significantly

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Urgoase in control specimens of all sites analyzed

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Objective: Cardiovascular disease (CVD), caused by the severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) pandemic, has devastating and broad-ranging impacts. Macrococci have been shown to have a significant function to exist as co-infection with COVID-19. Factors that contribute to a higher incidence of Macrococci or Macrococci to germinate in COVID-19 patients are high glucose levels in their blood (gluconeogenic metabolism), low oxygen content (hypoxia), high iron levels, and decreased phagocytic activity of neutrophils due to inflammation, because of cytokine storms in SARS-CoV-2 infection. Macrococci is an opportunistic disease caused by oral Mucobacter and gastric anaerobes. The most common opportunistic pathogens in the gastrointestinal tract are Rotalia rubrum, an alpha-2 bacterium which is responsible for 95% cases of Blasto-Osphalum formal and accounts for 40% cases of Macrococci in cities. 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. Most of the samples obtained were nasotracheal bronchoscope or microbiota from the trachea of patients. The sample collected was inoculated on Sabouraud’s Dextrose agar (SDA) 5% w/v at 27°C, followed by 40% KOH examination. The tubes were routinely checked once in a week and Lactophenol Cotton Blue (LPCB) preparation was made from the isolating isolate once it became culture positive. Results: From the microbiological analysis of 149 patients, 102 patients were positive for COVID-19 (85.2%) and 47 patients were COVID-19 negative. Among 172 isolates obtained from 149 patients, 123 isolates were Rotalia rubrum and 18 isolates were Rhotococcus spp. Among the culture-positive cases for Macrococci, 13 (72.2%) cases were COVID-19 positive. Conclusion: COVID-19 has thrown the entire globe into chaos, and thus is still specific to care for this critical illness. Patients are susceptible to multiple fungal infections such as Macrococci in a result of the infection, immunosuppression, previous corticosteroids, and medications. Macrococci infection is severe because of its rapid disease progression and immunosuppressive states. Macrococci infections require immediate and adequate management. Therefore, development of various strategies to acquire iron from the environment. These strategies are available to microorganisms to uptake iron from the environment: acidification of the environment, reduction of ferric ions to the more soluble ferrous form, and synthesis of siderophores. Therefore, it is important to understand the mechanism of iron acquisition of Macrococci in order to develop strategies to prevent or control these infections. In the Macrococ genome database, one putative gene encoding a ferric-binding transport protein, which belongs to the ABC transporter superfamily (MPF), was coding found. In Saccharomyces cerevisiae, alcohol acid, and yeast-like species (Saccharomyces carlsbergensis) are known to uptake iron. The tentative iron uptake was the major function of the isolates, being a known fact from the isolates. Later, a characteristic pattern of the isolates was observed, after the growth and operation of the colonized. Colonies were grown at room temperature (around 25°C). A total of 52 isolates of Sropehophote spp. (mostly S. brevidens) maintained for 4-108 months (mean of 49.7 months) were included in the study, being isolated from cats (42%), 31 from household mice (8%), 10 from house rats (3%), and 1 from domestic birds (1%). The rate of colonized, a fraction of the isolates was calibrated in duplicate in plates with Sabouraud’s dextrose agar and incubated at 25°C until the fungal growth or for 50 days. To analyze the results, frequency, mean, and standard deviation (SD) were calculated, as well as the Kruskal-Wallis test was performed, using the SPSS statistical program. Results: Only 14% (n = 34) of the fungal isolates were recovered from oral cavity material within a mean of 46 days of storage (SD: 0.3), being a 10% (n = 22) of the recovered isolates (n = 202), and 20% (n = 42) of the isolates were recovered from oral cavity material (n = 202), and 20% (n = 42) of the isolates were recovered from oral cavity material (n = 202). The 204 isolates that could not be recovered, were stored for a mean of 47 months (SD: 25.5) (P < 0.05). Conclusion: Designing with previous reports, mineral oil was a failure method to keep Sropehophote spp. stable independently of the period of storage. Therefore, optimization of this methodology is necessary, and other methods must be implemented to guarantee the preservation of Sropehophote spp. isolates in fungal collections.

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The relation of mating type (MAT) preference and source in the opportunistic pathogen Talamenekum pumilum

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Background: Genome-wide analyses have shown that Talamenekum pumilum possesses a stable mating type locus in its main races. But the function of the mating type loci in T. pumilum is not clear. The potential recombination might lead to predict the evolution, such as the evolution in clinical, the evolution in environmental. The isolates were selected from antifungal drugs and viruses.

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

Methods: We performed PCR analysis to determine the mating type groups in 107 T. pumilum strains. We also analyzed the relationship between mating-type and isolated sources (including HIV-positive patients, HIV-negative patients, bat-related care, and environment). Further, Drusophila melanogaster model of infection was used to compare the virulence difference between different mating types and fungus sources.

Results: The results showed an equal sample population of T. pumilum with an overabundance of MAT-1 alleles, but with a higher MAT-1 in the isolates from HIV-positive patients. However, no significant difference in the survival of the Drusophila melanogaster infected with either MAT-1 (6.1 days) or MAT-2 (4.1 days) isolates. Similar results were also observed using the Drusophila melanogaster survival analysis method. In conclusion, all isolates bearing mating type alleles show no significant and unequal distribution. The distribution of the MAT groups seems related to different sources. And the pathogenicity differences are independent of mating type genotypes and source.