

## “Human and environment exchanging microbes: a hospital insight”

**Parmesani Francesca**<sup>1</sup>, Fumagalli Sara<sup>1</sup>, Armani Alice<sup>1</sup>, Ghisleni Giulia<sup>1</sup>, Bruno Antonia<sup>1</sup> & Citerio Giuseppe<sup>2</sup>.

*E-mail: f.parmesani1@campus.unimib.it*

<sup>1</sup> Department of Biotechnology and Bioscience, University of Milan-Bicocca, Milan, Italy

<sup>2</sup> School of Medicine and Surgery, University of Milan-Bicocca, Milan, Italy

**Keywords:** hospital, microbiome, amplicon-based sequencing, microbial exchange

### Abstract:

The hospital environment imposes strong selective pressure for microbial life. Numerous studies indicate that human-microbiome interactions play a critical role in immune functions and that microbiome composition can serve as a potential indicator of chronic and infectious diseases.

As part of the ANTHEM project (AdvaNced Technologies for Human-centrEd Medicine), we investigated this human-microbiome synergy, analyzing both human and environmental samples from the pre-admission ward in Fondazione IRCCS San Gerardo dei Tintori Hospital in Monza (Italy), as an example of short-stay visit.

Over four consecutive days, microbiome samples were collected from patients' dominant hand and from multiple surfaces. The DNA of each sample was extracted and sequenced using an amplicon-based approach. Resulting reads were processed through a standardized bioinformatic pipeline to infer ASVs, and microbial community structure variations were quantified and compared at ASV-level taxonomic resolution.

Our results confirmed skin microbiome to be a highly subject-specific signature, while environmental samples from different surfaces and areas consistently showed distinct microbial profiles. Notably, a substantial proportion of taxa newly appearing on patients' skin after hospital exposure were also detected in the surrounding environment. We investigated the origin of these newly acquired ASVs and found that, although they were broadly distributed across the hospital environment, their distribution differed across surfaces with the floor containing the higher number of taxa. We then evaluated patient acquisition patterns and observed considerable inter-individual variability in the extent to which environmental taxa were gained. Finally, by assessing whether these new ASVs were already present in the other participants before their arrival in the hospital, we detected frequent potential sharing events, suggesting a dynamic and reciprocal microbial exchange among individuals.

Further studies are needed to assess the driving force responsible for inter-individual microbial exchange. Such insights will be critical for designing evidence-based environmental management strategies that foster a hospital ecosystem that is both safe and microbiologically balanced for its occupants.