Identification of Airborne Bacteria and Fungi on a Ship in Malaysia using Next-Generation Sequencing

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Abstract

The ship's indoor air quality (IAQ) is susceptible to bioaerosol contaminants, including bacteria and fungi, due to the humid and enclosed living environment. These bioaerosols cause inboard problems, such as ship-acquired infections (SAI) that can trigger allergic and inflammatory reactions. Besides that, they contribute property losses through microbiologically-induced corrosion (MIC) and materials biodegradation. Nevertheless, research on ships' bioaerosols remains limited, especially in Malaysia. Therefore, this study aims to identify airborne bacteria and fungi on a Malaysian ship to monitor inboard bioaerosol contamination, thus recognizing their potential harm. The bioaerosols at four ship compartments; cabin, common room (CR), electrical room (ER), and mess were sampled on media agar using SAS Super IAQ air sampler at 100L/min flow rate. After incubation, the bacterial and fungal DNA were extracted, amplified, and sequenced by amplicon sequencing using the Next-generation sequencing, Nanopore platform. Data was analysed using MicrobiomeAnalyst tool. Results found that the ship's indoor air was inhabited by percentages of opportunistic pathogens and cellulolytic bacteria, such as *Staphylococcus epidermidis* (CR: 3%, ER:15%), *Staphylococcus saprophyticus* (CR:10%, ER: 1%, mess: 0.01%), and *Bacillus spp.* (CR: 1%, ER: 10%, mess: 85%). Fungal identification revealed the presence of *Aspergillus spp.,* known to cause Aspergillosis and emit microbial volatile organic compounds (mVOCs), such as *A. alabamensis* (cabin: 52%) and *A. versicolor* (cabin: 0.2%, ER: 24%) onboard. In conclusion, this study discovered the biohazard and biodeterioration potential risks onboard, consequently highlighting the importance of having bioaerosol monitoring inside ships as the preliminary step to control and prevent bioaerosol-related problems onboard.

Keywords: Indoor air quality; Ship; Airborne bacteria; Airborne fungi; Next-generation sequencing.