17-ID-03

Committee: Infectious Disease

Title: Standardized Case Definition for *Candida auris* causing clinical infection and colonization in people

I. Statement of the Problem

Candida auris is an emerging fungus that presents a serious global health threat. Most strains of *C. auris* are resistant to at least one antifungal drug, and some strains are resistant to all three major classes of antifungal drugs. *Candida* infections are typically thought to reflect opportunistic infection from the host's normal flora. By contrast, *C. auris* can spread from patient to patient within healthcare facilities and contaminate healthcare environments. It has caused numerous healthcare-associated outbreaks with high mortality that have been difficult to control. In some hospitals abroad, *C. auris* has emerged as the leading cause of candidemia, accounting for up to 40% of Candida isolates. A consensus case definition would allow for standardized public health tracking of *C. auris* cases, which will be helpful in containing its spread within healthcare facilities and networks.

II. Background and Justification

Candida auris is an emerging multidrug-resistant (MDR) yeast that can cause invasive infections and is associated with high mortality. Some strains of *C. auris* have elevated minimum inhibitory concentrations (MICs) to the three major classes of antifungals, severely limiting treatment options. It can spread from patient to patient within healthcare settings and cause outbreaks, much like methicillin-resistant *Staphylococcus aureus* and multidrug-resistant *Acinetobacter*. *C. auris* requires specialized methods for identification and can be misidentified as other yeast (especially *Candida haemulonii)* by some testing methods (see Appendix 1). Unlike *C. auris*, strains of *C. haemulonii* are typically unable to grow above 37°C; therefore, *C. auris* should be suspected when *C. haemulonii* is identified on culture of invasive body sites (e.g., blood) unless the method used can reliably detect *C. auris*.

Known risk factors for *C. auris* infection are similar to those for invasive *Candida* infection in general, including central venous catheter use, recent surgery, diabetes, and recent broad-spectrum antibiotic or antifungal use. In the United States as of February 2017, *C. auris* has been observed predominantly among patients with extensive exposure to nursing homes and short-term and long-term acute care hospitals. *C. auris* is known to cause bloodstream infections, wound infections, and otitis, although it has also been cultured from urine and the respiratory tract, which may involve colonization or infection.

A standardized case definition will allow for public health tracking of *C. auris* cases, which will be helpful in containing its spread within healthcare facilities and networks. A sample case investigation form can be found in Appendix II.

III. Statement of the desired action(s) to be taken

1. Utilize standard sources (e.g. reporting*) for case ascertainment for *Candida auris*. Surveillance for *Candida auris* should use the following recommended sources of data to the extent of coverage presented in Table III.

Table III. Recommended sources of data and extent of coverage for ascertainment of cases of *Candida auris*.

Source of data for case ascertainment	Coverage	
	Population-wide	Sentinel sites
Clinician reporting	x	x
Laboratory reporting	x	x
Reporting by other entities (e.g., hospitals, veterinarians, pharmacies, poison centers)	x	x
Death certificates	x	x
Hospital discharge or outpatient records	x	x
Extracts from electronic medical records	x	x
Telephone survey		
School-based survey		
Other _____		

2. Utilize standardized criteria for case identification and classification (Sections VI and VII) for *Candida auris* but do not add *C. auris* to the *Nationally Notifiable Condition List*. If requested by CDC, jurisdictions (e.g. States and Territories) conducting surveillance according to these methods may submit case information to CDC.

IV. Goals of Surveillance

To assess the temporal, geographic, and demographic occurrence of *Candida auris* in the United States in order to facilitate its prevention and control. Surveillance will also help to identify cases of *C. auris* to help in better understanding the organism, including its transmission, pathogenicity, response to treatment, and resistance patterns. The ultimate aim is containment of *C. auris*.

V. Methods for Surveillance: Surveillance for *Candida auris* should use the recommended sources of data and the extent of coverage listed in Table III.

The primary source of data is the microbiology laboratory. Laboratories should report suspected and confirmed cases of *C. auris* to STLT public health agencies and submit suspect *C. auris* isolates to regional Antibiotic Resistance Laboratory Network (ARLN) laboratories or CDC via state public health laboratories for further characterization. Clinicians and healthcare facilities that become aware of a case of *C. auris* should report the case to STLT public health authorities. Other data sources, such as death certificates or hospital discharge data, may be used as supplementary case finding methods.

VI. Criteria for case identification

The primary source of data will be the microbiology laboratory. The laboratory should report *Candida auris* or suspect *C.auris* to public health authorities (and submit isolates for further characterization). Healthcare facilities and clinicians who become aware of patients with suspected or confirmed *C.auris* should report them to public health authorities. Other data sources (e.g., death certificates, medical records, infection control databases or hospital discharge data) may be used as supplementary case finding methods; their yield is unknown). Healthcare facilities should note that *C. auris* can be misidentified as other yeasts when using biochemical methods for yeast identification.

A. Narrative: A description of suggested criteria for case ascertainment of a specific condition.

Report to public health any of the following clinical evidence:

- Health care record diagnosis of *Candida auris* or *Candida haemulonii*
- Death certificate lists as cause of death or significant condition contributing to death: *C. auris* or *C. haemulonii*

Report to public health any of the following laboratory results detected from any bodily source, including blood, wound, skin, ear, urine, respiratory secretions, rectum, perirectal area, or other tissue or body fluids (and submit confirmed and suspect *C. auris* isolates to an ARLN laboratory or CDC via state public health laboratory for further characterization):

- *C. auris* identified on culture by a diagnostic instrument equipped to identify it (e.g., matrix-assisted laser desorption/ionization time-of-flight [MALDI-TOF], see Appendix I)
- *C. haemulonii* identified by a laboratory instrument not equipped to detect *C. auris* (as of February 2017, any method other than MALDI-TOF or ribosomal DNA sequencing)
- *Rhodotorula glutinis* identified by API 20C, and the characteristic red color of *C. glutinis* is not present
- *Candida sake* by API 20C
- *Candida catenulata* identified by BD Phoenix
- *Candida catenulata, Candida famata, Candida guilliermondii, or Candida lusitaniae* identified by Microscan
- *Candida* spp. (if unable to further speciate after validated method of *Candida* identification attempted)

Isolates may be detected by clinical cultures (i.e., collected for the purposes of diagnosing or treating disease in the normal course of care) or screening/surveillance cultures (i.e., collected for the detection of colonization and not for the purpose of diagnosing or treating disease).

Table VI-B. Table of criteria to determine whether a case should be reported to public health authorities.

Criterion		
Clinical Evidence		
Health care record diagnosis of *Candida auris*	S	
Health care record diagnosis of *Candida haemulonii*	S	
Death certificate lists as cause of death or significant condition contributing to death: *C. auris*	S	
Death certificate lists as cause of death or significant condition contributing to death: *C. haemulonii*	S	
Laboratory Evidence		
C. auris identified on culture by a diagnostic instrument equipped to identify it (e.g., MALDI-TOF or some phenotypic methods)		S
C. haemulonii identified by a laboratory instrument not equipped to detect *C. auris* (as of February 2017, any method other than MALDI-TOF or ribosomal DNA sequencing)		S
Rhodotorula glutinis identified by API 20C, and the characteristic red color of *R. glutinis* is not present		S
Candida sake identified by API 20C		S
Candida catenulata identified by BD Phoenix		S
Candida catenulata, Candida famata, Candida guilliermondii, or *Candida lusitaniae* identified by MicroScan		S
Candida spp. (if unable to further speciate after validated method of *Candida* identification attempted)		S

Notes:
S = This criterion alone is Sufficient to report a case.
* A requisition or order for any of the “S” laboratory tests is sufficient to meet the reporting criteria.

C. Disease-specific data elements
None

VII. Case Definition for Case Classification

A. Narrative: Description of criteria to determine how a case should be classified.

Clinical Description
Clinical manifestation of *C. auris* infection depends upon the site of infection. Patients with *C. auris* bloodstream infection typically have sepsis and severe illness. Other invasive infections, such as intraabdominal candidiasis can also occur. *C. auris* has also been found to cause wound infections and otitis. *C. auris* has been found to colonize the skin of asymptomatic people.

Clinical Criteria
None

Laboratory Criteria

Confirmatory laboratory evidence:

- Culture of *Candida auris* from any body site, including blood, wound, skin, ear, urine, rectum, respiratory secretions, or other body fluids.

Supportive laboratory evidence:

- Detection of *Candida haemulonii* from urine, respiratory tract, or normally sterile site (e.g., blood) by a laboratory instrument not equipped to detect *C. auris* (i.e., not MALDI-TOF or ribosomal DNA sequencing as of February 2017) and isolate is not available for further testing. See Appendix 1 for further details of performance characteristics of laboratory diagnostic tests.

C. auris cases should be stratified by:

- **Blood** vs **non-blood clinical isolates**

Epidemiologic Linkage

- Isolate from a person who is within same household, same healthcare facility, or in a healthcare facility that commonly shares patients with a facility, with another person with confirmatory laboratory evidence.

CASE CLASSIFICATION

***Candida auris* case, clinical**

Confirmed

Person with confirmatory laboratory evidence. Specimen was collected for the purposes of diagnosing or treating disease in the normal course of care. This includes cultures of body sites reflecting invasive infection (e.g., blood, cerebrospinal fluid). Culture of wounds, urine, central venous catheter tips, and the respiratory tract would be classified as clinical cases unless the laboratory report indicates that the culture was performed as part of screening or surveillance and not in the normal course of care. Specimen source is NOT a screening/surveillance swab, such as skin (e.g., axilla, groin), external ear canal, nares, rectum, or stool

Probable

Person with supportive laboratory evidence and evidence of epidemiologic linkage.

Suspect

Person with supportive laboratory evidence and no evidence of epidemiologic linkage.

***Candida auris* case, screening/surveillance**

Confirmed

Person with confirmatory laboratory evidence. Specimen was collected for the purpose of screening or surveillance. Specimen site is skin (e.g., axilla, groin), external ear canal, nares, rectum, stool, or other external body site. Cultures from other specimen sites, such as urine and respiratory cultures, collected specifically for screening or surveillance would be classified under this classification as well.

Criteria to distinguish a new case of this disease or condition from reports or notifications which should not be enumerated as a new case for surveillance

- Count a clinical case only once even if a patient has a new event in the future (i.e., a new clinical isolate from a patient reported as a previous case would not be counted again). If a person previously had a suspect case, he or she may subsequently be counted as having a probable or confirmed case; the suspect case would be deleted. Similarly, if a person previously had a probable case, he or she may subsequently be counted as having a confirmed case; the probable case would be deleted.
- For colonization (screening/surveillance culture), count patient only once regardless of the interval between testing (assumes patient is always colonized).
- A person with a screening/surveillance case can later be categorized as having a clinical case (e.g., asymptomatic person with skin colonization who later develops invasive infection would be counted in both categories)
- A patient with a clinical case should not be counted as having a screening case thereafter (e.g., a patient with a known infection who later has skin colonization is not counted as having more than one case)

Comments:

Many laboratory instruments are unable to differentiate *C. auris* from other *Candida* species, and *C. auris* phenotypically resembles *Candida haemulonii*. Unlike *C. auris*, strains of *C. haemulonii* are typically unable to grow above 37°C, so have been less commonly observed to cause invasive infections, whereas numerous wound infections with *C. haemulonii* have been reported. 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. See Appendix 1 for details on diagnostic methods for accurately identifying *Candida auris*.

B. Classification Tables

Table VII-B. Criteria for defining a case of *Candida auris*.

	CLINICAL			**SCREENING/ SURVEILLANCE**
Criterion	**Suspect**	**Probable**	**Confirmed**	**Confirmed**
Laboratory evidence				
Specimen source: normally sterile site (e.g., blood, CSF), or respiratory tract or urine	N	N		
Specimen source: swab from skin (e.g., axilla, groin), external ear canal, nares, rectum, or stool or other external body site (usually performed as part of screening/surveillance)				N

Specimen source is NOT a screening/surveillance swab such as skin (e.g., axilla, groin), external ear canal, nares, rectum, or stool	N	N	N	
Culture of *Candida auris*			N	N
Culture of *Candida haemulonii*, identified by a laboratory instrument not equipped to detect *C. auris,* and no other tests performed	N	N		
Epidemiologic evidence				
Exposed to healthcare facility with confirmed case(s)		O		
Exposed to healthcare facility that is linked to a healthcare facility with confirmed case(s)		O		
Household contact of confirmed case		O		
Absence of known epidemiologic link (household, healthcare facility) to confirmed case	N			
Criteria to distinguish a new case:				
Not previously counted as clinical case	N	N	N	N
Not previously counted as screening case				N

Notes:
N = All "N" criteria in the same column are Necessary to classify a case. A number following an "N" indicates that this criterion is only required for a specific disease/condition subtype (see below). If the absence of a criterion (i.e., criterion NOT present) is required for the case to meet the classification criteria, list the Absence of criterion as a Necessary component.
O = At least one of these "O" (One or more) criteria in each category (e.g., clinical evidence and laboratory evidence) in the same column—in conjunction with all "N" criteria in the same column—is required to classify a case. (These "O" criteria are alternatives, which means that a single column will have either no O criteria or multiple O criteria; no column should have only one O.) A number following an "O" indicates that this criterion is only required for a specific disease/condition subtype.

VIII. Period of Surveillance
Surveillance is expected to be ongoing, as this is an emerging pathogen .

IX. Data sharing/release and print criteria
At present, there are no expectations for sharing of case data with CDC. Because *C. auris* is a concerning and emerging pathogen, please notify CDC of new cases by email (candidaauris@cdc.gov).

X. Revision History
Not applicable

XI. References

1. Mizusawa et al. Can a multi-drug resistant Candida auris be reliably identified in clinical microbiology laboratories? Journal of Clinical Microbiology, 2016. doi:10.1128/JCM.02202-16
2. Vallabhaneni, S., et. al. Investigation of the first seven reported U.S. cases of Candida auris, a globally-emerging invasive fungus — United States, May 2013–August 2016(https://www.cdc.gov/mmwr/volumes/65/wr/mm6544e1.htm?s_cid=mm6544e1_w) . MMWR, 2016, Nov 4.
3. Lockhart, S., et al., Simultaneous emergence of multidrug resistant Candida auris on three continents confirmed by whole genome sequencing and epidemiological analyses. Clinical Infectious Dis, 2016, Oct 20.
4. European Centre for Disease Prevention and Control. Candida auris in healthcare settings – Europe – 19 December 2016. Stockholm: ECDC; 2016.
5. Lee, W.G., et al., First three reported cases of nosocomial fungemia caused by Candida auris. J Clin Microbiol, 2011. 49(9): p. 3139-42.
6. Laboratory Submission Information: http://www.cdc.gov/fungal/lab_submission.html

XII. Coordination

Agencies for Response

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Appendix I.

Candida auris requires specialized methods for identification and can be misidentified as other yeast (e.g., *Candida haemulonii)* by some testing methods. Molecular methods based on sequencing the D1-D2 region of the 28s rDNA can identify isolates of *C. auris*. Diagnostic devices based on MALDI-TOF can also differentiate *C. auris* from other *Candida* species, but not all devices may include *C. auris* in the reference database to allow for detection. Table 1 summarizes the yeast identification methods reported to identify *C. auris*, as of February 2017; note that some older versions of the Bruker and bioMérieux platforms may not be able to distinguish *C. auris* from other species. This list will likely change as biochemical identification systems update their databases.

Table 2 shows the misidentification of *C. auris* isolates using specific software versions of four commercially-available biochemical identification platforms (Mizusawa et al. 2016). As *C. auris* continues to gain recognition, updated versions of yeast identification platforms may be able to identify *C. auris*; please consult instrument manufacturers for the most up-to-date information.

C. auris should be suspected when an isolate is identified as *Candida haemulonii*, because *C. auris* is most commonly misidentified as this species, including by Vitek-2, BD Phoenix, and some MALDI-TOF databases. DNA sequencing and MALDI-TOF using certain databases can distinguish *C. auris* and other related species (*e.g., C. duobushaemulonii* and *C. pseudohaemulonii*) from *C. haemulonii*.

C. auris should also be suspected when an isolate is identified as follows:

- Simply reported as *Candida* spp. after a validated method of *Candida* identification was attempted
- As *Rhodotorula glutinis* by API 20C, and the characteristic red color of *R. glutinis* is not present
- As *Candida sake* by API 20C
- As *Candida catenulata* by BD Phoenix
- As *Candida catenulata, Candida famata, Candida guilliermondii,* or *Candida lusitaniae* by MicroScan
- Note that *Saccharomyces cerevisiae* does not appear to be a frequent misidentification for *C. auris* in the United States

All confirmed and suspected *C. auris* isolates should be forwarded to regional ARLN laboratories or CDC through state public health laboratories for further characterization.

Table 1. Diagnostic Methods Differ in Ability to Accurately Identify *Candida auris**

Methods that <u>do</u> identify *C. auris*	**Methods that <u>do not</u> currently identify *C. auris* reliably**
Whole genome sequencing or marker gene sequencing of the internal transcribed spacer and D1/D2 regions	API 20C AUX (bioMérieux, Marcy l'Etoile, France)
Bruker's 6903 MSP RUO databases for Biotyper	BD Phoenix (BD Diagnostics, Sparks, MD)
Specific bioMérieux identification platforms: - VITEK 2 YST (with Ver 8.01 software) - VITEK (MALDI-TOF) MS RUO (with Saramis Ver 4.14 database and Saccharomycetaceae update)	MicroScan (Beckman Coutler, Pasadena, CA)

*Methods are continuously evolving and advancing. This list is up to date as of February 16, 2017.

CDC's MicrobeNet (https://www.cdc.gov/microbenet/index.html) is a tool that provides information for the most relevant laboratory identification methods, including MALDI-TOF, which has been curated by subject matter experts. The Biotyper Classification Module, recently released as a collaboration between CDC and Bruker, provides MicrobeNet users with access to Bruker's most up-to-date database and CDC spectral libraries. The strains of *C. auris* represented in the MicrobeNet database have been proven to accurately classify to the species level on the Biotyper.

Table 2. Biochemical identification*

Isolate no.	Species tested	API[a]	BD Phoenix[b]	Vitek-2[c]	MicroScan[d]
1	*Candida auris*	*Rhodotorula glutinis*	*C. catenulata*	*C. haemulonii*	*C. famata*
2	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. famata*
3	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. famata*
4	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. lusitaniae*
5	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. guilliermondii*
6	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. famata*
7	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. guilliermondii*
8	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. parapsilosis*
9	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. guilliermondii*
10	*C. auris*	*R. glutinis*	*C. haemulonii*	*C. haemulonii*	*C. guilliermondii*
11	*C. duobushaemulonii*	*R. glutinis*	*C. parapsilosis*	*C. haemulonii*	*C. guilliermondii*
12	*C. duobushaemulonii*	*R. glutinis*	*C. parapsilosis*	*C. haemulonii*	*C. guilliermondii*
13	*C. haemulonii*	*R. glutinis*	*C. haemulonii*	*C. haemulonii / Kodamaea ohmeri*	*C. catenulata*
14	*C. duobushaemulonii*	*R. glutinis*	*C. parapsilosis*	*C. haemulonii*	*C. parapsilosis*
15	*C. haemulonii*	*R. glutinis*	No identification	*C. haemulonii / Kodamaea ohmeri*	*C. parapsilosis*

[a] Identification at 48 hours and 72 hours of incubation; API doesn't have *C. auris, C. haemulonii, C. duobushaemulonii in* its library.

*Mizusawa et al. Can a multi-drug resistant *Candida auris* be reliably identified in clinical microbiology laboratories? Journal of Clinical Microbiology, 2016. doi:10.1128/JCM.02202-16

Appendix II:
Case Report Form for *Candida auris*.
Attached is a case report form to assist in the investigation of potential *Candida auris* cases. This is also available electronically via REDCap. Please contact HAI.Health@tn.gov to receive a copy of the database.

Candida auris Case Report Form

ID number: ________________ Sex (M)(F) Age: __________ (years)(months)(days)
Place of residence City/Town: ________________ State: ____
Location where *C. auris* specimen was collected: Institution:________________ City: _________ State: ____
Date(s) of *C. auris* specimen collection: First (MM)(DD)(YY) Second): (MM)(DD)(YY) Third: (MM)(DD)(YY)
Type(s) of sample: (blood) (other sterile site: ___) urine) (sputum) (BAL) (wound) (other non-sterile site:_________)
Type of case: (Clinical) (Screening/Surveillance)
If clinical case, did person previously have a positive screening/surveillance culture? (Yes) (No) (Unknown)
Was antifungal susceptibility testing (AFST) performed? (Yes) (No) (Unk) If yes, MICs: Fluconazole:____
Voriconazole:____ Amphotericin:____ Caspofungin ____ Anidulafungin:____ Micafungin:____
What methods are used on-site for AFST? (Broth microdilution) (E-test) (Automatic) (Other:__________________)
Was it initially misidentified? (Yes) (No) (Unk)
Using what method? (API 20C Aux)(VITEK-2)(Phoenix)(MicroScan)(other: _______________)
If yes, as what? (*C. haemulonii*) (*C. famata*) (*C. sake*) (*Candida* spp.) (Other: ________________)
Was the patient known to be colonized with other multidrug-resistant organisms (e.g., CRE, MRSA)?
(Yes, specify: ______________________) (No) (Unknown)

Healthcare Encounters

At the time of C. auris specimen collection, was the patient admitted in a healthcare facility? (Yes) (No) (Unk)
If yes, Name of facility:_______________ City: ______________ State:____Country:____________
Type of facility: (Acute care hospital) (Nursing facility) (Other: ____________________)
Date of admission (MM)(DD)(YY) Date of discharge (MM)(DD)(YY) ☐ Still hospitalized
Condition at discharge: (Alive) (Dead) (Unk)
Where was the patient admitted from? (Home) (Facility, specify: _________________) (Other: _________) (Unk)
Where was the patient discharged to? (Home) (Facility, specify: _________________) (Other: __________) (Unk)
Was the patient admitted to the intensive care unit (ICU)? (Yes) (No) (Unk) If so, length of stay in ICU: ________ days
Date of admission to the ICU (MM)(DD)(YY) Date of discharge from the ICU (MM)(DD)(YY)
(*If multiple ICU admissions, please select stay closest to *C. auris* specimen date. Order of preference: (1) stay encompassing culture, (2) stay preceding culture.)
Locations of patient during hospitalization:
Unit/floor: ___________ room: ______ From: (MM)(DD)(YY) To: (MM)(DD)(YY) on Contact precautions:(Yes) (No)
Unit/floor: ___________ room: ______ From: (MM)(DD)(YY) To: (MM)(DD)(YY) on Contact precautions:(Yes) (No)
Unit/floor: ___________ room: ______ From: (MM)(DD)(YY) To: (MM)(DD)(YY) on Contact precautions:(Yes) (No)
Unit/floor: ___________ room: ______ From: (MM)(DD)(YY) To: (MM)(DD)(YY) on Contact precautions:(Yes) (No)
Unit/floor: ___________ room: ______ From: (MM)(DD)(YY) To: (MM)(DD)(YY) on Contact precautions:(Yes) (No)
Did the patient have roommate (or wardmates if general ward) at any point while not on Contact Precautions:(Yes) (No)

Risk Factors

Known exposure to confirmed *C. auris* case-patient (e.g., via healthcare of household) (Yes) (No) (Unknown)

<u>Medical Conditions</u>:

Diabetes (Yes) (No) (Unk)
Cancer: Solid tumor (Yes) (No) (Unk)
Cancer: Hematologic Malignancy (Yes) (No) (Unk)
Transplant: Bone Marrow (Yes) (No) (Unk)
Transplant: Solid Organ (Yes) (No) (Unk)
Chronic renal failure (Yes) (No) (Unk)
Hemodialysis (Yes) (No) (Unk)
Liver disease (Yes) (No) (Unk)
Respiratory disease (COPD) (Yes) (No) (Unk)
Neurologic disease (AMS, CVA) (Yes) (No) (Unk)
HIV/AIDS (Yes) (No) (Unk)
If yes, CD4: ________ Viral load: ______________
Other immunosuppressed state: (Yes) (No) (Unk)
If yes, specify: __________________
Premature at birth (Yes) (No) (Unk)
Congenital heart defect (Yes) (No) (Unk)
Other conditions (Yes) (No) (Unk)
If yes, specify: __________________

<u>Devices and procedures</u>:

In the **<u>2 weeks</u>** prior to *C. auris* specimen collection, did the patient have or experience any of the following:
Central venous catheter: e.g. PICC, triple-lumen, dialysis catheter (Yes) (No) (Unk)
Urinary catheter: e.g. Foley (Yes) (No) (Unk)
Gastrostomy tube: e.g. PEG tube (Yes) (No) (Unk)
Endotracheal intubation: (Yes) (No) (Unk)
Tracheostomy: (Yes) (No) (Unk)
Mechanical ventilation: (Yes) (No) (Unk)
Hemodialysis: (Yes) (No) (Unk)
Intra-abdominal drain or catheter (Yes) (No) (Unk)
Other surgical procedure or device (Yes) (No) (Unk)
If other procedure or device, specify: _______________________

<u>Travel History</u>:

Has the patient recently travelled to a different country? (Y)(N)(Unk)
If yes, which country? _______________ When? (MM)(YY)
Did the patient receive healthcare there? (Yes) (No) (Unk)
If yes, when: (MM)(YY)

Treatment

In the **2 weeks** prior to *C. auris* specimen collection,
Did the patient receive broad spectrum antibiotics? (Yes) (No) (Unk)
Did the patient receive antifungal medication? (Yes) (No) (Unk) If yes, specify antifungal (e.g. fluconazole):
_____
After *C. auris* was identified, did the patient receive antifungal medication? (Yes) (No) (Unk)
If yes, specify antifungal (e.g. micafungin) and dates: _____
Begin:(MM)(DD)(YY) End:(MM)(DD)(YY)