Detection of antimicrobial resistance genes in urban air

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Abstract

To understand antibiotic resistance in pathogenic bacteria, we need to monitor environmental microbes as reservoirs of antimicrobial resistance genes (ARGs). These bacteria are present in the air and can be investigated with the whole metagenome shotgun sequencing approach. This study aimed to investigate the feasibility of a method for metagenomic analysis of microbial composition and ARGs in the outdoor air. Air samples were collected with a Harvard impactor in the PM10 range at 50 m from a hospital in Budapest. From the DNA yielded from samples of PM10 fraction single-end reads were generated with an Ion Torrent sequencer. During the metagenomic analysis, reads were classified taxonomically. The core bacteriome was defined. Reads were assembled to contigs and the ARG content was analyzed. The dominant genera in the core bacteriome were Bacillus, Acinetobacter, Leclercia and Paenibacillus. Among the identified ARGs best hits were vanRA, Bla1, mphL, Escherichia coli EF-Tu mutants conferring resistance to Pulvomycin, BcI, FosB, and mphM. Despite the low DNA content of the samples of PM10 fraction, the number of detected airborne ARGs was surprisingly high.

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