Algorithm to identify *Candida auris* based on phenotypic laboratory method and initial species identification

**PURPOSE**

*Candida auris* is a multidrug-resistant yeast that has been found in multiple countries, including the United States. *C. auris* can cause invasive infections, be passed from person to person, and persist in the environment. Its severity, communicability, and drug resistance makes correctly identifying *C. auris* crucial to treating patients and preventing infections. However, this is challenging because traditional phenotypic methods frequently misidentify *C. auris*. This algorithm details the steps needed to determine the correct *Candida* spp. based on the tests and equipment available in your lab.

**Table of Contents – Algorithms by Method**

1. Bruker Biotyper MALDI-TOF
2. bioMérieux VITEK MS MALDI-TOF
3. VITEK 2 YST
4. API 20C
5. BD Phoenix
6. MicroScan
7. RapID Yeast Plus
8. GetMark ePlex Blood Culture Identification Fungal Pathogen (BCID-FP) Panel
9. Summary of this algorithm in table form

Please note that these algorithms are based on our current knowledge about misidentification of *C. auris* and may change as we learn new information.
**Identification Method**

Bruker Biotyper MALDI-TOF

**Database/Software**

- RUO libraries (Versions 2014 [5627] and more recent)
- CA System library (Version Claim 4)

**Initial finding**

- C. auris

**Determination**

- C. auris confirmed
- C. auris

**Next steps**

*C. auris confirmed:*

Place patient in transmission-based precautions, report to CDC (candidauris@cdc.gov), and notify state and local health departments.
C. auris confirmed:
Place patient in transmission-based precautions, report to CDC (candidaauris@cdc.gov), and notify state and local health departments.
**VITEK 2 YST**

**Software version 8.01**

**C. auris** confirmed:
Place patient in transmission-based precautions, report to CDC (candidaauris@cdc.gov), and notify state and local health departments.

**C. auris possible:**
Further work-up needed to determine if actually **C. auris**. Send isolates to a reference lab, a state public health lab, a regional lab, or CDC for further identification. Place patient in transmission-based precautions and notify state and local health departments and CDC (candidaauris@cdc.gov).

**C. auris** possible:
Needs further work-up
**API 20C**

- **Rhodotorula glutinis**
  - Characteristic red color present? [No] [Yes]
    - [No] C. auris possible: Needs further work-up
    - [Yes] Likely not C. auris

- **C. sake**
  - C. auris possible: Needs further work-up

- **Candida spp. not identified**
  - C. auris possible: Needs further work-up

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**Next steps**

**C. auris suspected:**
Place patient in transmission-based precautions and notify state and local health departments and CDC (candidaauris@cdc.gov). Send any isolates suspected to be C. auris to a reference lab, a state public health lab, a regional lab, or CDC for further identification.

**Likely not C. auris:**
No further C. auris-related action required.
**Initial finding**

- C. catenulata
- C. haemulonii
- Candida spp. not identified

**Determination**

- C. auris possible: Needs further work-up
- C. auris possible: Needs further work-up
- C. auris possible: Needs further work-up

**Next steps**

**C. auris possible:**
Further work-up needed to determine if actually C. auris. Send isolates to a reference lab, a state public health lab, a regional lab, or CDC for further identification. Place patient in transmission-based precautions and notify state and local health departments and CDC (candidauris@cdc.gov).
**Identification**

**Method**

- MicroScan

**Initial finding**

- C. lusitaniae
- C. guilliermondii
- C. parapsilosis
- C. famata
- Candida spp. not identified

**Test using cornmeal agar**

- No hyphae or pseudohyphae present
- Hyphae or pseudohyphae present

**Determination**

- Can rule-out C. lusitaniae, C. guilliermondii, and C. parapsilosis. 
  C. auris possible: Needs further work-up
- Likely to be C. lusitaniae, C. guilliermondii, or C. parapsilosis, but cannot rule-out C. auris. Some C. auris strains have had hyphae or pseudohyphae, so consider further work-up
- C. auris possible: Needs further work-up

**Next steps**

C. auris possible: 
Further work-up needed to determine if actually C. auris. Send isolates to a reference lab, a state public health lab, a regional lab, or CDC for further identification. Place patient in transmission-based precautions and notify state and local health departments and CDC (candidauris@cdc.gov).
**RapID Yeast Plus**

- **C. parapsilosis**
  - **No hyphae or pseudohyphae present**
    - Can rule-out *C. parapsilosis*. *C. auris* possible: Needs further work-up
  - **Hyphae or pseudohyphae present**
    - Likely to be *C. parapsilosis*, but cannot rule-out *C. auris*. Some *C. auris* strains have had hyphae or pseudohyphae, so consider further work-up

- **Candida spp. not identified**
  - *C. auris* possible: Needs further work-up

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**C. auris possible:**
Further work-up needed to determine if actually *C. auris*. Send isolates to a reference lab, a state public health lab, a regional lab, or CDC for further identification. Place patient in transmission-based precautions and notify state and local health departments and CDC (candidauris@cdc.gov).
Identification Method

GenMark ePlex BCID-FP Panel

C. auris confirmed:
Place patient in transmission-based precautions, report to CDC (candidaauris@cdc.gov), and notify state and local health departments.
### Identification Method

<table>
<thead>
<tr>
<th>Identification Method</th>
<th>Database/Software, if applicable</th>
<th>C. <em>auris</em> is confirmed if initial identification is <em>C. auris</em>.</th>
<th>C. <em>auris</em> is possible if the following initial identifications are given. Further work-up is needed to determine if the isolate is <em>C. auris</em>.</th>
</tr>
</thead>
<tbody>
<tr>
<td>Bruker Biotyper MALDI-TOF</td>
<td>RUO libraries (Versions 2014 [5627] and more recent)</td>
<td>C. <em>auris</em></td>
<td>n/a</td>
</tr>
<tr>
<td></td>
<td>CA System library (Version Claim 4)</td>
<td>C. <em>auris</em></td>
<td>n/a</td>
</tr>
<tr>
<td>bioMérieux VITEK MS MALDI-TOF</td>
<td>RUO library (with Saramis Version 4.14 database and Saccharomycetaceae update)</td>
<td>C. <em>auris</em></td>
<td>n/a</td>
</tr>
<tr>
<td></td>
<td>IVD library (v3.2)</td>
<td>C. <em>auris</em></td>
<td>n/a</td>
</tr>
</tbody>
</table>
|                       | Older IVD libraries | n/a | C. *haemulonii*  
C. *lusitaniae*  
No identification |
| VITEK 2 YST | Software version 8.01 | C. *auris* | C. *haemulonii*  
C. *duobushaemulonii*  
*Candida* spp. not identified |
|                       | Older versions | n/a | C. *haemulonii*  
C. *duobushaemulonii*  
*Candida* spp. not identified |
| API 20C | | n/a | Rhodotorula glutinis (with characteristic red color present)  
C. *sake*  
*Candida* spp. not identified |
| BD Phoenix | | n/a | C. *catenulata*  
C. *haemulonii*  
*Candida* spp. not identified |
| MicroScan | | n/a | C. *lusitaniae*  
C. *guilliermondii*  
C. *parapsilosis*  
C. *famata*  
*Candida* spp. not identified |
| RapID Yeast Plus | | n/a | C. *parapsilosis*  
*Candida* spp. not identified |
| GenMark ePlex BCID-FP Panel | | C. *auris* | n/a |

* *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, the isolate should raise suspicions of being *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 work-up should be considered.

If **C. auris** is **confirmed**: Place patient in transmission-based precautions, report to CDC (candidaauris@cdc.gov), and notify state and local health departments.

If **C. auris** is **possible**: Further work-up is needed to determine if actually *C. auris*. Send isolates to a reference lab, a state public health lab, a regional lab, or CDC for further identification. Place patient in transmission-based precautions and notify state and local health departments and CDC (candidaauris@cdc.gov).