Chennai Metro's Transit Microbiome: Findings of the IIT Madras Study

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Why in the news

November 13, 2026: A study by researchers at the Indian Institute of Technology (IIT) Madras on the microbial communities of the Chennai Metro is in the news. According to the study, published in mSphere, a peer-reviewed journal of the American Society for Microbiology, the Chennai Metro has a distinct 'transit microbiome' that shows microbial patterns different from other urban transit systems of the world. It is the first study of its kind on the microbiome and antimicrobial resistance (AMR) genes of the Chennai Metro.

How the study was conducted

In two phases, in December 2021 and January 2022, the research team collected 96 surface swabs from 12 stations and trains on the Blue and Green Lines of Chennai Metro Rail Limited (CMRL). The samples were taken from four high-touch surfaces - station handrails (banisters), ticket vending machines (kiosks), train handrails (rods) and ticket counters. Of these, 47 samples that passed quality checks underwent shotgun (whole-genome) metagenomic sequencing, and 41 samples with more than one million reads were included in the final analysis.

For context, the Blue Line is 32.65 km long and connects Wimco Nagar Depot with Chennai International Airport, while the Green Line is 22 km long and connects Chennai Central with St. Thomas Mount.

Key findings

The study found that the type of surface meaningfully influences the composition of the microbial community, and the highest microbial diversity was found on ticket kiosks. On comparison with a

global urban dataset (MetaSUB), nine species were found to be especially more prevalent in the Chennai samples, indicating the regional distinctiveness of the city. Species from the classes Actinobacteria, Alphaproteobacteria and Gammaproteobacteria dominated most samples.

AMR genes were in low relative abundance but widely distributed - at least one AMR gene was present in more than 80 per cent of the samples, including genes linked to the rifamycin, multidrug resistance and sulfonamide families. According to the researchers, this is not an immediate cause for concern; the study highlights the need for continued surveillance to limit the risk of disease transmission in high-density transit systems, and offers a baseline framework for understanding India's urban microbiomes.

Concepts relevant for the exam

Microbiome: The combined community of all microorganisms (bacteria, fungi, viruses, etc.) living in a particular environment (such as the human body, soil or a metro surface), together with their genetic material.

Metagenomics: Direct analysis of the genetic material of all microorganisms present in an environmental sample; it allows microbes to be identified without culturing them in a laboratory. In shotgun sequencing, the entire DNA of the sample is broken into random fragments and read.

AMR (antimicrobial resistance): The condition in which microorganisms begin to survive the effect of antimicrobial drugs. The World Health Organization counts it among the major threats to global public health, and environmental sampling is one tool for monitoring it.

Prelims practice questions

Question 1. Consider the following statements with reference to the recent IIT Madras study on the microbial communities of the Chennai Metro:

1. It is the first study of its kind on the microbiome of the Chennai Metro rail network.

2. It used shotgun (whole-genome) metagenomic sequencing of the samples.

3. It was published in mSphere, a peer-reviewed journal.

(a) Only 1 and 2

(b) Only 2 and 3

(c) Only 1 and 3

(d) 1, 2 and 3

Answer and explanation

Answer: (d)

All three statements are correct. The study is the first of its kind on the microbiome and AMR genes of the Chennai Metro; the samples that passed quality checks underwent shotgun metagenomic sequencing; and it was published in mSphere, a journal of the American Society for Microbiology.

Question 2. With reference to the samples collected in the above study, consider the following statements:

1. The samples were taken from stations and trains of the Blue and Green Lines.

2. The highest microbial diversity was found on ticket vending kiosks.

3. All 96 samples collected were used in the final analysis.

(a) Only 1 and 2

(b) Only 2 and 3

(c) Only 1 and 3

(d) 1, 2 and 3

Answer and explanation

Answer: (a)

Statements 1 and 2 are correct. Statement 3 is incorrect - only 47 of the 96 samples passed quality checks and were sequenced; 41 samples were included in the final analysis.

Question 3. With reference to the findings of the study on AMR genes, consider the following statements:

1. AMR genes were in low relative abundance but widely distributed.

2. At least one AMR gene was present in more than 80 per cent of the samples.

3. The study recommended immediate public health intervention.

(a) Only 1 and 2

(b) Only 2 and 3

(c) Only 1 and 3

(d) 1, 2 and 3

Answer and explanation

Answer: (a)

Statements 1 and 2 are correct - the AMR genes (linked to the rifamycin, multidrug resistance and sulfonamide families) were in low abundance, yet at least one was present in more than 80 per cent of the samples. Statement 3 is incorrect - the researchers did not call for immediate action; they stressed continued surveillance.

Frequently Asked Questions (FAQ)

Summary answer: According to the IIT Madras study (published in mSphere), the Chennai Metro has its own distinct transit microbiome. The team sequenced 47 of 96 surface samples; the highest microbial diversity was found on ticket kiosks; AMR genes were in low abundance but present in more than 80 per cent of the samples. The researchers say there is no cause for alarm, but continued surveillance is needed.

Question: What did the Chennai Metro microbiome study find?

The study found that the microbial pattern on Chennai Metro surfaces differs from other urban transit systems of the world - nine species were especially more prevalent here. Ticket kiosks showed the highest microbial diversity, and at least one AMR gene was present in more than 80 per cent of the samples.

Question: How were the samples collected for the study?

In December 2021 and January 2022, 96 surface swabs were taken from 12 stations and trains on the Blue and Green Lines - from handrails, ticket vending kiosks, train handrails and ticket counters. The 47 samples that passed quality checks underwent shotgun metagenomic sequencing, and 41 samples made it to the final analysis.

Question: Is the presence of AMR genes in the metro dangerous?

According to the study, no. The AMR genes were in low relative abundance, though widely distributed. The researchers did not call for immediate action; they described it as baseline information for public health surveillance.

Sources

- mSphere (American Society for Microbiology) - Chennai Metro transit microbiome and AMR study

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