

## Original Article

# Amplicon Sequencing Reveals Bacterial Diversity of Indoor Air Microbiome in Hospital Buildings

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**ABSTRACT:** Airborne transmission of pathogens in hospitals poses a significant risk for healthcare-associated infections. Traditionally, assessing microorganisms in hospital air relies on culture methods, limiting the identification process. Advances in genome sequencing technology now allow for more accurate and unbiased identification of microbial content. This study employed amplicon sequencing to analyse the bacterial community in the indoor air microbiome of Sultan Ahmad Shah Medical Centre (SASMEC). Dust samples from 12 randomly selected air-handling unit (AHU) rooms were collected, and genomic DNA was extracted and sequenced targeting the V3 region of 16S rRNA. The Illumina NovaSeq 6000 system performed short-read amplicon sequencing. The results revealed diverse bacterial communities in AHU supply and return units, with Proteobacteria, Firmicutes, and Actinobacteria being the most common phyla. Dominant bacterial species included *Methylobacterium* spp., *Nesterenkonia* spp., *Rubrobacter A bracarensis*, *Flavobacteriaceae* spp., and *Salinisphaera* spp., with *Methylobacterium* spp. posing concerns due to its association with opportunistic infections. The study highlights the importance of using next-generation sequencing and culture-independent methods to monitor indoor air microbiomes. This provides crucial insights for managing biological contaminants, including airborne transmission, and enhances infectious disease surveillance in healthcare settings.

**Keywords:** Air Microbiome, Amplicon Sequencing, Bacteria, Culture-Independent Method, Hospital, Malaysia

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