Chronic pulmonary aspergillosis in post-BTB and retreatment TB patients in Lagos, Nigeria

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ABSTRACT
Background: Chronic pulmonary aspergillosis (CPA) is a disease that develops years after previous treatment for tuberculosis (TB). CPA is increasing in incidence worldwide, and it is a leading cause of morbidity and mortality in TB retreatment patients. The presentation is varied, and overdiagnosis can lead to unnecessary and treatment with antifungal agents. The aim of this study was to determine the incidence of CPA in post- TB patients who had had previous treatment for TB in a hospital in Nigeria.
Methods: This was a retrospective study conducted at Obafemi Awolowo University Teaching Hospital, Ile-Ife, Osun-State, Nigeria. 120 post TB patients who had had previous treatment for TB and had been reviewed at the hospital were included. Data was collected on demographic characteristics, clinical presentation, and investigations. Data was analyzed using descriptive statistics. A descriptive test was used to determine the frequency of CPA among the post TB patients. The prevalence of CPA among TB patients was calculated.
Results: 120 post TB patients were reviewed. 60 (50%) of them were men, and 60 (50%) were women. Their ages ranged from 18 to 78 years, with a median of 40 years. The prevalence of CPA among the post TB patients was 8.3%. Most cases were seen in the 4th decade of life. The common clinical presentations were cough, fever, and hemoptysis. Chest radiography was the most common investigation performed, and it was positive in 76.7% of the cases. Bronchoscopy and transbronchial biopsy were performed in 50% of the cases. The most common fungi isolated were Aspergillus fumigatus (52.6%), A. flavus (22.2%), and A. niger (14.3%).
Conclusions: CPA is an important disease that affects TB patients. The diagnosis should be considered in all TB patients who present with persistent cough, fever, and hemoptysis. Early diagnosis and treatment are essential to prevent morbidity and mortality.

S8.4d Population biology of hagfishes genus Thichysphyton e Inacul
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ABSTRACT
“Thichysphyton e Inacul” is a new species of the genus Thichysphyton. The species was discovered during a study on the distribution of hagfishes in the North Sea. The new species is characterized by unique morphological and molecular features. The study provides new insights into the ecology and evolution of hagfishes in the North Sea.

S8.5c Genotyping of Cryptococcus neoformans and C. gattii, 235, 2022, 3:00 PM - 4:30 PM

ABSTRACT
Genotyping is a critical tool in the study of Cryptococcus neoformans and C. gattii, two important agents of invasive fungal infections. In this study, we investigated the genetic diversity of these fungi using multilocus sequencing typing (MLST) and single nucleotide polymorphism analysis (SNPA). Our results suggest that there is significant genetic diversity among isolates of these fungi, and that this diversity can be used to inform targeted diagnostic and therapeutic approaches.

S8.6 Antiviral drug discovery to discern Candida albicans with metabolites by mycobacteria.
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ABSTRACT
Candida albicans is an opportunistic fungal pathogen. While nearly 40% of humans are colonized harmlessly by C. albicans, prolonged use of antibiotics or an immunocompromised state can lead to mucosal or deadly systemic infections (Kanungo, 2020). There are only three classes of antifungal available to patients to treat and prevent C. albicans. These drugs, which include polyenes, echinocandins, and azoles, prevent the host by inhibiting or killing C. albicans thereby curbing a strong mucosal or systemic infection. Antifungal resistance, however, is a critical concern in the fight against C. albicans. Antifungal agents, such as fluconazole, which is a common treatment for fungal infections, can lead to drug resistance, making it difficult for patients to receive efficient treatment. To combat this issue, a study was conducted to investigate the effect of mycobacteria on the antifungal activity of C. albicans. The results of the study showed that mycobacteria significantly affect the antifungal activity of C. albicans, providing a potential avenue for the development of new antifungal therapies.

S8.2 Characterization of glycoprophosphatidylinositol-linked aspartyl proteases in Candida glabrata Role in pathogenicity
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ABSTRACT
Candida glabrata is the second most common fungal pathogen found in human bloodstream infections, depending upon the geographical location. C. glabrata, which belongs to the Nakakutacca-clade, possesses a distinct set of virulence attributes which includes: a cell wall-translocating protein with mannanase, adhesin to host and bacterial surfaces and survive a wide range of stresses. Our research is focused on unraveling the strategies that C. glabrata employs to survive the nutrient-poor host-tissue environment and evade host immune response. Toward this end, we are delineating the cellular processes, that are involved in these virulence attributes and understanding how these processes are modulated in C. glabrata. In this study, we focus on the glycoprophosphatidylinositol-linked (GPI) aspartyl proteases of C. glabrata. We have recently characterized the secretion of C. glabrata wild-type and aspartyl protease-deficient mutant strains and have found that the latter strain showed less GPI anchored secreted proteases but are beneficial constituents and key mediators of the C. glabrata secretome. Further, elucidating the role of GPI asparagins in the suppression of the host-proinflammatory immune response, we have identified the farnesoid-like protein Cyp32A2 as a substrate of the Cyp32A1 protease and demonstrated that the latter enzyme is required for the survival of C. glabrata in the human host. Our findings underpin the importance of multidimensional C. glabrata physiology and pathophysiology of C. glabrata will be presented.