Fatal anti-macrophage colony-stimulating factor (Anti-GM-CSF) antitubercules— the underrecognized cause of Cryptococcosis in non-HIV individuals: Thai case series from a tertiary care hospital

Tuvanent Pongdumib1, Pornpit Treepchapunakitakul1, Pirklow Unrom1, Wathai Tambidebdyangrii2, Mathie Chayalukkeret1

1Division of Infectious Diseases, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand
2Department of Medicine, Faculty of Medicine Siriraj Hospital, Mahidol University, Bangkok, Thailand

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Background: Cryptococcosis is an opportunistic fungal infection in immunocompromised patients. Granulocyte-macrophage colony-stimulating factor (GM-CSF) regulates the functions of phagocytes and absolute macrophages, which are crucial in the intracellular control. Anti-granulocyte-macrophage colony-stimulating factor (Anti-GM-CSF) antitubercules have been found to be associated with cryptococcosis in non-HIV individuals; however, this syndrome has never been described in Thai population.

Methods: We report here the case series of patients hospitalized in a tertiary care hospital in Northern Thailand. Results: Three apparently immunocompetent patients, 34, 38, and 45 years old, were presented with neurological manifestations. Brain computed tomography scans and lumbar punctures were performed and the results showed evidence of cryptococcal meningitis. Two of the patients also had pulmonary cryptococcosis. We performed anti-GM-CSF antitubercules ELISA assays in the patient’s sera and all of these serum samples revealed a high titre of anti-GM-CSF antitubercules. The patients were treated with amphotericin B. Deoxycholate with or without flucytosine for induction antifungal therapy, followed by flucytosine consolidation treatment. All patients were cured and had favorable outcomes.

Conclusions: Anti-GM-CSF antitubercules syndrome is underrecognized in Thai patients and is a new entity of immunodeficiency associated with cryptococcal meningitis and disseminated cryptococcosis in Thai patients.

Fatal secondary fungemia due to Trichosporon asahii onychomycosis in a diabetic patient

Saeed Taj-Alden1,2, Elaine Francisco3,4, Muna Al-Malikam3,4, Bari Theiner3,4, Duong Vu3, Teun Beekhuijsen2,4, Ferry Hagen2,4

1MycoMycology Laboratory, Department of Medicine and Pathology, Hamad Medical Corporation, Doha, Qatar
2University of Babylon, Hilla, Iraq
3Division of Infectious Diseases, École Paulista de Medicine-Universidade Federal de São Paulo, São Paulo, Brazil
4Westerdijk Fungal Biodiversity Institute, Utrecht, The Netherlands

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Objectives: We describe a fatal case of onychomycosis caused by Trichosporon asahii in a diabetic patient. The aim was to molecularly characterize the T. asahii strains from blood and tissue samples to investigate their genetic relationships.

Case: An 85-year-old morbidly obese female with a prior cerebrovascular accident, hypertension, and diabetes mellitus was admitted to a peripheral hospital with type II respiratory failure, metabolic acids, and chronic anemia. Three weeks post-hospitalization the patient remained febrile, physical examination showed that the patient had paronychia, nail pigmentation, subungual onychomycosis, and a diabetic foot ulcer. Blood cultures, as well as nail and ulcer samples, became positive for Trichosporon sp.

Methods: Trichosporon strains were subjected to molecular identification by sequencing the intergenic spacer (IGS1) region. Minimal inhibitory concentrations (MICs) were determined by the Etest microdilution method. Long-read nanopore sequencing was performed for the three clinical strains, the type-strain of T. asahii (CBS2479), and two ITS-1 gene sequences. 16S rRNA (CBS2936, CBS7812) using the native base calling kit v2 (SQK-LSK112, Oxford Nannopore Technologies). Raw data were base-called with Guppy v6, FliXX v2.9 was used to de novo assemble the genome of CBS2479, this was used as a reference for variant calling using the genomic reads of all strains.
Invasive fungal infection during COVID era at tertiary care hospital

Kumari Seema1, Abhay Kumar1, Manoj Kumar1, Ashok Sharma2, Manju Boipai3
1RIMS, Ranchi, Ranchi, India
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Introduction: Invasive fungal infection is a leading cause of morbidity and mortality in COVID patients as a secondary infection. Invasive fungal infections are often rapidly life-threatening and require specialist consultation for prompt diagnosis and therapy. The reporting of these invasive fungal infections (Mucormycosis, aspergillosis, and candidiasis) is less than its occurrence.

Objective: This study was undertaken to diagnose invasive fungal infections in COVID patients during the first, second, and third COVID-19 pandemic waves by conventional methods.

Materials and Methods: From March 2020 to December 2020 was considered the first wave pandemic. March 2021 to May 2021 was the second wave pandemic and December 2021 to February 2022 was considered the third wave pandemic era for this region. A total of 42, 146, and 87 samples were collected from patients clinically suspected to have invasive fungal infections during these pandemic waves from Covid indoor patients of RIMS, Ranchi. Among a total 24 were tissue samples, 13 BAL and 200 were usual cerebrospinal fluid samples collected from suspected patients. KOH screening of all samples was done followed by culture on SDA media.

Results: A total of 83297 (27.94%) cases were positive for KOH screening. In all, 91297 (30.4%) samples showed culture positivity. A majority of growth was for Mucorales (44.2%), Aspergillales species (28.3%), Candida species (13%), and Rhizomucor (5.7%). Among Mucorales, Rhizopus was identified in 64% followed by Mucor (28%), Absidia (15%), and Rhizomucor (3%). Among Aspergillales species, majority were A. fumigatus (48%) followed by A. niger (37%), and A. flavus (15%). Maximum positivity for invasive fungal infections was observed during the second wave pandemic (62%) followed by the third wave (27%), and the first wave (11%) respectively.

Discussion: Maximum cases were observed during and after the second wave COVID pandemic era due to encounter use of steroids during COVID treatment and cases were decreased during the third wave as compared with second wave timeframe due to the use of COVID vaccine, and many asymptomatic cases and home quarantine policy.

Conclusion: Early diagnosis and treatment of invasive fungal infections with antifungal therapy and surgical debridement are necessary to reduce mortality and end-organ damage.

Functional genomics in Candida glabrata, new tools to study stress, pathogenesis and drug resistance

Jane Uchal2
1University Of Exeter, Exeter, United Kingdom
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The pressures of life are dynamic and change on a molecular level enable organisms to grow but to adapt and survive in different environments, such as the ability to cause disease within a human host. My research focuses on the human fungal pathogen, Candida glabrata, which can cause illnesses in humans ranging from allergic reactions, infections such as thrush which affects ~75% of women or least once, to serious disease in patients that have impaired immune systems. These fungi are increasing in incidence and the reason for this increase is not understood. However, it is clear that the fungus can defend itself against high levels of stress and antifungal drugs used in treatment regimes. My hypothesis is that C. glabrata has evolved the capabilities to withstand a challenge from the combination of environmental and imposed drug stresses.

To look at C. glabrata, I will take advantage of my recent discovery of the sexual cycle in this fungus which offers novel methods to test hypotheses about evolution and pathogenesis. Pathogens of humans, such as C. glabrata, are successful because