

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



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INTRODUCTION

Candida auris is an emerging, potentially multidrug-resistant organism linked to healthcare outbreaks¹. Clinical and screening isolates have been identified in at least 24 countries since its characterization in 2009². 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-TOF³. As of 20 April, 2018, only one commercial test has been authorized by the U.S. FDA for identification of *C. auris*⁴.

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

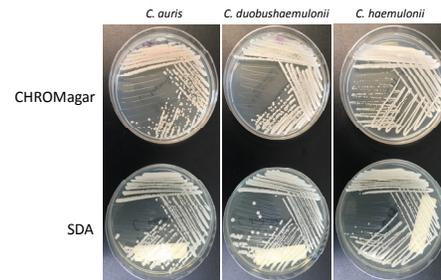
- A panel of 20 yeast isolates, including 10 *C. auris* isolates, were obtained from the National Microbiology Laboratory (Table 1)

Table 1. Testing Panel

Yeast	Number of Isolates
<i>Candida auris</i>	10
<i>Candida duobushaemulonii</i>	3
<i>Candida haemulonii</i>	2
<i>Candida krusei</i>	1
<i>Candida lusitanae</i>	1
<i>Saccharomyces cerevisiae</i>	2
<i>Kodamaea ohmeri</i>	1

- 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

Figure 1. Morphology of *Candida* species



RESULTS

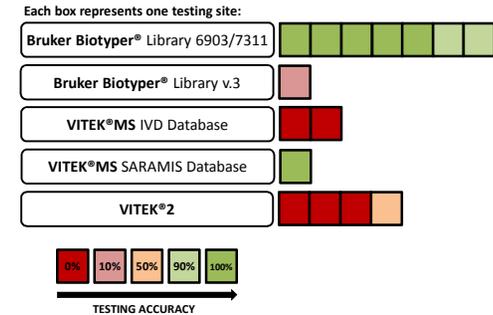
MALDI-TOF

- 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 lab 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”

Figure 2. Results of *C. auris* Testing by ID Method



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 spot extraction, consistent with prior evidence in the literature³
- 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

- 1) CDC. Clinical alert to U.S. healthcare facilities—June 2016: global emergence of invasive infections caused by the multidrug-resistant yeast *Candida auris*. Atlanta, GA: US Department of Health and Human Services, 2016. Available: <http://www.cdc.gov/fungal/diseases/candidiasis/candida-auris-alert.html>
- 2) Jeffery-Smith A, et al. 2018. *Candida auris*: a review of the literature. Clin Microbiol Rev 31:e00029-17.
- 3) Misraevska M, et al. 2017. Can multidrug-resistant *Candida auris* be reliably identified in clinical microbiology laboratories? J Clin Microbiol 55:638-640
- 4) FDA News Release: FDA authorizes new use of test, first to identify the emerging pathogen *Candida auris*. Available: <https://www.fda.gov/news-events/press-announcements/ucm625336.htm>



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