



Since January 2020 Elsevier has created a COVID-19 resource centre with free information in English and Mandarin on the novel coronavirus COVID-19. The COVID-19 resource centre is hosted on Elsevier Connect, the company's public news and information website.

Elsevier hereby grants permission to make all its COVID-19-related research that is available on the COVID-19 resource centre - including this research content - immediately available in PubMed Central and other publicly funded repositories, such as the WHO COVID database with rights for unrestricted research re-use and analyses in any form or by any means with acknowledgement of the original source. These permissions are granted for free by Elsevier for as long as the COVID-19 resource centre remains active.

PFM-006

A case report on the first documented case of *Candida auris* fungemia in a tertiary hospital in Philippines

Lydia Linggowaty, Gwen Marcellana*, Gelza Zabat, Ralph Villalobos. *St. Luke's Medical Center Global City, Taguig City, Philippines*

Background: *Candida auris* is a recently emerging nosocomial multidrug resistant pathogen that poses a threat to global health, particularly for hospital infection control in critical care units.

Method: We report the first documented case of *C. auris* fungemia from a tertiary care hospital in the Philippines.

Case: Patient is a 76 year old male, French national, diabetic, post-coronary artery bypass graft and aortic valve replacement, transferred from another institution after bilateral chest tube insertion due to pleural effusion from heart failure and parapneumonic process. On further work-up, he was subsequently diagnosed with a biopsy proven-Follicular B-cell lymphoma and received chemotherapy in the form of R-CHOP.

Result/Discussion: On the 104th hospital day, due to febrile and hypotensive episodes, the patient underwent septic work-up revealing *Candida auris* on two separate blood culture sites, detected by matrix-assisted laser desorption ionization time-of-flight mass spectrometry. Central tunneled catheter was removed and initial empiric antibiotics and antifungal (fluconazole) were shifted to anidulafungin. Repeat blood culture after five days of anidulafungin showed persistence of *C. auris*.

Conclusion: Nosocomial outbreaks and multiple drug resistance to *Candida auris* have been reported worldwide despite enhanced infection control protocols in hospital. Our case highlights the importance of an emerging infections other than COVID-19 pneumonia that we should be concerned of because its tendency to be multidrug resistant, difficult to be identified and has caused outbreaks in healthcare.

PFM-007

COVID-19 associated mucormycosis – unprecedented experience from a developing country

V. Shwetha, C. Sneha*, R. Ambica, S. Deepa, A. Aashish, P. Harshita, R. Shruthi, N. Shruti, P. Jyothirmai, G. Sunil, Chakravarthi, M. Silpa, B. Viswanatha, S. Nagarathna. *BMCRI & NIMHANS, Bangalore, India*

Mucormycosis is an aggressive, life-threatening infection requiring prompt diagnosis and treatment. Prevalence of mucormycosis in India was 70 times more than global prevalence, even before COVID-19 and has drastically increased at present. Our hospital is among the largest designated COVID Hospitals and has treated around twelve thousand COVID-19 patients till date. Since May 2021, COVID-19 associated mucormycosis (CAM) patients were also admitted, with predominant rhino-orbito-cerebral presentation. Among 198 CAM patients admitted, age ranged from 27 to 83 years, M: F ratio was 2:1. Majority of them hadn't taken COVID-19 vaccination. 45 had severe, 25 had moderate, 22 had mild course of COVID-19. 90% were known diabetic, many were hypertensive, had chronic kidney disease, hypothyroidism. 84 were given steroids for COVID-19, 71 were on oxygen support. Biopsy tissue/ nasal swabs were sent for KOH and fungal culture. Out of 198 samples, 111 were positive for fungal elements by KOH; most of them showed broad aseptate ribbon like hyphae suggestive of mucorales. KOH mount provided rapid diagnosis of CAM. Fungal culture showed growth in 37 samples, of which 14 were Mucorales. Slide cultures identified 10 as *Rhizopus* species, 02 as *Rhizomucor* and 02 as *Mucor*. *Rhizopus* species were predominant and identified as *R. arrhizus* by MALDI-TOF. Other fungal isolates were *Aspergillus* species and *Candida* species, *C. albicans* being commonest and fluconazole resistant. All the cases were treated with Amphotericin B and recovered, except for 02 who succumbed. Study shows that diabetes & steroid therapy can be predisposing factors for CAM. Cost effective, rapid evidence-based diagnosis of CAM by KOH can be useful in resource limited scenarios. Given the expensive therapy, challenges in managing CAM are important concerns in India.

PGN-001

Taking AIM-(1) at carbapenem resistance in *Pseudomonas aeruginosa*

Anteneh Amsalu, Sylvia A. Sapula, Jon J. Whittall, Bradley J. Hart, Jan Bell, John Turnidge, Henrietta Venter*. *Department of Microbiology, University of South Australia*

Carbapenems are potent broad-spectrum β -lactam antibiotics reserved for the treatment of serious infections caused by multi-drug-resistant Gram-negative bacteria such as *Pseudomonas aeruginosa*. The surge in *P. aeruginosa* resistant to carbapenems is an urgent threat as very few treatment options remain. Resistance to carbapenems is predominantly due to the presence of carbapenemase enzymes that deactivate the antibiotic.

Carbapenem resistant isolates of *P. aeruginosa* (n=32) were screened for carbapenem resistant genes using PCR. Carbapenemase encoding genes were detected in two isolates, the New-Delhi metallo beta-lactamase (*bla*_{NDM-1}) and the Adelaide imipenemase (*bla*_{AIM-1}) were detected in a clinical and a wastewater isolate, respectively. The sensitivity profile revealed that AIM-1 conferred much higher (>128 fold increased) levels of resistance to carbapenems when compared to NDM-1.

A further investigation using wastewater samples from various local healthcare and non-healthcare sources as well as water from a river, using probe-based qPCR revealed the presence of the *bla*_{AIM-1} gene in all the samples analysed. The widespread occurrence of *bla*_{AIM-1} throughout Adelaide hinted at a possible more widespread