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# The resistome of human-associated microbial communities, its mobility and temporal dynamics

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*Motivation and Aim*: Complex microbial communities associated with the human body such as intestinal and respiratory microbiomes contain many antibiotics resistance genes (ARGs). Some of them are thought to be mobile and able to spread from one species to another. Considering rampant antibiotics resistance reported worldwide, we find it necessary to assess resistomes of human-associated microbial communities. In this study, we aimed to characterize sets of ARGs present in oropharyngeal and fecal samples of 182 patients using a targeted gene sequencing panel based on 4937 antibiotics resistance genes.

*Methods and Algorithms*: We have used sequencing reads obtained from 94 oropharyngeal and 88 fecal samples collected in different time points during the antibiotics course. Those reads were sequenced with Illumina HiSeq platform based on targeted gene sequencing panel of 4937 antibiotics resistance genes. We have aligned sequencing reads to the reference MEGARes v.2.0. database using bwa mem tool and calculated the numbers of mapped reads with samtools. Gene coverage calculation and the visualization of the results were carried out in R language. We have also assembled reads into contigs using metaspades v.3.15.4. In order to identify possible mobile elements in the proximity of antibiotics resistance genes, we have used a set of 5970 insertion sequences (ISs) from the ISFinder database.

*Results*: In each sample, 113 to 1440 AR-associated genes were covered with at least one read. The most abundant and common genes identified in fecal samples were class C beta-lactmases, lincosamide nucleotidyltransferases and macrolide phosphotransferases, while chloramphenicol acetyltransferase and quinolone resistance peptides Qnr were abundant in oropharyngeal samples. Class A beta-lactamases and various efflux pump genes were abundant both in fecal and oropharyngeal samples. Interestingly, most samples demonstrated no obvious temporal dynamics during the antibiotics. While analyzing assembly contigs, we have identified sequences presumably belonging to insertion sequence (IS) elements from IS1, IS6, IS5, IS30 and IS605/IS200 families. Of those contigs, the ones with the highest coverage contained putative IS5 family sequences in the proximity of class A beta-lactamase genes. Another set of contigs with high coverage contained putative IS6 family sequences in the proximity of streptothricin acetyltransferase genes.

*Conclusion*: The use of targeted gene sequencing panels based on the sequences of known resistance determinants allows us to assess the resistomes of human-associated microbial communities and explore the changes it might undergo over time. In our study, we have identified resistome patterns that might be specific to intestinal and oropharyngeal microbial communities. We have also shown that the resistomes of the microbial communities analyzed are likely to maintain stable composition over time. We have also identified several associations of ARGs with putative mobile genetic elements that require further exploration.

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