attributed to C. albicans (Edwards, 1990). However, the prevalence of candidemia caused by non-albicans Candida species has been
**Table 1.** Distribution of yeast isolates according to different type of hospital and source

<table>
<thead>
<tr>
<th>Type of hospital</th>
<th>Number of hospital</th>
<th>Number of isolates</th>
<th>Source [number of isolates (percentage)]</th>
</tr>
</thead>
<tbody>
<tr>
<td></td>
<td></td>
<td>Total</td>
<td>Mean</td>
</tr>
<tr>
<td>Total</td>
<td>24</td>
<td>945</td>
<td>39</td>
</tr>
<tr>
<td>Medical Center</td>
<td>9</td>
<td>508</td>
<td>56</td>
</tr>
<tr>
<td>Regional Hospital</td>
<td>15</td>
<td>437</td>
<td>29</td>
</tr>
<tr>
<td>North total</td>
<td>7</td>
<td>229</td>
<td>33</td>
</tr>
<tr>
<td>Medical Center</td>
<td>1</td>
<td>64</td>
<td>64</td>
</tr>
<tr>
<td>Regional Hospital</td>
<td>6</td>
<td>165</td>
<td>28</td>
</tr>
<tr>
<td>Middle total</td>
<td>7</td>
<td>374</td>
<td>53</td>
</tr>
<tr>
<td>Medical Center</td>
<td>3</td>
<td>199</td>
<td>66</td>
</tr>
<tr>
<td>Regional Hospital</td>
<td>4</td>
<td>175</td>
<td>44</td>
</tr>
<tr>
<td>South total</td>
<td>7</td>
<td>247</td>
<td>35</td>
</tr>
<tr>
<td>Medical Center</td>
<td>4</td>
<td>189</td>
<td>47</td>
</tr>
<tr>
<td>Regional Hospital</td>
<td>3</td>
<td>58</td>
<td>19</td>
</tr>
<tr>
<td>East total</td>
<td>3</td>
<td>95</td>
<td>32</td>
</tr>
<tr>
<td>Medical Center</td>
<td>1</td>
<td>56</td>
<td>56</td>
</tr>
<tr>
<td>Regional Hospital</td>
<td>2</td>
<td>39</td>
<td>20</td>
</tr>
</tbody>
</table>

*p ≤ 0.05, comparison of percentage for each location/source vs. percentage in total population, CVP: Central venous pressure catheter
increasing as shown in our study (55.4%, 72/130) as well as other studies (Cheng et al., 2004; Peman et al., 2005; Pfaller et al., 2000). Of the 130 candidemia in our study, 31 (23.8%) and 24 (18.5%) candidemia were caused by C. tropicalis and C. parapsilosis, respectively. Candida parapsilosis is now the second most common species causing candidemia in Canada, Spain and other countries in Europe, and Latin America (Krmery and Barnes, 2002; Peman et al., 2005). Interestingly, only 13 (10%) candidemia were caused by C. glabrata even though this species is the second most common species causing candidemia in the USA and The Netherlands (Pfaller et al., 2000; Voss et al., 1996).

The distribution of C. parapsilosis when according to the source of isolation was different from that of other Candida species. The two most common sources of C. parapsilosis were blood and wound. Unlike other Candida species, C. parapsilosis has a wide distribution in nature and can be isolated from various non-human sources (Abi-Said et al., 1997; Levin et al., 1998). Thus, the distribution of C. parapsilosis in humans was different from other species maybe because it can be part of the normal flora of the human skin (Hedderwick et al., 2000).

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References


臺灣臨床酵母菌的分佈

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摘 要

臺灣 24 家參與臺灣黴菌抗藥性監測計畫第二期合作醫院 (Taiwan Surveillance of Antimicrobial Resistance of Yeasts, TSARY) 所分離 3,926 株臨床致病性酵母菌中，以念珠菌為多。而不同念珠菌種所佔的比例亦有不同，Candida albicans 佔 69.1%，成爲最多的菌種，其它依序爲 12.9% 的 C. tropicalis、8.3% 的 C. glabrata、2.7% 的 C. parapsilosis、0.6% 的 C. krusei 及 6.4% 的其它菌種。爲進一步探討臺灣臨床酵母菌在不同檢體來源的分佈，此監測計畫一共收集有關 945 株菌的資料做詳細的分析，結果顯示，以來自尿液的菌株最多 (39.6%)，其它依序爲痰液 (22.3%)、血液 (13.7%)、導管 (5.1%)、傷口 (5.0%) 以及其它部位 (13.7%)。不同菌種好發的部位也有所不同，有 72.2% 的 C. glabrata、60% 的 Trichosporon species 以及 45.9% 的 C. tropicalis 則來自尿液。大部分的 C. albicans 不是來自痰液 (31.3%) 就是尿液 (26.3%)，而 C. parapsilosis 則是以來自血液 (38.1%) 及傷口 (19%) 爲主。

關鍵詞：念珠菌、酵母菌、檢體來源。