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Updated of Macromycetes in COVID-19—A retrospective study in a tertiary care hospital in Pune
Sangeeta Mohan
Christian Medical College, Ludhiana, India
Poster session 5, September 23, 2022, 12:30 PM - 1:30 PM

Objectives: Coronavirus disease 2019 (COVID-19), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), is a highly contagious and lethal coronavirus pandemic. Macromycetes have been reported as one of the main fungal pathogens to exist as co-infection with COVID-19. Factors that contribute to a higher incidence of Macromycetes or Mucorales in COVID-19 patients are high-glucose levels in their blood (glucomony, minor hypoxia, high lipids, and increased blood viscosity). The presence of these factors may encourage Mucorales to infect human tissues, leading to the development of a potentially life-threatening infection. The most common types of Macromycetes are those that cause filamentary disease, which is responsible for 90% of fungal-Behavioral Clinical forms and accounts for 60% of cases in multiple macromycetosis cases in India.

Methods: A retrospective study was conducted at Christian Medical College and Hospital, Ludhiana from May 1, 2021 to February 28, 2022 for a duration of 10 months. The samples obtained were necrotic bone marrow or mucor from the thoracic and upper extremities. The sample obtained was sent on Sabouraud’s Dextrose Agar (SDA) at 25°C ± 2°C, followed by 40% KOH examination. The tubes were routinely checked once in a week and Lactophenol Cotton Blue (LPCB) preparation was made from using the isolate once it becomes culture positive.

Results: 11 fungal samples were positive for yeast and 20 were positive for filamentous fungi. The most common types of Macromycetes were Mucorales, which include Rhizopus species, Rhizomucor species, and Absidia species. Among these, the commonest pathogenic Mucorales were Rhizopus sp., Mucor sp., and Phialophora sp., respectively.

Conclusion: COVID-19 has increased the prevalence of fungal infections and the spectrum of filamentous fungi remains essential in nosocomial care units in order to implement appropriate precautions and therapeutic strategies.

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Aspergillus spp. in atypical environments with different salinity
Emila Andrade1, Dr. Vanessa Poester2, Jessica Holíga1, Dr. Manuel Souza1, Dr. Jessica Bemelfim1, Prof. Melissa Xavier1
1Laboratory of Mycology, Faculdade de Medicina (FAMED), Universidade Federal do Rio Grande (UFRG), Rio Grande, Brazil
2Programa de Graduação em Ciências Básicas de Saúde, Universidade Federal do Rio Grande do Sul (UFRGS), Porto Alegre, RS, Brazil
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Objectives: Aspergillus flavus is a fungus found in several environments due to its ubiquitability characteristics. The emergent antifungal resistance of these fungi and their relation with animal and human pathogens turned necessary a One Health approach, which unites animal, human and environmental health as one. In this context, the ocean can be an inhabitable environment in view of the high salinity and other variables like pH and temperature. However, Aspergillus spp. is reported as a pathogen of marine animals, and the ocean can be a reservoir and/or creator of resistant strains considering the unfavorable conditions found there.

Purpose: We aimed to evaluate the seasonal frequency of Aspergillus spp. in different coastal environments in southern Brazil.

Methods: Samples of surface seawater were collected monthly from July 2021 to April 2022 at three coastal environments in the municipality of Rio Grande/RS: the locations were 1) Lagoh thano estrutural das Pias (~5°05'57".-30°56'49".S, 2) Lagoh thano (~32°14'52".-32°10'09".S) and 3) Saco ao mar (32°20'44".-13°13'58".W). Water samples (100 mL) were collected in sterile bottles, refrigerated and cultured within 12 h. An adapted technique of filtering marine bacteria (0.45 μm) culture by vacuum filtration system was performed. Briefly, after filtration, the membrane was transferred to a Falcon tube with 10 μl of sterile saline and stored at 4°C for later. Subsequently, the membrane was disposed of Sabouraud dextrose (SDA) slants. Sabouraud dextrose and albicans agar slants were cultured at 25°C for 5 days from the environment. To evaluate the rate of recovery, a fragment of colon sections was cultured in duplicate by spreading on SDAC agar plates. Incubated at 30°C for 7 days, being evaluated daily for fungal growth. Aspergillus spp. were identified at species level by macro and molecular morphological characteristics. The determination of the water salinity in the samples was performed with a TSM multiparameter (PRODIS).

Results: The average salinity of the water samples (n = 10) was 18.19 PSU (SD ± 1.482) at point 1 (Lagoh thano), 19.41 PSU (SD ± 1.900) at point 2 (Lagoh thano), and 31.31 PSU (SD ± 1.581) for point 3 (Saco ao mar). Aspergillus spp. were cultured in 23%, 37%, and 40% of the samples at points 1, 2, and 3, respectively. A total of 30 isolates were obtained, being 13 Aspergillus, 10 Fusarium, 3 Sclerotinia, and 3 Sclerotinia. In point 1 and 2, the Fusarium section predominated (37.5% and 34%, respectively). In point 3, the Fusarium section, point 3, Flavus section (32%) and Penicilli section (32%) predominated. And in point 3, Fusarium section (32%) predominated.

Conclusion: Although pathogenic Aspergillus spp. can be isolated from environments with distinct salinity sections, the salinity section seems to have less frequent to isolate salinity positive ones. Their respective antifungal susceptibility profile will be pondered.

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Low rate of Sporothrix spp. recovery from storage in mineral oil along period study
Vanessa Poester2, Beatriz Roca1, Mariana Vieira1, Mariana Trápaga1, Lívia Mouchão3, Gabriel Kielke3, Melissa Xavier1
1Universidade Federal do Rio Grande (UFRG), Faculdade de Medicina (FAMED), Rio Grande, Brazil
2Pós-Graduação em Ciências da Saúde, FAMED, UFRG, Rio Grande, Brazil
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Background: An essential goal in the concept of storage is the conservation of the mycological material for possible retrieval during the course of the investigation. The mycological material must be stored in conditions that ensure the best chances for a future microscopical and molecular identification. Previous studies have demonstrated the importance of Sporothrix species in the diagnosis of sporotrichosis, a chronic infection caused by S. schenckii. The use of mineral oil has been predominantly used for long-term storage of mycological material. A study conducted by AOAC International reported the mineral oil to be the storage medium with the highest storage efficiency of fungal material, followed by glycerol and lyophilization.

Methods: Sporothrix species were isolated in potato dextrose agar, incubated at 30°C for 30 days and stored in mineral oil for 10 years. The mycological material was recovered from mineral oil and isolated in Sabouraud dextrose agar, incubated at 30°C for 21 days along the same incubation as sporotrichosis patients and confirmed using morphological and molecular analysis. All fungal isolates were submitted to a 16S-28S rDNA sequencing, and a phylogenetic analysis was performed using the BLAST algorithm.

Results: A total of 10 Sporothrix isolates were recovered from mineral oil storage along 10 years. A total of 10 isolates of Sporothrix schenckii were confirmed for the analysis, and all isolates were positive for the fungus Sporothrix schenckii. All isolates were submitted to a 16S-28S rDNA sequencing, and a phylogenetic analysis was performed using the BLAST algorithm. The results showed that 95% of the isolates were identified as Sporothrix schenckii, with 100% similarity.

Conclusion: The low rate of Sporothrix spp. recovery from storage in mineral oil along period study is an important finding for the field of mycology, as it highlights the importance of proper storage conditions for mycological material. The results of this study suggest that Sporothrix spp. can be successfully stored in mineral oil along period study, and future studies should be conducted to evaluate the long-term storage of other fungal species under similar conditions.

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The relation of mating type (MAT) preference and source in the opportunistic pathogen Talaromyces marneffei
Sha Liu1, Lü Shuo2, Xi Liyang3, Xin Zhou2
1Department of Dermatology, The Sun Yat-sen Memorial Hospital, Guangzhou, China
2Department of Dermatology, Southern Medical University, Guangdong, China
3Rashbroid University Medical Center, Nijmegen, Netherlands

Introduction: Talaromyces marneffei is an emerging opportunistic pathogen that causes disseminated infections in immunocompromised patients, particularly in patients with human immunodeficiency virus (HIV) infection. The non-mating type (MAT) of T. marneffei is the most common mating type detected in clinical isolates. However, the mating type (MAT) preference and source of T. marneffei remain unclear.

Objectives: To determine the mating type of Talaromyces marneffei in a sample of 107 strains and to explore the possible relationship between mating type and fungus virulence.

Methods: We performed PCP analysis to determine the mating type distribution of Talaromyces marneffei in 107 strains. We also analyzed the relationship between mating type and isolated sources (including HIV-positive patients, HIV-negative patients, cancer patients, and environment). Further, the Talaromyces marneffei model of infection was used to test the virulence differences between different mating types and source environments.

Results: The results showed the entire sample population of T. marneffei with an overabundance of MAT1-2 alleles, with MAT1-2 and MAT1-1 in the isolates from HIV-negative patients. However, no significant differences in the survival of the Talaromyces marneffei infected larva with either MAT1-1 (6 days) or MAT1-2 (4 days) isolates. Similar results were also observed in the fungal growth and virulence analysis results. The results of this study will help to determine the virulence differences between different mating types and source environments.

Conclusion: The results show that Talaromyces marneffei has a preference for MAT1-2, which is the most common mating type detected in clinical isolates. The results of this study will help to determine the virulence differences between different mating types and source environments.