P289 A teenage with Pythium keratitis—a case report

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Introduction: Pythium is an oomycete found in an aquatic environment and is considered to be a plant pathogen. However, it is able to cause ocular and systemic infections in humans and animals. Keratitis or corneal ulceration caused by Pythium species closely resembles fungal keratitis and is known as a pseudo-fungal infection. It is associated with high ocular morbidity owing to the difficulty in diagnosis and treatment.

Case Report: A 13-year-old adolescent from rural Sri Lanka presented with pain and tearing from left eye for 3 weeks’ duration. He was previously healthy and had no history of trauma to the eye. He had fished in a lake recently. On examination, visual acuity was only perception of light and there was a corneal ulcer in the left eye. Since the ulcer had a poor response to medical therapy, penetrating keratoplasty was performed twice with failure of the graft.

Direct smear of both corneal buttons revealed broad-spectrum fungi with occasional branch-like angles that mimic fungi of zygomycetes. Culture on Sabouraud Dextrose Agar yielded expanding white submarginal colonies. In the true mold, hyaline, occasionally septate broad fungal filaments were visible. Therefore, the organism was identified as Pythium species in the Mycology Reference Laboratory.

Repealed intracameral and intrastromal antifungal and topical and systemic antibiotic treatment resulted in a quiet, vascularized eye with the retained perception of light.

Discussion: Pythium keratitis carries a significant challenge in laboratory diagnosis due to its unicellular-like appearance. Normal PCR has higher accuracy than standard culture identification. Not being a true fungus, Pythium lacks ergosterol. Therefore, it is usually resistant to many commonly used antifungal agents which target ergosterol. High degree of suspicion is important for accurate identification in the laboratory and the clinicians should be informed for early, aggressive surgical intervention along with antimicrobial therapy in order to achieve a satisfactory outcome.

P290 Public health treatment due to rise in Candida auris candidemia infection

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Introduction: Isolation of Candida spp. from a blood sample in patients is known as candidemia. Candida albicans is the most common causative agent of candidemia globally while C. tropicalis is the most common causative agent in India. Candida parapsilosis complex, C. glabrata, and C. krusei are the other three common causative agents of candidemia. Candida auris was described in 2009 and is a public health treatment. It is multidrug-resistant and causes localized hospital outbreaks.

Objective: To determine the fungal profile of candidemia in a tertiary care hospital.

Methods: Institute ethics approval was taken. All patients admitted to the Jawaharlal Institute of Postgraduate Medical Education & Research (JIPMER), Puducherry, India from January 2020 to January 2021, whose blood culture samples yielded yeast were included in the study. The patient’s demographic details were recorded. Yeast isolates were identified by Matrix-Assisted Laser Desorption Ionization-Time of Flight Mass Spectrometry (MALDI-TOF MS) as per the manufacturer’s instruction. The antifungal susceptibility testing (AST) was performed by broth microdilution method for fluconazole, voriconazole, amphotericin B, and caspofungine as per Clinical and Laboratory Standards Institute (CLSI) M27 and interpreted by CLSI M19 and M9 and M7 document. AST of C. auris was interpreted as per Centers for Disease Control and Prevention (CDC) criteria. Results were expressed in percentages.

Results: A total of 248 blood culture samples yielded yeast cells during the study period. Approximately 43% of samples were obtained from male patients, while 57% were obtained from female patients. Most of the patients were between 41 to 60 years or under 10 years of age. A total of 122/243 (15.8%) were diabetics, and 30 (12.4%) were positive for severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). Candida tropicalis (34.7%) was the most common causative agent. It was followed by C. parapsilosis complex (20.5%), Candida albicans (16.5%), C. glabrata (13.5%), C. krusei (6.5%), and other C. spp. (3.9%). Candida auris is no longer observed as one of the top five agents of candidemia and it replaced by C. auris. The rise of candidemia due to C. auris is a cause of concern, and its prevalence is observed more than that of C. albicans in our tertiary care hospital. The antifungal resistant pattern of the top four candidemia isolates is depicted in Figure 1. The antifungal resistance was maximum in C. auris isolates, followed by C. parapsilosis complex isolates. A total of 12.2% of C. auris isolates were resistant to amphotericin B, and 4.8% of C. auris isolates were multidrug-resistant.

Conclusion: Candida tropicalis was the most common causative agent of candidemia. But the increased prevalence of C. auris over C. albicans is a cause of concern as 4.9% of C. auris isolates were multidrug-resistant.
Aspergillosis is a ubiquitous fungus in the human environment. Spores are constantly circulating in hospital and community environments alike. Infections like COVID-19 which affect not only the immune system but also lead to local immune-compromises especially in the respiratory system make the patient vulnerable to infections like Aspergillosis. Hereby, we present the prevalence of Aspergillosis infection in a tertiary care centre over a period of 1 year with special reference to co-infections with COVID-19 in Aspergillosis or mixed infection (Aspergillosis and Mucormycosis).

Material and Methods: All the samples which were submitted to Mycology Laboratory during the time period of 1 year from January 2021 to December 2021 were included in the study. The samples were processed as per the standard mycological techniques for direct examination and culture. Those patients which had direct KOH instant positive for septate hyphae and grew Aspergillus on culture were included for the purpose of this study. Records of Aspergillosis patients who were positive for COVID-19 too were assessed to look for significant associating factors.

Results: Out of a total of 6863 samples, 66 samples came out to be positive for Aspergillus sp. Out of which, 55 were identified phenotypically as A. flavus, 3 A. fumigatus, 2 A. terreus and 1 was A. niger. In five of the strains, species could not be identified even phenotypically and were reported as Aspergillus sp. Minimum isolates (43) were from sputum and paranasal sinuses (nasal discharge, nasal tissue, nasal polyp, nasal sinuses, oral cavity, mandibular means etc) 16 were pulmonary samples (sputum, tracheal aspirate, bronchoalveolar lavage, pleural fluid, lung tissue), two were corneal scrapings, two samples were dental tissue and palatal necrosis material and two were soil samples. One sample was from a patient with ear discharge. A total of 15 patient had COVID-19 infection at the time of diagnosis or within 3 months prior. In all, 12 patients had co-infections of Aspergillus and Mucormycetes (9 being COVID positive too), and 2 patients had co-infections of Aspergillus and Candida. Records of COVID-19 patients revealed that all 12 patients with co-infection of Aspergillus and Mucormycetes were treated as per guidelines for Mucormycosis infection. One of other three, two were confirmed CAPA as per the criteria. One patient was treated for COVID-19 infection only.

Conclusions: Mucormycosis was another infection during COVID-19 times, which was a huge wave, enveloping all attention. Rather Aspergillosis infections got shadowed by mucormycosis despite the fact that during COVID-19 times, as many as 15% of cases were found to be positive for Aspergillosis in COVID-19 positive patients, especially in ICU areas. In the times to come, it is speculated that sequelae of Aspergillosis infections may be seen among COVID-19 patients. Emerging drug resistance among Aspergillus can worsen the situation further.