Candida famata as a Cause of Invasive Candidiasis: Misidentification in Two Global Surveillance Systems

C. famata (Candida famata)

Introduction

Candida famata (C. famata) is a yeast-like fungus that is commonly found in various habitats, including dairy products. C. famata is a rare human pathogen that is associated with bloodstream infections, peritonitis, cutaneous and bone infections. In the decade-long ARTENEX survey, C. famata was identified only in a few cases, which may indicate that C. famata is much less common as an etiologic agent of invasive candidiasis than other species of the Candida genus.

Methods

In total, 63 strains were initially identified as C. famata by Vitek 2 and other commercial methods. These isolates were further identified using MALDI-TOF (MALDI) and aspergillosis. C. famata was sent to the SENTRY Antifungal Surveillance Program for the year 2010, and a total of 14 isolates were identified with high confidence as C. famata (Table 1). One isolate was unknown and not reliably identified by the Vitek 2 and the MALDI and was not identified as C. famata/C. guilliermondii (1). One isolate was unknown with very good confidence and a score value of 1.97, suggesting that the occurrence of this species in fungal surveillance programs in the United States is only 0.3% of the total isolates. Our recent experience was similar in that five isolates of C. famata were correctly identified as such by phenotypic methods, and molecular methods demonstrated agreement of only 55.6% agreement with DNA sequencing whereas the Vitek 2 displayed only 56.6% agreement with DNA sequencing (Table 2).

Discussion

C. famata was found to be less common as an etiologic agent of invasive candidiasis than other species of Candida. Our recent experience was similar in that five isolates of C. famata were correctly identified as such by phenotypic methods, and molecular methods demonstrated agreement of only 55.6% agreement with DNA sequencing whereas the Vitek 2 displayed only 56.6% agreement with DNA sequencing (Table 2).

Results

Among the 53 isolates originally identified as C. famata by the subtyping laboratory, only 16 (30.2%) were correctly identified with confidence using the Vitek 2 yeast identification card (Table 1). These isolates were identified as C. famata/C. guilliermondii by sequencing, MALDI-TOF (MALDI) and as DNA sequencing (1) using ITS (low discrimination between D. hansenii and D. guilliermondii) and MALDI sequencing (1) (Table 2).

Table 1: Identification by DNA sequencing, Vitek 2, MALDI-TOF and phenotypic methods for 5 isolates of Candida famata from different public health laboratories.

<table>
<thead>
<tr>
<th>Isolate</th>
<th>DNA Sequencing</th>
<th>Vitek 2</th>
<th>MALDI-TOF (MALDI)</th>
<th>Reference ID (no. of isolates)</th>
</tr>
</thead>
<tbody>
<tr>
<td>I</td>
<td>C. famata</td>
<td>neg</td>
<td>neg</td>
<td>(1)</td>
</tr>
<tr>
<td>II</td>
<td>C. famata</td>
<td>neg</td>
<td>neg</td>
<td>(1)</td>
</tr>
<tr>
<td>III</td>
<td>C. parapsilosis</td>
<td>pos</td>
<td>pos</td>
<td>(1)</td>
</tr>
<tr>
<td>IV</td>
<td>C. parapsilosis</td>
<td>pos</td>
<td>pos</td>
<td>(1)</td>
</tr>
<tr>
<td>V</td>
<td>C. parapsilosis</td>
<td>pos</td>
<td>pos</td>
<td>(1)</td>
</tr>
</tbody>
</table>

Acknowledgments

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References