SARS-CoV-2-associated invasive fungal sinus infection: the Sri Lankan perspective
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Objectives: With the advent of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) sequencing, the public health mandates in the pandemic's context to rapidly identify and surveil scenarios that have informed for a variety of pathogens. For SARS-CoV-2, the U.S. Centers for Disease Control and Prevention (CDC) is working with global partners to stand up PangNet, a network that aims to equip scientists with laboratory, bioinformatics, and information resources to harness genomic data. PangNet partners will have immediate access to data, enabling cross-sectional analyses, and characterizing transmission of fungal infections. In 2022, PangNet aims to expand nine site and local health departments in the United States and two global network members, the Northern Netherlands in the Netherlands and the Instituto Nacional de Salud in Colombia and the National Institute for Communicable Diseases in South Africa, with a focus on Candida auris.

Methods: To streamlining the evolving pipeline, CDC generated standardized operating procedures (SOPs) specific to C. auris. SOPs were created for workflows using the Zyme Research QuickDNA v3. For PangNet, the data were processed using the data pre-processing framework, and Perl scripts, and a C. auris-specific NextC and a C. auris-specific analysis were run. Further, the C. auris-specific datasets and C. auris-specific databases are the most challenging activities with the instrumentation of MycoSNP and the ability to back up each step of the process is the main barrier. Next steps will focus on the validation of information methods to link genomic and epidemiologic data.

Results: To date, 11 partners have committed to building capacity for C. auris genomic sequencing and analysis as a PangNet partner. Of these, seven have validated methods for DNA extraction, and nine have generated high-quality sequencing data. Only one partner has installed and locally run MycoSNP, and nine have submitted raw sequence data to NCBI. Challenges currently, 11 PangNet partners are working to subcategorize C. auris genomic sequencing and bioinformatics analysis in 2022. This process is complex, requiring several laboratories, bioinformatics, and informatics workflow partners. For many partners, bioinformatics analysis and C. auris reference databases are the most challenging activities with the instrumentation of MycoSNP and the ability to back up each step of the process.

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 sinus samples from all SARS-CoV-2 PCR-positive patients received at the Mycology Reference Laboratory at University of Colombo School of Medicine were included in the study. The presence of fungal pathogens in the samples collected from the patients was considered significant for fungal infection. The clinical characteristics of patients, the associated symptoms and signs of sinusitis, and the type of fungal pathogens isolated from the samples were noted.

Results: A total of 135 sinus samples were received from 102 SARS-CoV-2 PCR-positive patients during the third wave. All 45 patients (44%, 63/135) had positive findings indicating fungal sinusitis. The median age was 54 (IQR 40–61) years in the patients with positive results. The most common symptom associated with fungal sinusitis was headache in 35 (4% 35/135) patients. Culture-proven mucormycosis was seen in 20 patients while direct microscopic evidence was seen in 28 patients. All mucormycosis patients isolated Rhizopus arrhizus which was identified by morphological and molecular methods. A total of 15 cases of mucormycosis grew in the cultures, 2 patients with A. fumigatus and 1 with A. niger. In 1 patient, A. terreus sinus infection was seen. Mixed growth of A. fumigatus and Rhizopus arrhizus was seen in 1 patient. Risk factors associated with fungal sinusitis were hypertension and diabetes mellitus. Diabetes mellitus was seen in 31 (23% of 135) COVID-19-associated sinus infections. However, further studies are required to establish the risk factors on mucormycosis.

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 sinus infections. However, further studies are required to establish the risk factors on mucormycosis.