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The Second Candida auris Isolate from Aural Discharge in Japan

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Candida is one of the most common causative agents of mycoses identified in autopsy cases in Japan (1). Candidosis is known as a hospital-acquired infection which is sometimes refractory. Candida auris is a rapidly emerging, life-threatening, fungal pathogen that is difficult to identify and shows multi-antifungal drug resistance (MDR). C. auris was first identified in 2009 from the external ear canal discharge of a patient admitted to a hospital in Japan (2). However, for reasons that remain unclear, it has not since been isolated in Japan. Meanwhile, C. auris has been identified and reported in other countries, including South Korea, India, Venezuela, the USA, Colombia, the UK, South Africa, Kuwait, Pakistan, Kenya, and Israel (3).

We have identified the second isolate of the C. auris strain (TWCC 58191) from the tympanic cavity discharge of an outpatient who presented with a history of chronic otitis media and type 1 diabetes mellitus and no history of antifungal agent usage. The cultured strain appeared slightly light pink on the CHROMagar Candida medium (Becton Dickinson, Baltimore, MD, USA) after 2 days of culturing at 35°C and was initially erroneously identified as either Candida haemulonii (99%, excellent identification) using VITEK 2 Yeast (bioMérieux, Marcy l’Etoile, France) or Saccharomyces kluyveri (45.1%, T = 0.69) using API ID 32C (bioMérieux). This strain was later determined to be a C. auris strain, using a matrix-assisted laser desorption/ionization time-of-flight mass spectrometry (MALDI-TOF MS, Microflex LT with Biotyper ver 3.0; Bruker Daltonics, Bremen, Germany) with a species level score value of 2.07. Species identification was confirmed using an internal spacer (ITS) and D1/D2 region of 26S rDNA sequences (DDBJ accession no. LC318417). The phylogenetic analysis of ITS sequences with neighbor-joining analysis, using Geneious R9 (Biomatters, l’Etoile, France) or CLUSTALW (1), was performed. The phylogenetic tree was drawn using Tamura-Nei genetic distance model and neighbor-joining bootstrap analysis (bootstrap value over 50% from 1,000 bootstrap samples).

Fig. 1. ITS sequences of Candida auris and closely related species were aligned using ClustalW. Phylogenetic tree drawn using Tamura-Nei distance model and neighbor-joining bootstrap analysis (bootstrap value over 50% from 1,000 bootstrap samples).

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174
cies, as follows: FLC 32 µg/mL, AMB 2 µg/mL, MCFG 4 µg/mL, and caspofungin (CPFG) 2 µg/mL (5). In a study conducted by the CDC, 2 µg/mL for voriconazole (VRC), 8 µg/mL for echinocandins, and 128 µg/mL for flucytosine (5FC) have been established as break points (7). C. auris is generally resistant to FLC and exhibits variable susceptibility to other classes of antifungal agents. On the other hand, 2 strains in Japan have shown significant susceptibility to antifungal agents. C. auris is phylogenetically closely related to C. haemulonii, Candida krusei, and Candida lusitaniae, which show intrinsic or inducible resistance to FLC, AMB, or both (7). Therefore, C. auris may have inducible resistance to antifungal agents, and multidrug resistance strains may possibly emerge in Japan. For this reason, our patient was not treated with any antifungal agents, and the tympanic tube was removed to irrigate the tympanic cavity.

If C. auris infection is treated empirically, echinocandin may be a relatively good option until the specific susceptibility of the strain is known (3). Following determination of the drug susceptibility, antifungal agents are required to be administered, based on these results. In case of MDR (defined as multiple antifungal agent class, including azole, echinocandin, and polyene), some experts prefer more than 2 antifungal agent administrations, notwithstanding the lack of evidence supporting such an approach (3). To prevent major outbreaks, standard and contact infection control procedures and patient quarantine are required for C. auris. A strong emphasis on adherence to appropriate hygiene, as well as cleaning and disinfecting the patient care environment, is required. A culture-negative confirmation method for patient colonization is suggested at a sampling interval of 3 months (if the last culture is positive), and at least twice, at intervals of 1 week (if the last culture is negative), by the CDC (8).

Whole-genome sequence analysis, including isolates from different geographical zones, shows that this strain has independently emerged in multiple locations (7). Basically, mechanisms of resistant strain emergence are assumed to be due to hospitalized or medical care exposure patients in endemic areas acquiring these strains which become resistant to antifungal agents and may subsequently lead to potential outbreaks (3). Because of the increasing number of inbound tourists, medical tourism, and so on, attention should be paid to the emerging C. auris strains with the aim of preventing its spread.

Conflict of interest None to declare.

REFERENCES