Conclusion: FUNI has emerged as an important cause of morbidity and mortality in neonates. Reporting of fungal bloodstream infections and the spectrum of infections caused by these organisms are essential measures in neonatal intensive care units in order to implement appropriate preventive and therapeutic strategies.

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Aspergillus spp. in coastal environments with different salinity

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Background: FUNI is a genus found in several environments due to its ubiquitous characteristics. The emerging 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. Our aim was 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 July 2022 at three coastal environments in the municipality of RioGrande. The locations were 1) Lagoinha extraflora das Patos (~52.0557°S, 12.9860°W); 2) Lagoa com ~32.1492°S, 12.1009°W; and 3) Saco/Canavial beach (~32.2064°S, 12.1719°W). Water samples (~1000 mL) were collected in sterile bottles, refrigerated and cultured within 12 h. An adapted technique of filtering bacteria (~0.45 μm) culture by vacuum filtration system was performed. Briefly, after filtration, the membrane was transferred to a falcibus tube with 10 mL of sterile saline and stored at 4°C for 48 h. Subsequently, the membrane was disposed on Sabouraud dextrose (SDM) agar, and fungi and albicans colonies were counted. To evaluate the rate of recovery, a fragment of the precipitate (100 μL) was also cultured in duplicate by spreading on SMAC plates. Plates were incubated at 37°C for 5 days, being evaluated daily for fungal growth. Aspergillus spp. were identified at species level by macro and microbiological characteristics. The determination of the water salinity in the samples was performed with a TSM multiparameter (ProDOS).

Results: The average salinity of the water samples (~10) was 18.19 PSU (SD = 14.06) at point (1), 18.94 PSU (SD = 12.04) at point (2), and 15.63 PSU (SD = 11.10) at point (3). The Aspergillus spp. isolated were 23%, 37%, and 40% of the samples at points 1, 2, and 3, respectively. A total of 30 isolates were obtained, being 13 Sansef, 10 Paecilomyces, 4-108, and 3 T. longo. The Aspergillus spp. were isolated as 23%, 37%, and 40% of the samples at points 1, 2, and 3, respectively. A total of 30 isolates were obtained, being 13 Sansef, 10 Paecilomyces, 4-108, and 3 T. longo. The Aspergillus spp. were isolated as

Conclusions: Although pathogenic Aspergillus species can be isolated from environments with different salinities, the salinity factor seems to be less frequent in low-salinity waters. Their antifungal susceptibility profile will be redundantly presented.

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

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The relation of mating type (MAT) preference and source in the opportunistic pathogen Talassomonas marinae

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Background: Genome-wide comparisons have shown Talassomonas marinae possessed a stable mating type locus in its massive genes. But the function of the mating type locus in T. marinae is not clear. The potential recombination might lead to prototrophic strain, such as the evolution in clinical, and the evolution in the environmental. The stability of the mating mode of T. marinae is of great interest.

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

Methods: We performed PCR analysis to determine the mating type of strains in 107 T. marinae strains. We also analyzed the relationship between mating type and isolates including (HIV-positive patients, HIV-negative patients, healthy individuals, and environment). Further, Drosophila melanogaster model of infection was used to compare the virulence differences between different mating type and fungi virulence.

Results: The results showed an entire sample population of T. marinae with a predominance of MAT1-1 alleles, but with a high frequency of MAT1-1 in the isolates from HIV-negative patients. However, no significant differences in the survival of the Drosophila melanogaster infected with either MAT1-1 or MAT1-2 isolates. Similar results were also observed in the virulence analysis with mouse models. Analyses revealed no significant differences in pathogenicity of mating types.

Conclusions: All isolates bearing mating type idiomorphs and unequal distribution. The distribution of the MAT gene seems unrelated to different sources. And the pathogenicity differences are independent of mating type genotypes and source.