A study of the ecology, evolution and resistance mechanisms of Candida auris at a tertiary care center in North India
Sonakshi Gupta1, Immaculata Xeas3, Gagandeep Singh2, Saumya CS4, Adva Irani1, Manish Soneja2
1Department of Microbiology, All India Institute of Medical Sciences, New Delhi, India
2Department of Medicine, All India Institute of Medical Sciences, New Delhi, India
3Department of Pathology, Imam Khomeini Hospital Complex, Tehran University of Medical Sciences, Tehran, Iran
4Department of Infectious Diseases and Tropical Medicine, Imam Khomeini Hospital Complex, Tehran University of Medical Sciences, Tehran, Iran

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Aim: To study the ecology, evolution, and resistance mechanisms of Candida auris, using samples from patients, healthcare workers, and environmental sites, using amplified fragment length polymorphism (AFLP) and antifungal susceptibility testing (AST).

Methods: A total of 720 samples were screened for C. auris, including clinical samples from patients (mucous, body fluids), surveillance samples from patients (auricular exploration swabs), and water samples from environmental sites and objects, surface smears from hospital locations, and screening samples from healthcare personnel for hand carriage of C. auris. Samples were cultured on Sabouraud Dextrose agar (SDM) and CHROMagar Candida. Morphology and susceptibility were then confirmed using MALDI-TOF and biochemical staining techniques (API). The reference strains were identified using the VITEK 2 system. The susceptibility of isolated strains was tested using the microdilution method according to the Clinical and Laboratory Standards Institute (CLSI). The following antifungal agents were tested: fluconazole, amphotericin B, voriconazole, and caspofungin.

Results: Of the 720 samples, C. auris was identified by MALDI-TOF from 30, including 27 from routine patient samples, 128 from auricular exploration swabs, and 166 from samples from hands of healthcare workers. C. auris was not isolated from any environmental samples or hospital surfaces.

The highest rates of resistance to amphotericin B, and azoles were observed in isolates from blood (59.5% of isolates) and auricular swabs (44.3% of isolates). Resistance to caspofungin was seen in 14.28% of isolates from both groups.

Conclusion: C. auris is a growing threat in healthcare settings, and it is crucial to identify and characterize the species of C. auris to prevent the spread of this fungus. The methods used in this study included a combination of molecular and biochemical techniques to accurately identify the species and determine their susceptibility to antifungal agents.

Identification and characterization of cryptic species of Aspergillus isolated from clinical samples
Sruti Janani R1, Gagandeep Singh1, Immaculata Xeas1, Bimal Kumar Das1
AIMS, New Delhi, India

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Background and Objectives: Molds are emerging as a major cause of life-threatening infections in immunocompromised patients. There is an increasing recognition of the cryptic Aspergillus species, which are organisms that are morphologically indistinguishable yet can be differentiated by molecular methods. These organisms have been known to show a higher minimal inhibitory concentrations for the majority of the antifungal agents in vitro. Therefore, correct identification of these cryptic species is very important to administer the proper antifungal agents.

Methods: In this study, we sought to identify and characterize the cryptic species of Aspergillus from all clinical samples. The methods used to identify and characterize the cryptic species of Aspergillus included molecular and biochemical techniques. The identification of the isolates was done using the VITEK 2 system and the MALDI-TOF mass spectrometry method. The susceptibility of the isolated strains was tested using the microdilution method according to the CLSI guidelines.

Results: Of the 720 isolates, using molecular methods, 53 were identified as A. fumigatus, 53 were identified as A. flavus, 3 as A. niger, 2 as A. terreus, and 1 as A. Angrace MALDI-TOF (Vitek MS database) misidentified 2 isolates of A. nidulans and 1 isolate of A. ornithia as A. fumigatus. The 4-plex sequence analysis for the identification of cryptic species revealed that 2 isolates (12.99%) were cryptic, one was A. terreus morphologically identified as A. niger and another one was A. chroogriseus morphologically identified as A. niger.

Conclusions: Our study demonstrated the importance of identifying the cryptic species of Aspergillus. The identification of these species is crucial to administering the appropriate antifungal agents.