

LETTERS

The authors respond to “*Candida auris* can be identified accurately”

We thank Dr. Yeung for his interest in our primer for Canadian clinicians on *Candida auris*.^{1,2} Given word-limit constraints, we were unable to elaborate further in our article, and so we welcome the opportunity to provide clarification regarding limitations in the ability of diagnostic laboratories to identify *C. auris*.

Dr. Yeung claims that our statement that some matrix-assisted laser desorption/ionization time of flight (MALDI-TOF) mass spectrometry systems cannot accurately identify *C. auris* is misleading. However, it is essential to understand that the accuracy of *C. auris* identification by MALDI-TOF mass spectrometry is only as good as the database the instrument uses for identification. Although MALDI-TOF mass spectrometry research-use-only (RUO) databases have been able to accurately identify *C. auris* for some time,³ many clinical laboratories in Canada do not use RUO databases because of the need for additional validation before clinical implementation and the technical difficulty to use these databases.

Among microbiologists from diagnostic laboratories across Canada who are members of the Canadian MALDI-TOF Users Group (CMUG) and who responded to a 2018 survey, 28 of 60 (46.7%) used the VITEK MS (bioMérieux) and 32 of 60 (53.3%) used the Bruker Biotyper (Bruker Daltonics) platforms. Among VITEK MS users, just 1 of 28 reported occasional use of the RUO library, whereas the RUO database is obligatory with the Bruker Biotyper (Dr. Philippe Lagacé-Wiens, CMUG chair, Winnipeg; personal communication, 2019).

In 2017, CMUG member laboratories were sent a *C. auris* isolate as an unknown to identify for quality assurance. Among 27 Bruker Biotyper users who participated, 25 (92.6%) correctly reported the identification as *C. auris*, 1 (3.7%) identified but did not report *C. auris* because of low confidence, and 1 (3.7%) could not obtain a reliable identification. In contrast, among 24 VITEK MS users, just 1 (4.2%) — the laboratory with access to the VITEK MS in vitro diagnostic (IVD) version 3.2 database — reported *C. auris*, whereas 7 (29.2%) reported *Candida haemulonii*, 1 (4.2%) each reported *Candida pulcherrima* and *Candida rugose*, and 14 (58.3%) reported no identification (Dr. Philippe Lagacé-Wiens: personal communication, 2019).

Fortunately, both the Bruker Biotyper and VITEK MS systems have recently had their US Food and Drug Administration- and Health Canada-approved libraries updated to include *C. auris* (Bruker Biotyper CA version Claim 4 and VITEK MS IVD version 3.2).⁴ However, not all laboratories have updated their databases to enable accurate *C. auris* identification.

It is important for microbiologists and physicians to be aware of the possibility of inaccurate identification when using older MALDI-TOF mass spectrometry database versions, and to understand which databases are used by their local clinical microbiology laboratory. Furthermore, the specific MALDI-TOF database versions used should be considered when interpreting published studies on *C. auris* identification. The Centers for Disease Control and Prevention keeps an updated list on its website of the database library versions that can accurately identify *C. auris*,⁴ and Public Health Ontario has also indicated which database versions provide accurate identification in its January 2019 statement.⁵

Finally, common phenotypic biochemical identification methods, including the VITEK 2 YST, API 20C and BD Phoenix yeast identification systems, and MicroScan can misidentify *C. auris*.^{4,6} These systems continue to be used in smaller clinical laboratories without MALDI-TOF mass spectrometry systems.

Tanis C. Dingle PhD

Assistant professor, Division of Diagnostic and Applied Microbiology, Department of Medicine, University of Alberta, Edmonton, Alta.

Ilan S. Schwartz MD PhD

Assistant professor, Division of Infectious Diseases, Department of Medicine, University of Alberta, Edmonton, Alta.

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