5.4d Antifungal prophylaxis in children with cancer and HSCT, September 22-22, 2022 | 4:45 PM - 6:15 PM
Objectives: Documentation and dissemination of findings of a rare fungal isolate in an immunosuppressed child.
Methods: A case study with rare fungal isolate in correlation to age, clinical condition, sample, and comorbidity was done. A 4-year-old child was admitted for routine management of B cell acute lymphoblastic.
The patient completed induction chemotherapy in July 2021. The patient was planned for consolidation in the last week of July and to rule out any infection and blood samples were sent. Patol blood samples were received in pediatric automated BacT/Alert blood culturing system and both the blood and bone marrow samples, with blood ones going to show more. No pseudohyphae were seen. Septicemia was noted. The patient was process further on HECOZAM agar showing secondary colonies at 37°C, compatible with V, with lower 100 for Dilata technology showed only viable to globule yeast cells with Hanoiastaci, enlarged cells appearing as chlamydospores without pseudohyphae or true hyphae were seen. Glucose and sucrose fermentation and then was reduced to false negative. Urac and negative was isolated as Candida equina/Canadisolate. Antifungal susceptibility showed Streptococcus for Fluconazole but susceptible to amphotericin B, voriconazole, and caspofungin. As part of routine collaboration with reference center PMIS, Bloodstream Candida isolates were sent for confirmation, and a report was generated.
Results: The isolate phylogenetically suspected as Candida lacticasea funguse was confirmed by the reference center as C. auris. Currently, patient is on routine follow-up and doing well. On reviewing of available literature on C. magnoliae, biofilm formation on fungal colonies from Brazil, used immunocompetent child with cryoglobulins from the USA, and a tandem cytologic patient from Italy were noted.
In a Chinese study of 2007, phylogenetic analysis showed a close relationship of C. magnolaic Candida dicrois. Comparison. Susceptibility with longstanding or repeated hospital admissions is a risk for nosocomial fungal infections, especially, bloodstream infections. Additionally confirming phenotype identification among C. auris, C. ananeus, and C. auris. Management of fungal infections arising from this fungal yeast is highly important.
5.5a Stand up Penguin: Genomic epidemiology and surveillance of fungal diseases
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5.5b SARS-CoV-2 associated invasive fungal sinus infections in the Sri Lankan perspective
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5.5.3 Genetic Epidemiology of Fungal Infections, September 22, 2022, 2:00 PM - 4:30 PM
Objectives: With the advent of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) sequencing the public health implications of fungal epidemiology and surveillance has been enhanced for the variety of pathogenic. For fungal agents, the U.S. Centers for Disease Control and Prevention (CDC) is working with global partners to stand up, Penguin Network, a platform that aims to equip scientists with laboratory, bioinformatics, and information resources to harness genomic data. Fungal partners are sharing genomic and epidemiological data to detect outbreaks, identify introductions, and characterize transmission of fungal infections. In 2022, Penguin Network aims to expand nine states and local health departments in the United States and two global consortia, the Boston University, Aids in India, and the National Institute for Communicable Diseases in South Africa, with a focus on Candida auris.
Methods: To streamline the enoufrastructure, CDC generated standardized operating procedures (SOPs) specific to C. auris. For Sars-CoV-2, SOPs were created for workflow and the Zero-Research QuickSTART (ZRS). Penguin/Mycologue, Quincy Deane Blood and Tissue, and Epitome (Blanca) MasterPure Yeast DNA Purification Kits. For library preparation and Illumina sequencing, PinyaNet methods used for fungal and pathologic were validated for C. auris. For NCR data submission, defined data elements were defined. For NCR-associated metadata, the following are noted: coliform was adapted to use Nextflow software and the Terra platform. For visualization with epidemiologic data, genome databases are currently being used in Microglobe. Following the methods have been done in RDcP and in laboratory information management systems to rapidly share genomic related data.
Results: To date, 11 partners have committed to building capacity for C. auris genomic sequencing and as a Penguin Partner On, seven have validated methods for DNA extraction, and nine have generated high-quality sequencing data. Only one partner has installed and locally run MycoSNAP, and none have submitted sequence data to NCBI. Conclusions: Currently, 11 Penguin partners are working to onboard C. auris genomic sequencing and bioinformatics in 2022. This process is complex, requiring several laboratories, bioinformatics, and information where feasible. For many partners, bioinformatics. The challenges are most likely to be the validation of information methods to link genomic and epidemiologic data.
5.5.4 SARS-CoV-2 associated invasive fungal sinus infections in Sri Lanka
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5.5.5 Genetic Epidemiology of Fungal Infections, September 22, 2022, 2:00 PM - 4:30 PM
Introduction: The spread of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) has led to 663,424 reported cases as of May 1, 2022, in Sri Lanka, recording the widest pandemic of the modern era. Coronavirus 2019 (COVID-19) associated mucormycosis has been on the rise within the pandemic in the neighboring India leading to soaring cases numbers estimated at 140 million population reducing 80% higher prevalence in comparison to developed countries. In Sri Lanka, has not seen a case in COVID-19 associated fungal infections on a similar scale, even though geographic conditions are closer.
Objective: The study was done with the aim of exploring the epidemiology of COVID-19 associated invasive sinus infections in Sri Lanka.
Methods: A retrospective study was done on the sinus samples received from patients suspected of having COVID-19 associated invasive sinus infections. The study was done during the third wave of the pandemic in Sri Lanka from May 1, 2021 to March 31, 2022. Multiple sinuses samples from all SARS-CoV-2 PCR positive patients received at the Mycology Reference Laboratory, Department of Microbiology and Research Foundation were included in the study. As there was presence of broad fungal flora with wide angle branching was considered suggestive of mucormycosis and the presence of macroconidial fungi in the culture of the specimen was considered confirmatory for mucormycosis. Similarly, the presence of thin branched emerging spores fungal filaments was considered suggestive of fungal infection, and the specimen was confirmed by the presence of growth in the culture. Following the details on the request forms were analyzed to identify demographic data and risk factors in COVID-19 associated invasive sinus infections.
Results: A total of 135 sinus samples were tested from 102 SARS-CoV-2 PCR positive patients during the pandemic. All 45 patients (44%, 49/102) had positive findings indicating fungal sinusitis. The median age was 56 (IQR 49-61) years in the positive cases (Table 1). The study was done by the percent of the positive cases of sinus infections 10.5% (5/135) the most common species was documented in 35 (34%, 1/102) patients. Culture proven mucormycosis was seen in 20 patients while direct microscopic evidence was seen in 28 patients. All mucormycosis isolates were identified using biochemical tests were identified by methylation patterns and the ability to form a 3-rayed, 4-rayed, or 5-rayed hairpin. Of fungus growing in the cultures, 2 patients with A. flavus and 1 with T. terreus infection were seen. Mixed growth of A. flavus and R. rhodochrous was seen in 1 patient. Risk factors were diabetes mellitus, hypertension, and chronic kidney disease. Diabetes mellitus was seen in 35 (31%) of 102 patients with mucormycosis, while 2 patients had chronic kidney disease and 5 had hypertension.
Conclusion: This study demonstrates that fungal sinusitis is a significant entity in Sri Lanka with 34% proven mucormycosis infection in the samples received at the Mycology Reference Laboratory from SARS-CoV-2 PCR positive patients. Diabetes mellitus was seen in 31% of the COVID-19 associated mucormycosis cases. However, further studies are required to establish the effect of risk factors on infections.