Rhizomucor infections occurrence.

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Results:

Among the samples, A. flavus was identified in 64%. followed by Mucor (28%), Absidia (17%), and Rhizomucor (5%). A majority of growth was for Macerar (48.2%), Aspergillus species (24.3%), Candida species (15%), and mixed growth (12.7%). Among Macerar, Rhizopus was identified in 64%, followed by Mucor (28%), Absidia (17%), and Rhizomucor (5%). Among Aspergillus species, majority were A. fumigatus (48%) followed by A. niger (37%), and A. fumigatus (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 (13%) respectively.

Discussion:

Maximum cases were observed during and after the second wave COVID pandemic era due to coexistence of stresses 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.

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Imvasive fungal infection during COVID era at tertiary care hospital

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Poster session 3, September 23, 2022, 12:30 PM - 1:30 PM

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 (Mucoraceae, aspergillus, and candida) 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 82, 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 endoscopists collected from suspected patients. KOH screening of all samples was done followed by culture on SDA media.

Results: A total of 83/297 (27.9%) cases were positive for KOH screening, in all, 91/297 (30.6%) samples showed culture positivity. A majority of growth was for Macerar (44.2%), Aspergillus species (24.3%), Candida species (15%), and mixed growth (12.7%). Among Macerar, Rhizopus was identified in 64% followed by Mucor (28%), Absidia (17%), and Rhizomucor (5%). Among Aspergillus species, majority were A. fumigatus (48%) followed by A. niger (37%), and A. fumigatus (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 (13%) respectively.

Discussion:

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Conclusion:

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

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

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The pressures of life are dynamic and changes 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 ~5% of women at least once, to serious diseases in patients that have impaired immune systems. These fungi are increasing in incidence and the reasons for this increase are 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
they adapt effectively to environmental stresses encountered within the host body. Upon recognition by host immune cells, C. glabrata is engulfed and exposed to a combination of stresses. Its contrast to other pathogenic fungi, C. glabrata is highly resistant to stress allowing it to maintain the host immune defenses. This suggests that resistance to both antifungal drugs and natural host-induced stress are essential for the establishment and progression of infection. The molecular mechanisms underlying antifungal resistance and the response to individual stress have been investigated in isolation, however, little is known about how C. glabrata adapts to combinatorial stress. The mechanistic explanation of stress adaptation will yield new insights into Candida infection.

Using a newly discovered sexual cycle in C. glabrata, I have generated a series of related strains of the same fungal pathogen that have increased resistance to combinatorial drug stress. I will sequence their genomes to identify the critical genes involved in stress response and characterize the mechanisms of C. glabrata stress response. My preliminary data demonstrate that the C. glabrata response to a combinatorial stress is similar to that observed upon phagocyte engulfment. At the level of gene expression, there is an up-regulation of genes encoding functions related to stress adaption and nutrient recycling overlap. Understanding this regulatory network and the role that selected components (different genes) play in stress resistance, is essential to the development of future drug regimens.

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Comparison of Candida colonization in intensive care unit patients with and without COVID-19: First prospective cohort study from Turkey

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Purpose

Objectives: Candida species, as the main component of human mycobiota, are the most common cause of fungal infections in intensive care units (ICU). ICU patients with COVID-19 are more prone to fungal infections, due to various causes like mechanical ventilation, use of steroids, and long-term hospitalization. There is yet no extended prospective study examining Candida colonization rates, epidemiology of species, and predisposing factors in this population. This is the first prospective cohort study comparing the strain varying colonization features of Candida species in ICU patients with and without COVID-19.

Methods: This study was performed between March 2021–December 2021 in ICUs of Istanbul University, Istanbul Faculty of Medicine, Department of Anesthesiology and Reanimation. COVID-19 and non-COVID-19 ICU patients who were ≥18 years and expected to stay in the ICU for at least 7 days were included in the study.

Samples were taken at certain time intervals from different body parts of the patients (mouth, skin [axilla], rectum, and urine) (Table 1) and evaluated at Istanbul University, Istanbul Faculty of Medicine, Department of Medical Microbiology, Microbiology Laboratory. All specimens were inoculated on CHROMagar Candida media (CHROMagar Candida, France) to detect mixed growth and CHROMagar Candida Plus media (CHROMagar Candida Plus, France) to avoid missing Candida aeri.

Cultures were incubated at 35-37°C for 48 h and phenotypically different colonies on primary media were subcultured on corn meal-msoon-80 agar for determining their morphology. All strains were identified to the species level using MALDI-TOF MS (Version 4.1.8, Bruker Bremen, a subsidiary of Bruker Daltonics). The results were recorded in the database of the hospital.

Results: The study consisted of 122 ICU patients including 62 COVID-19 (25 female, 37 male, mean age 63.29 years) and 60 non-COVID-19 (24 female, 36 male, mean age 60.9 years).

A total of 1464 samples (754 COVID-19 and 708 non-COVID-19 patients) were taken (Table 1) and fungi grew in 340 (23.2%) samples. Mixed growth was observed in 108 cultures, was more frequently in COVID-19 patients (P < 0.05) and significantly higher in oral specimens (P < 0.05).

Conclusion: In this study, we found significantly higher oral, rectal, and urine Candida colonization rates in COVID-19 ICU patients compared with non-COVID-19 individuals. Increased oral Candida colonization can be the result of insufficient oral care application to those patients in the ICUs due to infection control anxiety, and also mechanical ventilation. Because non-albicans Candida strains were found significantly more frequent in patients with COVID-19 in oral, rectal and urinary regions (P < 0.05).

Contamination of wind instruments: A potential threat to musicians

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Purpose

The aim of the present study was to examine the presence of Candida species in medical and brass wind instruments to determine whether these instruments can serve as a potential source of infection and to evaluate the prevalence of Candida species in medical and brass wind instruments.

Methods: This study was conducted in the Department of Music and Dance at the Anadolu University Eskişehir Campus. The study included 150 wind instruments, including 75 medical and 75 brass wind instruments.

Results: The prevalence of Candida species in medical and brass wind instruments was found to be 28.0% and 25.3%, respectively. The most common species isolated was Candida albicans, followed by Candida tropicalis and Candida glabrata. The findings of this study suggest that medical and brass wind instruments may serve as a potential source of infection and should be handled with caution.

Conclusion: The present study highlights the importance of proper maintenance and cleaning of wind instruments to prevent the spread of Candida species and other potential pathogens. Educating musicians and instrument care providers about the potential risks associated with the use of these instruments is crucial to ensure the safety and well-being of all individuals who come into contact with them.