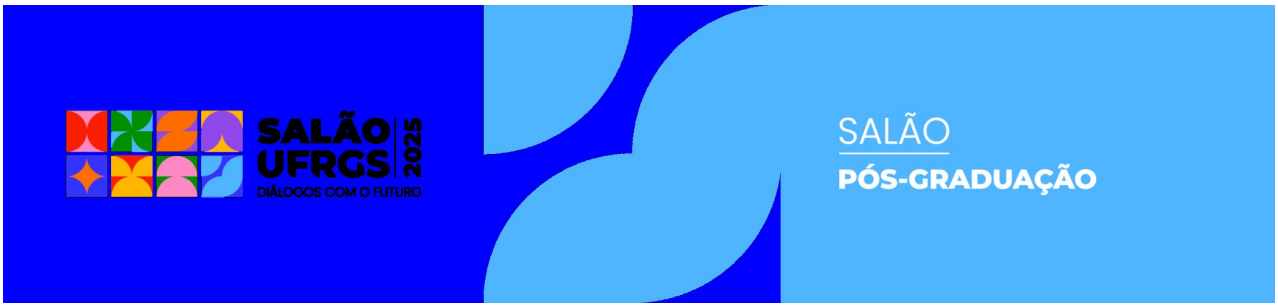


Evento	Salão UFRGS 2025: I SALÃO DA PÓS-GRADUAÇÃO
Ano	2025
Local	Campus do Vale - UFRGS
Título	Characterization of microbial interactions and resistance among respiratory infection isolates
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RESUMO: Respiratory infections are often caused by polymicrobial communities, where fungi and bacteria interact in complex ways. These interactions, particularly relevant when associated with pathogenic microorganisms, ranging from antagonism to synergism, can lead to dysbiosis and affect the progression of infections. Additionally, polymicrobial associations are capable of modulating the expression of genes related to virulence and antimicrobial resistance, thereby influencing interspecies signaling processes and the host immune response. However, understanding the molecular mechanisms underlying these interactions and their role in respiratory infections remains a challenge. Polymicrobial interactions are diverse and complex, occurring not only between species of the same kingdom but also among microorganisms from different kingdoms. Therefore, this study aims to characterize the interactions among three microorganisms—*Pseudomonas aeruginosa*, *Staphylococcus* sp., and *Candida albicans*—isolated from the bronchoalveolar lavage of a patient with a polymicrobial respiratory infection, to analyze the biophysical dynamics of polymicrobial interactions, and identify genetic determinants associated with antimicrobial resistance. The microorganisms were identified by MALDI-TOF, followed by genomic DNA extraction using the phenol-chloroform method and subsequent sequencing on the Illumina Novaseq 6000 platform. Growth curves of the monocultures were performed in 96-well plates, starting from cultures adjusted to an initial optical density of OD_{600} = 0.01, including serial dilutions down to 1:1000, in Luria-Bertani (LB) and Brain Heart Infusion (BHI) for the bacteria, and LB, BHI, Potato Dextrose Agar (PDA), and Yeast extract Peptone Dextrose (YPD) for the yeast. Optical density readings were taken every 15 minutes over a 60-hour period using a microplate reader, with plate agitation performed before each reading. Data were analyzed using the *Growthcurver* package in the R environment to obtain parameters for the logistic equation with the best fit for the data. Antimicrobial susceptibility tests using diffusion disks were performed according to EUCAST guidelines (for bacteria) and NCCLS guidelines (for yeast). Biofilm formation assays with crystal violet were conducted in monoculture and pairwise co-culture (50:50 and 95:5 ratios) in BHI medium. Data analysis and visualization were performed in R. The growth curves revealed distinct trends in proliferation dynamics among the three isolates. At lower dilutions, in BHI, *C. albicans* and *Staphylococcus* sp. showed higher growth rates (r = 0.204 and r = 0.212, respectively), while *P. aeruginosa* reached the highest rate in LB (r = 0.228). Under the same conditions, the carrying capacity (K) values for *C. albicans*, *Staphylococcus* sp., and *P. aeruginosa* were K = 0.618, K = 0.966, and K = 0.743, respectively. Among the three microorganisms, *Staphylococcus* sp. exhibited a relevant antimicrobial resistance profile, showing resistance to all antibiotics tested by disk diffusion. The panel included compounds from different classes, such as β-lactams, aminoglycosides, fluoroquinolones, carbapenems, and sulfonamides. The *Staphylococcus* sp. isolate, in monoculture (100%), exhibited the highest levels of biofilm production. In contrast, *P. aeruginosa* and *C. albicans* showed little to no adherence capacity when grown individually. Several co-inoculations revealed synergistic or antagonistic effects, indicating that specific microbial interactions strongly influence this behavior, suggesting potential cooperative or antagonistic relationships among the tested isolates. Future perspectives include genomic analysis of the isolates and characterization of the biofilm produced in triple co-culture, along with its composition and properties. The data obtained so far demonstrate that the microorganisms studied have clinical relevance, emphasizing the importance of microbial interactions in shaping disease progression and therapeutic outcomes.

PALAVRAS-CHAVE: interactions; biofilm; resistance