Appendix 1

Identification of *Candida auris* (as of August 20, 2018). This appendix will be updated as new information about *C. auris* identification becomes available.

Some yeast identification methods are unable to differentiate *C. auris* from other yeast species. *C. auris* can be misidentified as a number of different organisms when using traditional biochemical methods for yeast identification such as VITEK 2 YST, API 20C, BD Phoenix yeast identification system, and MicroScan.

The most common misidentification of *C. auris* is *Candida haemulonii. C. haemulonii* have been less commonly observed to cause invasive infections. Therefore, *C. auris* should be suspected when *C. haemulonii* is identified on culture of blood or other normally sterile site unless the method used can reliably detect *C. auris*. *Candida* isolates from the urine and respiratory tract ultimately confirmed as *C. auris* have been initially identified as *C. haemulonii*; less data are available about the ability of *C. haemulonii* to grow in urine or the respiratory tract, although true *C. haemulonii* infections in general appear to be rare in the United States.

The table below summarizes common misidentifications based on the yeast identification method used. If any of the species listed below are identified using the specified identification method, or if species identity cannot be determined by any method, further characterization using appropriate methodology should be sought.

Common misidentifications for *C. auris* by yeast identification method	
Identification Method	**Organism *C. auris* can be misidentified as**
Bruker MALDI Biotyper (FDA database)	No misidentifications of *Candida auris*. Bruker MALDI-TOF is able to accurately identify *C. auris*
bioMérieux VITEK MS (IVD/RUO database)	*Candida haemulonii*
VITEK 2 YST (Ver. 8.01 or older)	*Candida haemulonii* *Candida duobushaemulonii*
API 20C	*Rhodotorula glutinis* (characteristic red color not present) *Candida sake*
BD Phoenix yeast identification system	*Candida haemulonii* *Candida catenulata*
MicroScan	*Candida famata* *Candida guilliermondii** *Candida lusitaniae** *Candida parapsilosis**
RapID YEAST PLUS	*Candida parapsilosis**

**C. guilliermondii, C. lusitaniae,* and *C. parapsilosis* generally make hyphae or pseudohyphae on cornmeal agar. If hyphae or pseudohyphae are not present on cornmeal agar, this should raise suspicion for *C. auris* as *C. auris*

typically does not make hyphae or pseudohyphae. However, some *C. auris* isolates have formed hyphae or pseudohyphae. Therefore, it would be prudent to consider any *C. guilliermondii, C. lusitaniae,* and *C. parapsilosis* isolates identified on MicroScan and any *C. parapsilosis* isolates identified on RapID YEAST PLUS as possible *C. auris* isolates and further identification should be sought.

How to identify *C. auris*

Diagnostic devices based on matrix-assisted laser desorption/ionization time-of-flight (MALDI-TOF) can differentiate *C. auris* from other *Candida* species, but not all the reference databases included in MALDI-TOF devices allow for detection. Currently, accurate identification of *C. auris* can be performed using the Bruker Biotyper brand MALDI-TOF using the updated Bruker FDA-approved MALDI Biotyper CA System library (Version Claim 4) or their "research use only" libraries (Versions 2014 [5627] and more recent) and VITEK (MALDI-TOF) MS RUO (with Saramis Ver 4.14 database and Saccharomycetaceae update). VITEK 2 with software version 8.01 is also able to accurately detect *C. auris*, though misidentifications may still be possible. Molecular methods based on sequencing the D1-D2 region of the 28s rDNA or the Internal Transcribed Region (ITS) of rDNA also can identify *C. auris*.