

Unveiling Airborne Microbiomes through Metagenomic Sequencing

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Abstract: *This study aimed to characterise the variety of bacteria present in air samples collected in the Sahara Desert, Barbados, Cyprus, and during the Air Quality and Climate Change in the Arabian Basin (AQABA) ship voyage that travelled across the Mediterranean Sea and around the Arabian Peninsula. A metagenomic analysis was conducted using 16s rRNA gene sequences from the MGnify database (study ID: PRJEB26788). Human health, atmospheric chemistry, and environmental processes are all significantly influenced by airborne microbial communities. The microbial diversity and composition of air samples taken from a variety of sites, including desert, marine, and urban settings, were examined in this work using metagenomic analysis. To identify important bacterial taxa including Streptomyces, Nocardioidaceae, Burkholderiaceae, and Mycobacteriaceae, we processed and analysed sequencing data using programs like FastQC, Trim Galore, Kraken2, and Krona. The findings demonstrated the impact of environmental conditions on airborne microbiomes by revealing a notable variance in microbial abundance between locales. Our results also imply that long-distance atmospheric transport plays a role in the worldwide spread of microbial species, which may have consequences for the stability of ecosystems and the spread of disease. This research highlights the importance of metagenomics for high-resolution microbial community analysis and emphasizes the need for continued surveillance of airborne microorganisms to better understand their ecological functions and health implications.*

Keywords: 16S rRNA gene sequences, airborne, metagenomics, analysis.

