Assessment of Identification Methods for Candida auris in Microbiology Laboratories in British Columbia

INTRODUCTION

Candida auris is an emerging, potentially multidrug-resistant organism linked to healthcare outbreaks. Clinical and screening isolates have been identified in at least 24 countries since its characterization in 2009. In September 2017, the first C. auris isolate was identified in a clinical specimen in British Columbia.

Studies have shown that the organism can be challenging to identify accurately using commercial platforms, including phenotypic methods and MALDI-TOF. As of 20 April, 2018, only one commercial test has been authorized by the U.S. FDA for identification of C. auris.

OBJECTIVES

1) Assess the abilities of front-line clinical laboratories in B.C. to identify accurately and reliably C. auris isolates
2) Investigate factors affecting successful identification

METHODS

A panel of 20 yeast isolates, including 10 C. auris isolates, were obtained from the National Microbiology Laboratory (Table 1)

<table>
<thead>
<tr>
<th>Yeast</th>
<th>Number of isolates</th>
</tr>
</thead>
<tbody>
<tr>
<td>Candida auris</td>
<td>10</td>
</tr>
<tr>
<td>C. duobushaemulonii</td>
<td>3</td>
</tr>
<tr>
<td>C. haemulonii</td>
<td>2</td>
</tr>
<tr>
<td>C. krusei</td>
<td>1</td>
</tr>
<tr>
<td>C. lusitaniae</td>
<td>1</td>
</tr>
<tr>
<td>Saccharomyces cerevisae</td>
<td>2</td>
</tr>
<tr>
<td>K. phaffii</td>
<td>1</td>
</tr>
</tbody>
</table>

Ten front-line laboratories received the full panel; two received an abbreviated panel of 8 yeast isolates, which included 2 C. auris isolates. Figure 1 shows morphology of C. auris and two closely related species on CHROMagar and Sabouraud Dextrose Agar.

Laboratories were instructed to work-up the unknown samples as per their local protocol for yeast identification from sterile sites.

After results were returned, a questionnaire was distributed in order to elucidate factors associated with successful identification of the unknown samples.

RESULTS

MALDI-TOF

Three laboratories utilized the Vitek®-MS MALDI-TOF:
- The standard IVD database failed to correctly identify C. auris
- The SARAMIS RUO database accurately identified all isolates
- Common Misidentifications: “No ID”

Seven laboratories utilized the Bruker Biotyper® MALDI-TOF:
- Six laboratories correctly identified C. auris with ≥90% using the 6903 library or later. The seventh laboratory initially used the v.3 library and correctly identified 10% of C. auris isolates; this improved to 100% after updating to the 6903 library
- Common Misidentifications: “No Reliable ID”; Candida sp.

Laboratories reported improved ID scores when using a full tube sample extraction, compared to spot formic acid extraction.

PHENOTYPIC SYSTEMS

Two laboratories utilized Vitek®-2 exclusively, while other laboratories used this as a secondary identification system:
- Labs using Version 7.01 did not accurately identify any C. auris isolates
- One lab using Version 8.01 identified a single C. auris isolate; a second lab using the same version did not accurately identify any isolates
- Common Misidentifications: Candida haemulonii; Cryptococcus neoformans; “Low Discrimination”

CONCLUSIONS

The identification of C. auris can be made by MALDI-TOF systems but is dependent on database and extraction methods used:
- C. auris can reliably be identified by Vitek®-MS using the SARAMIS (Research Use Only) database
- Reliable identification on the Bruker Biotyper® requires updating to the 6903 library or later
- Tube formic acid extraction improved ID scores on MALDI-TOF compared to evidence consistent with prior evidence in the literature
- Vitek®-2, a phenotypic system, did not reliably identify C. auris using Version 7.01/8.01
- This assessment has helped reinforce confidence in the capacity of microbiology laboratories in the province to accurately and reliably detect C. auris as clinical cases emerge

FUTURE DIRECTIONS

This collaborative and voluntary coordinated assessment may be applied to other emerging pathogens to help ensure B.C. remains prepared for future public health threats

REFERENCES