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Harnessing next-generation sequencing to monitor unculturable pathogenic bacteria in the indoor hospital building
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Abstract
The hospital indoor air microbiome, a diverse range of microorganisms, gains prominence amid the COVID-19 pandemic. Elevated awareness underscores implications for patient and staff well-being. Concerns about risks to indoor air quality persist due to prolonged indoor exposure, necessitating further research on specific threats within the hospital environment. In this study, an independent culture-based approach was used to analyze the baseline core microbiome present in hospital environments, utilizing amplicon sequencing on the next-generation sequencing technology to target the V3 region of the 16S rRNA gene. Firmicutes, Proteobacteria, and Actinobacteria were the main bacterial phyla that were most isolated from the wards and clinics with different orders of abundance; Firmicutes being associated more in clinics and Actinobacteriota in wards. The bacteria Niallia taxi, Methyloversatilis universalis, unclassified Rummeliibacillus, unclassified Clostridium, and unclassified Sphingomonadaceae dominated the clinic area while ward areas reported Pseudonocardia bannensis, Rubrobacter aplysinae, unclassified Brachybacterium, unclassified Bradyrhizobium, and unclassified Mycobacterium to be the top five features. While the alpha-diversity index showed no significant differences, the beta-diversity analysis showed a significant difference between clinic and ward areas ($p<0.05$). Certain bacterial species associated with opportunistic pathogens as well as normal skin flora such as Methylobacterium spp., Cutibacterium spp., unclassified Sphingomonadaceae, and Anoxybacillus B spp., were also identified across all samples. The methods described in this research aim to establish a rapid and sensitive screening process that could be valuable for disease surveillance within the healthcare setting, shedding light on the potential impacts of the hospital microbiome on human illness. © 2024 The Authors

Author Keywords
Core microbiome; Culture-independent; Indoor microbiome; Next- generation sequencing

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