

# Subway and Passenger Micro-biomes Relationships: Where the Environment meets its Host?

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## ABOUT THE STUDY

The subway is a mass transit system where millions of people travel every day, they enter different wagons and touch different surfaces each time. The subway micro-biomes depend on the same factors as those of any other building. The subway occupants are people, some urban animals such as rats and cockroaches, and usually no plants. The number of people they transport and how they flow is relevant for each line and station. Ventilation is very different in each system, from the railroad aboveground and wagons with open windows to wagons heated and sealed in winter. The exchange of microorganisms through the air depends on cities' environment, particularly their land cover. Construction materials, temperature, humidity, season, and sunlight may also be playing a relevant role in micro-biome composition.

Around the world, there are 12 studies of the subway's micro-biomes. Nowadays, there is an international consortium for subway micro-biome research named MetaSUB (The MetaSUB International Consortium, 2016). In these studies, bacteria are usually identified at the genus level. Most of the bacteria belong to the Phyla Actinobacteria, Firmicutes, and Proteobacteria. The quantity and diversity of microorganisms are mainly due to anthropogenic activity and depending on the city is the proportion of environmental microorganisms. In the subways of Boston, Hong Kong, Oslo, and Mexico City, the dominant genera on the surfaces relate the skin (e.g., Cutibacterium, Staphylococcus, Streptococcus, Corynebacterium). While in the New York and Moscow subways, the dominant bacteria come from the soil (e.g., Stenotrophomonas, Pseudomonas).

Half of the studies of High Throughput Sequencing (HTS) have been carried out on surfaces. In New York, and Hong Kong, and Oslo, the dominant genera also correspond to skin associated bacteria (Staphylococcus, Micrococcus, Kocuria, Enhydrobacter, Cutibacterium); while in Barcelona and Athens, the dominant genera are environmental (e.g., Methylobacterium, Bradyrhizobium, Paracoccus, Arthrobacter, Rubellimicrobium).

This brief study only addresses bacterial diversity, although efforts have recovered fungal diversity by sequencing Internal Transcribed Spacer (ITS). Besides, viruses have been identified by Meta transcriptomics in the Barcelona subway.

Although the most abundant genera are shared in different cities and countries, there is great diversity in its particular Operational Taxonomic Unit (OTU) or Amplicon Sequence Variant (ASV) and rare organisms for each sample. There are variations between lines, stations, and types of surfaces; however, there is a specific fingerprint for each city subway system. The subway identity has been detected in different ways by analyzing the 16S rRNA gene and through metagenomes.

From the subway micro-biome analysis, it is evident that there is an interaction between passengers and these spaces. However, much remains to be done to understand interactions, their relevance, and how they are carried out.

The study in Mexico City goes a little further by analyzing the differences between the hands' palms when entering the subway and exiting. People modified their micro-biome without losing their personal signal. When exiting the subway, people's hands resemble those of the other passengers and the subway itself. These results are in agreement with those of Selway and collaborators. They observed that when people expose themselves 15 min to green spaces, it modifies their skin's micro-biome, increasing its diversity and making it more similar to the soil. The vast majority of this acquisition of new bacteria must be transitory since people have their micro-biome fingerprints. The skin micro-biome is stable; even recently, the skin micro-biome can be used to identify in crime scenes.

It is a large reservoir for antibiotic resistance. This has been analyzed in two ways, through culturable bacteria where the percentages of resistance can reach up to 75%; in addition, bacteria resistant to all the antibiotics evaluated have been found. There have been studies where the following antibiotics were tested, ampicillin, chloramphenicol, ciprofloxacin, kanamycin, nalidixic, nitrofurantoin, penicillin, streptomycin,

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tetracycline, and trimethoprim (Bactrim). An alternative way has been by searching for Antibiotic Resistance Genes (ARG) in metagenomic shotgun sequences. In Hong Kong, genes for efflux pumps and genes for resistance to fluoroquinolone, tetracycline, vancomycin, and erythromycin have been found; while in Boston, genes for efflux pumps and genes for resistance

to tetracycline and beta-lactams were detected. The ARG amounts were very different in both studies. In Hong Kong, an average of 469 ARGs per million reads was found, while in Boston, only 1.17 ARGs per million reads were found.