

# Antibiotic resistance genes in the gut microbiome of worldwide populations

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## Abstract

The human lifestyle and the environment have a direct impact not only on the taxonomic and functional profiles of the human gut microbiome but also on its collection of antibiotic resistance genes (ARGs), the resistome. ARGs have been identified even in the microbiomes of human populations that were never exposed to commercial antibiotics. This is correlated with the fact that microbial resistance has always been naturally occurring in the environment. To explore the resistome profiles of distinct populations worldwide, we analyzed 1072 human gut microbiomes from 21 human populations with different diets, lifestyles, and genetic backgrounds. This study is original considering the metagenomes dataset analyzed and the approach performed. The programs ARIBA and ABRICATE were used to screen for ARGs in the metagenomes with paired-end and single-end reads, respectively. The ARGs identified were grouped and sequence redundancy was removed using CD-HIT, which generated an ARGs catalogue with 328 sequences. Each metagenome was mapped against this catalogue with BMAP. DESeq was used to normalize the counts of the reads mapped. PcoA and cluster analysis showed a discernible separation among westernized and non-westernized groups. Genes that confer resistance to tetracycline are the most prevalent genes in most of the westernized and non-westernized groups, but the westernized groups show a higher abundance of these genes. Considering the 21 groups, it was possible to identify 182 significantly discriminative features among them. Interestingly, relevant ARGs commonly found in clinical isolates were found in remote or semi-isolated groups, as TEM, OXA, Cfx, aadS. The characterization of the resistome of worldwide populations and the understanding of the routes of ARGs spread are particularly relevant to global public health.

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