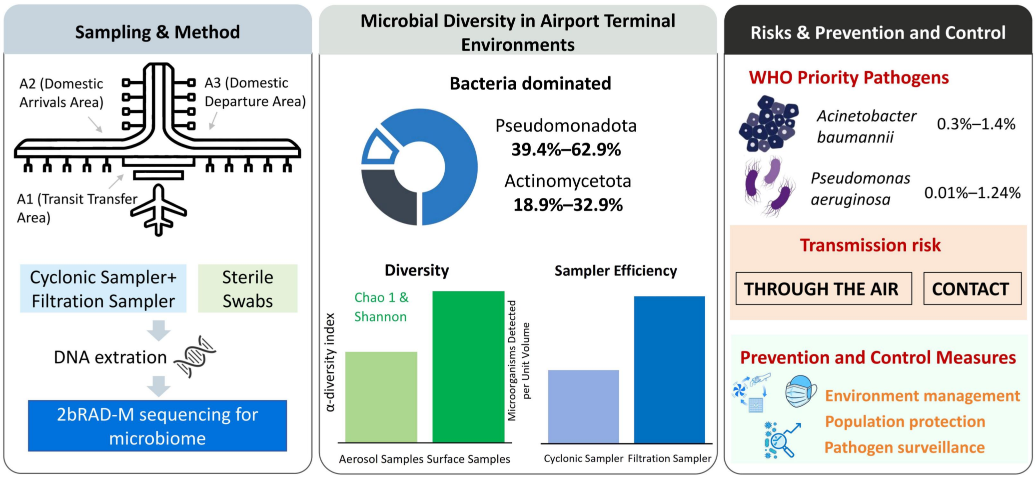
SUPPLEMENTARY MATERIALS



Graphical Abstract.

Calculation of Relative Abundance

For the identification of microbial species in each sample, quality-controlled 2bRAD sequencing tags were aligned to a reference database of unique species-specific markers. This custom database comprises theoretically distinct 2bRAD tags corresponding to 86,022 microbial species. Alignment was performed using an integrated Perl script. To minimize false-positive identifications, a G-score metric was calculated for each detected species within a sample. The G-score represents the harmonic mean of two values: the sequencing read coverage observed for the species' markers and the total number of possible marker targets for that species in the database. A detection threshold was applied, whereby species with a G-score below 5 were considered potential false positives and thus excluded from further analysis.

$$G\ score_{species\ i} = \sqrt{S_i \times t_i}$$

Where S is the number of reads assigned to all 2bRAD markers belonging to species i within a sample; t is the number of all 2bRAD markers of species i that have been sequenced within a sample.

Subsequently, the mean sequence coverage depth across all species-specific markers was determined for each microbial taxon. This value serves as a quantitative proxy for the estimated number of individuals of that species within the sample at the achieved sequencing depth. Following this, the relative abundance of a species was derived as the proportion between its estimated individual count and the cumulative sum of individuals from all identifiable species detected in that sample.

$$Relative\ abundance_{species\ i} = \frac{S_i/T_i}{\sum_{i=1}^{n} S_i/T_i}$$

Where S is the number of reads assigned to all 2bRAD markers of species i within a sample; T is the number of all theoretical 2bRAD markers of species i.

Data Analysis

(1) Chao1:

$$S_{chao1} = S_{obs} + \frac{n_1(n_1 - 1)}{2(n_2 + 1)}$$

Where S_{Chao1} is the estimated number of species; S_{obs} is the actually observed number of species; n_1 is the number of species with only one sequence; n_2 is the number of species with two sequences.

(2) Shannon Wiener:

$$H_{shannon} =- \sum_{i=1}^{S_{obs}} \frac{n_i}{N} \ln \frac{n_i}{N}$$

Where N is total number of sample sequences; n_i is the number of sequences of the i-th species; S_{obs} is total number of species detected in the sample.

(3) Simpson:

$$D_{simpson} = 1 - \sum_{i=1}^{S_{obs}} \frac{n_i(n_i - 1)}{N(N - 1)}$$

Where S_{obs} is the number of actually observed species; n_i is the number of sequences of the i-th species; N is total number of all sequences.

The adaptors and primers used in 2bRAD-M sequencing are provided in Supplementary Table S1.

Supplementary Table S1. The adaptors and primers used in 2bRAD-M sequencing(5’-3’)

Name	**Adaptor Sequence**
Adap-1 sense	ACACTCTTTCCCTACACGACGCTCTTCCGATCTNN
Adap-2 sense	GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCTNN
Adap antisense	AGATCGGAAGAGC
	Primer Sequence
Primer1	ACACTCTTTCCCTACACGACGCT
Primer2	GTGACTGGAGTTCAGACGTGTGCT
5UDI Primer	AATGATACGGCGACCACCGAGATCTACACXXXXXXXXACACTCTTTCCCTACACGACGCTCTTCCGATCT
7UDI Primer	CAAGCAGAAGACGGCATACGAGATXXXXXXXXGTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT

The environmental monitoring results are provided in Supplementary Table S2.

Supplementary Table S2. Monitoring results of environmental factors in different areas of the airport

Locations	**Temperature (℃)**	**Humidity (% RH)**	**Wind speed (m/s)**	**Average number of biological particles (particles)**
A1	25.8–26.2	53.6–57.0	0–0.3	357
A2	25.4–25.8	47.3–49.7	0.58–0.86	336
A3	25.6–26.4	53.0–56.9	0.42–1.00	327

The alpha diversity analysis results of surface samples and airborne aerosol samples (filtration sampling) are provided in Supplementary Table S3.

Supplementary Table S3. Alpha diversity of surface samples and airborne aerosol samples (filtration sampling)

Sample	**Chao1**	**Shannon**	**Simpson**
Surface_A1	4,857	8.29	0.98
Surface_A2	3,453	7.44	0.96
Surface_A3	4,020	8.45	0.98
P_A1_$PM_{2.5}$	1,040	6.79	0.95
P_A1_PM_{10}	1,866	7.92	0.98
P_A2_$PM_{2.5}$	1,197	6.71	0.95
P_A2_PM_{10}	1,791	7.96	0.98
P_A3_$PM_{2.5}$	1,014	6.61	0.95
P_A3_PM_{10}	1,576	7.84	0.98