Spatially and temporally resolved monitoring of microbial communities in hospital intensive care units: Insights into colonization and antimicrobial resistance

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INTRODUCTION

In care settings such as hospitals, vulnerable patients are exposed to a wide array of microbial species, with some harmful species presenting antimicrobial resistance (AMR). Often these exposures can result in infections, called hospital-acquired infections (HAIs). In those who are immunocompromised, HAIs can result in severe complications and fatal outcomes.

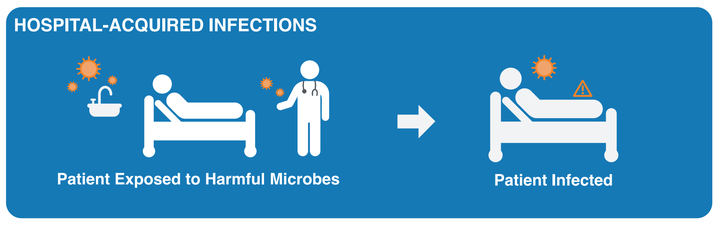

Figure 1. Vulnerable patients are exposed to microbial communities from other patients, care staff, and the built environment of the facility, leading to HAIs which can be life-threatening.

Careful reporting of the microbial species present and the AMR they present is vital to preventing HAIs. In hospitals, monitoring is completed through culture-based approaches, and reporting is typically compiled annually in antibiograms.

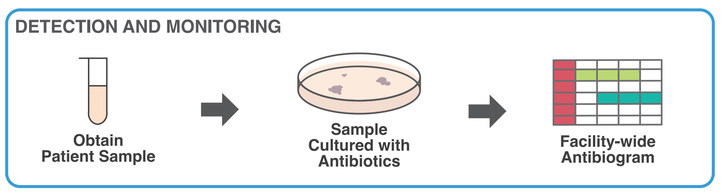

Figure 2. Detection and monitoring of the microbial communities present and AMR is completed with culture-based approaches and reported annually in antibiograms.

PROJECT OVERVIEW

In 2023, a tertiary care hospital opened a new intensive care unit (ICU). This provided the opportunity to, investigate the spatial and temporal dynamics of microbial communities in the built environment.
The success of the proposed investigation hinges on the following aims:

1. **Successfully characterize the microbial community dynamics in a high-risk clinical setting.**
2. **Investigate how microbial communities shift in response to patient activity by comparing the change in profile over time.**
3. **Assess the prevalence and variation of AMR-associated genes in high-risk clinical settings.**

METHODS

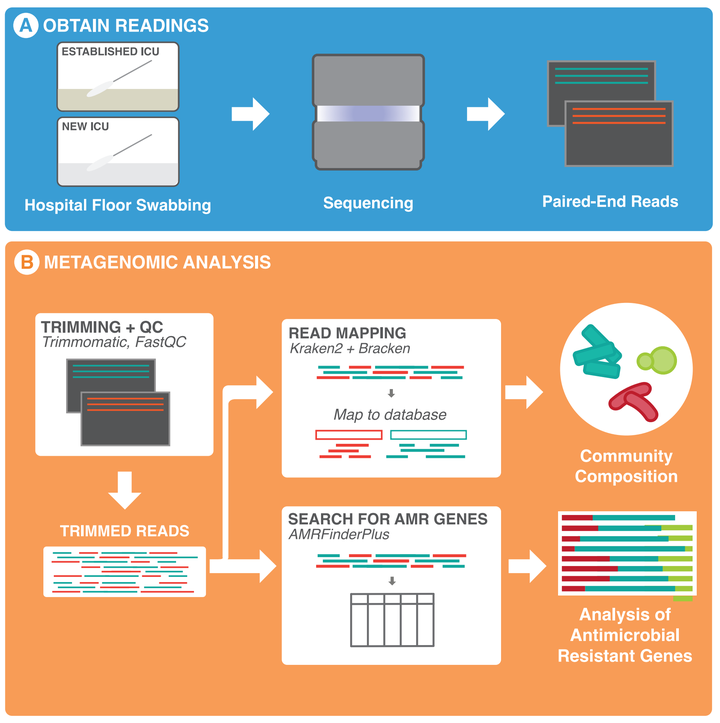

Figure 3. Graphical overview of the methods employed to assess spatial and temporal differences of microbial communities in established and newly opened ICUs of a hospital. After swabbing, sample processing, and sequencing, the paired end read files were mapped to a database of known genes for taxonomic classification. Investigations into the microbial community composition, as well as the prevalence of AMGs was then performed computationally.

Table 1. Floor swabbing approach of the established and newly opened ICU units.

DATE	ICU LOCATION *ESTABLISHED*	*NEW*	ADDITIONAL NOTES
28-04-2023	11	8	
05-05-2023	9	10	*E-110, E-200 missed, N-30, N-32, N-35 added*
12-05-2023	9	10	
19-05-2023	9	10	
26-05-2023	0	10	*Established ICU sample collection halted*
01-06-2023	0	10	

38 ESTABLISHED ICU + 58 NEW ICU FLOOR SWABS: **96 SAMPLES IN TOTAL**

RESULTS

Microbial communities present varied greatly across sampling locations and time points

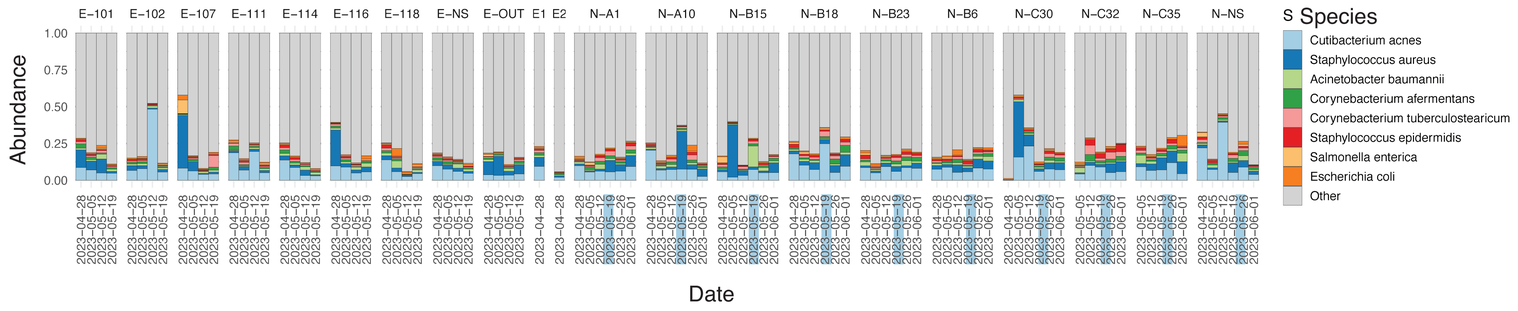

Figure 4. Microbial species abundance for the samples taxen each week within the established (E) and new ICUs (N). Blue shading indicates two days after patients were introduced within the new ICU. Nursing stations noted with an NS, and OUT indicating that swabs were performed just outside the doors of the ICU. E1 and E2 were rooms 110 and 200 of the established ICU, respectively.

Generally, the established ICU demonstrated more diversity than the new ICU

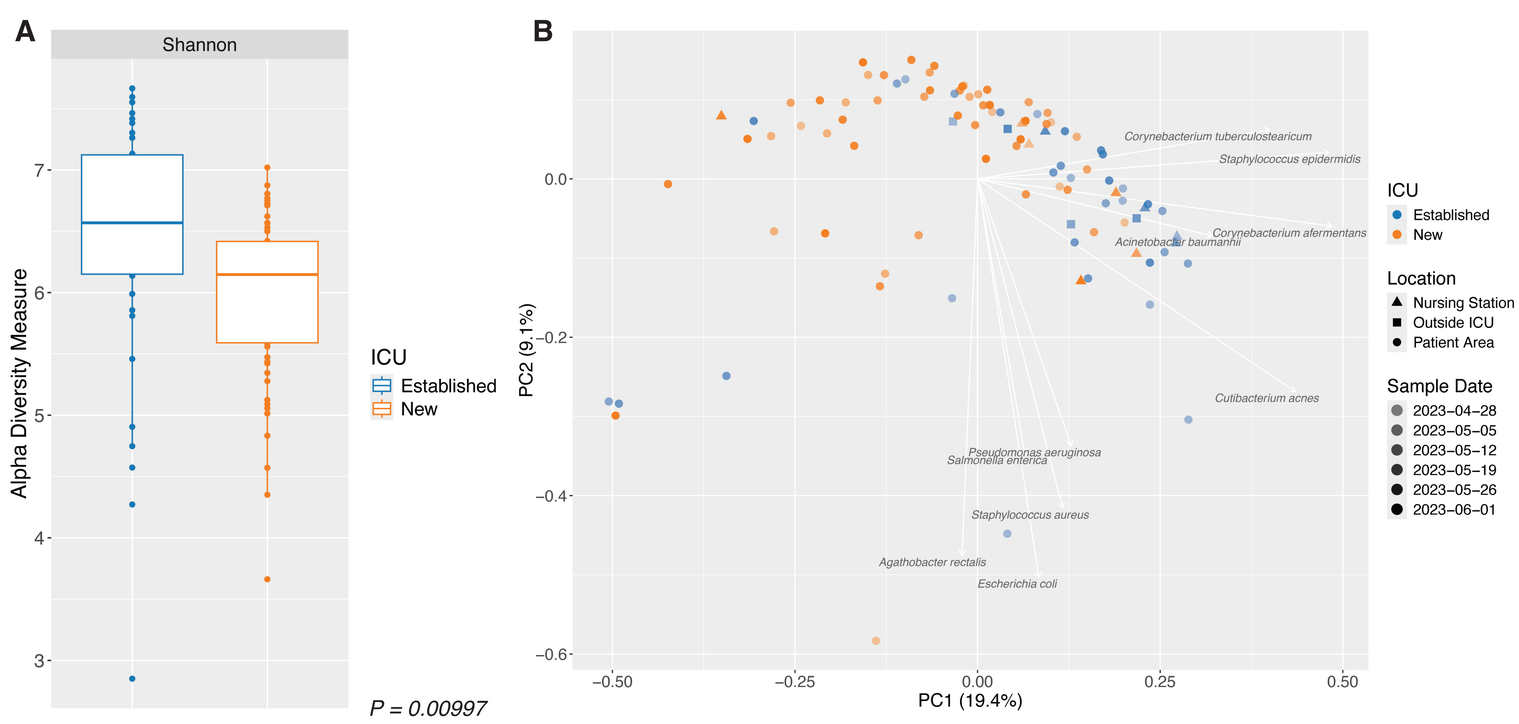

Figure 5. A Box plot of Alpha Diversity Measure for Jensen-Shannon difference between the new and established ICUs' distributions. **B** Visualization of the relationship between samples through Principal Coordinate Analysis (PCoA) of the swabs taken from each ICU. The top 10 species driving divergence and their contributions are demonstrated with the arrows.

Clinically relevant species were present within samples

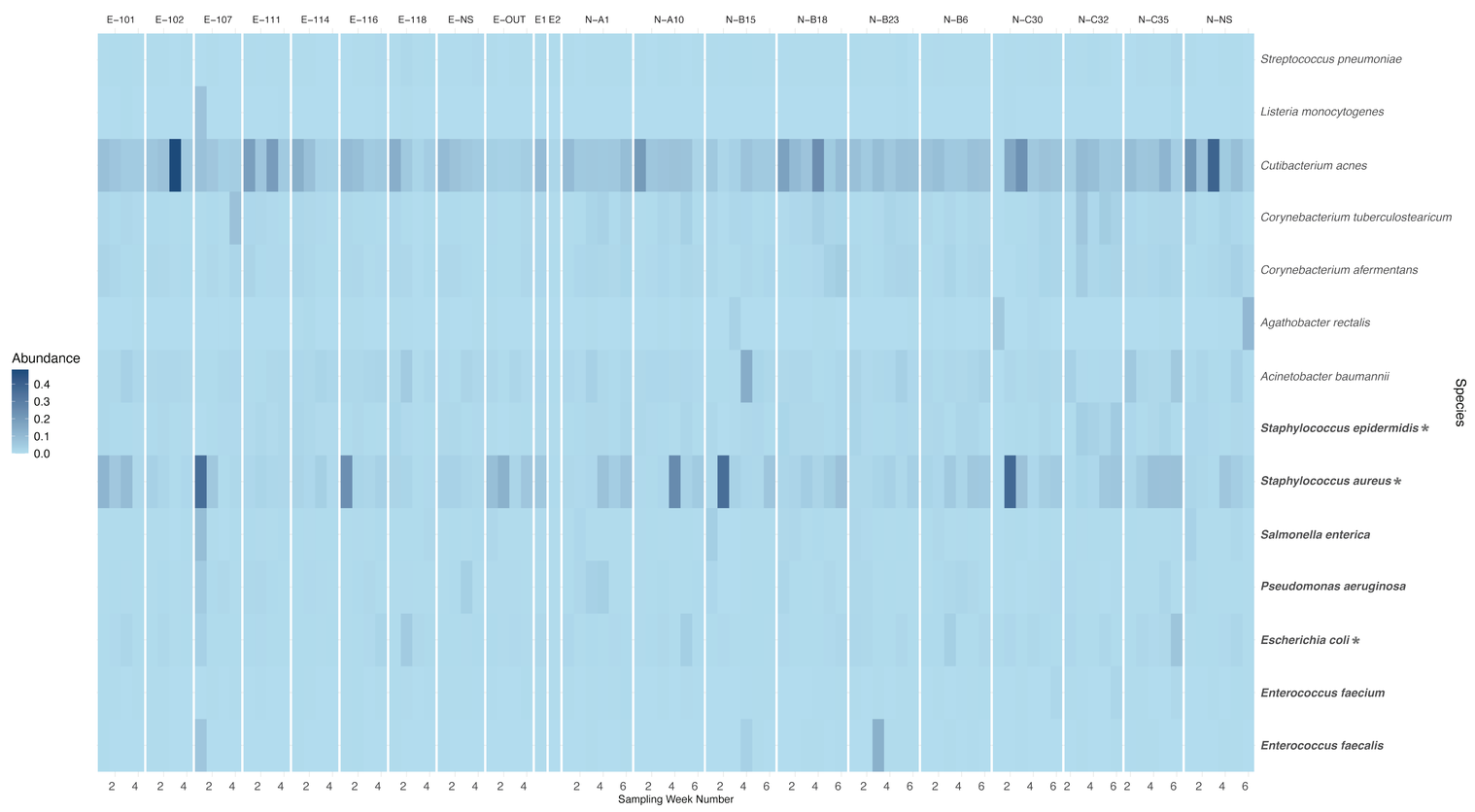

Figure 6. Heat map of clinically relevant (shown in bold bold) microbial species as well as the top 10 that drove divergence, across the weeks that samples were taken. Established ICU samples are indicated with an E, and new with an N. Asterisks indicate species that fell into both groups.

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