Conclusions: Fungal BSI has emerged as an important cause of morbidity and mortality in neonates. Reporting of fungal bloodstream infections and the spectra of infecting molds and yeasts are essential measures in neonatal intensive care units in order to implement appropriate preventions and therapeutic strategies.

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Aspergillus spp. in neonatal environments with different salinity

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

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

Methods: Samples of surface water were collected monthly from July 2021 to April 2022 at five coastal environments in the municipality of Rio Grande. The locations were 1) Lagoinha ostrearia das Patos (0°52′30″.5–12°58′00″.6, 2° Lagoinh 12.34922°S, 12.09983°W); 2) Sun/camau beach (12°2044.6°–12°17.983°W); 3) Water samples (100 mL) were collected in sterile bottles, refrigerated and cultured within 12 h. An adapted technique for harvesting fungal spores (0.45 μm) by culture in vacuum filtration system was performed. Briefly, after filtration, the membrane was transferred to a Falcon tube with 10 mL of sterile saline and vortexed (3 min) for elution. Subsequently, the membrane was disposed on Sabouraud dextrose (5% Bacto dextrose) and aliquot of it was transferred to 3500 rpm (5 min) and the precipitate (100 μL) also was cultured in duplicate by spreading on SMAC plates. Plates were incubated at 30°C for 7 days, being evaluated daily for fungal growth. Aspergillus spp. were identified at species level by macro and macro-mycological characteristics. The determination of the water salinity in the samples was performed with a YSI multiparameter (ProDSS).

Results: The average salinity of the water samples (n = 10) was 18.19°PSU (SD = 14.40) at point 1 (Lagoinh), 18.84°PSU (SD = 16.80) at point 2 (Lagoinha Ostrearia das Patos), 13.31 PSI (SD = 3.81) for point 3. 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 Fusarium, 10 Penicillium, 4 Aspergillus, and 3 Talaromyces. In point 1 and 2, the Penicillium section predominated (33.3% and 34%, respectively). In point 3, Fusarium predominated, with Penicillium corresponding to just 21%.

Conclusions: Although pathogenic Aspergillus species can be isolated from environments with distinct salinities, the section Penicillium may be less to frequent in high salinity waters. Their aspergillus17 specificity profile would be trend promisingly.

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Low rate of Sporothrix spp. recovery from storage in mineral oil after period storage

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Objectives: We aimed to evaluate the recovery rate of isolates of Sporothrix spp. maintained for years in the mineral oil after the mineral oil was a fungal collection.

Methods: Sporothrix spp. isolates were originally cultured in tubes with potato dextrose agar, incubated at 30°C for 14 days. One isolate from each culture was frozen at -80°C and recovered, were transferred to mineral oil and stored for 5 years. The isolates were cultured on Sabouraud dextrose agar, 7 days at 30°C.

Conclusions: Differenting with previous reports, mineral oil was a failure method to keep Sporothrix spp. isolates stable independent of the period of storage. Therefore, optimization of this methodology is necessary, and other methods must be implemented to guarantee the preservation of Sporothrix spp. isolates in fungal collections.

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The relation of mating type (MAT) preference and source in the opportunist pathogen Talaromyces marneffei

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Objectives: We analyzed the distribution of mating-type genes in T. marneffei strains. We also analyzed the relationship between mating-type genes and fungal isolates (including HIV-positive patients, HIV-negative patients, non-HIV patients, and environment). Further, Drosophila melanogaster model of infection was used to study the virulence difference between different mating-type strains and fungus virulence.

Methods: We performed PCR analysis to determine the distribution of mating-type genes in T. marneffei strains. We also analyzed the relationship between mating-type genes and fungal isolates (including HIV-positive patients, HIV-negative patients, non-HIV patients, and environment). Further, Drosophila melanogaster model of infection was used to study the virulence difference between different mating-type strains and fungus virulence.

Results: The results showed that the main population of T. marneffei was with an overabundance of MAT1-1 alleles, but with high ratio of MAT1-1 isoforms from HIV-negative patients. However, no significant difference in the survival of the Drosophila melanogaster infected either with MAT1-1 (64%) or MAT1-2 (48%) isoforms. Similar results were also observed in the analysis of virulence analysis results using Talaromyces marneffei model. Objective: To determine mating type in a sample of 107 strains and to explore the possible relationship between mating-type and fungus virulence.

Results: We performed PCR analysis to determine the distribution of mating-type genes in T. marneffei strains. We also analyzed the relationship between mating-type genes and fungal isolates (including HIV-positive patients, HIV-negative patients, non-HIV patients, and environment). Further, Drosophila melanogaster model of infection was used to study the virulence difference between different mating-type strains and fungus virulence.

Conclusions: This study supported the hypothesis that T. marneffei has a mating type preference and the analysis of different mating type strains could be important for understanding the risk factors of the disease.