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The Human Gut Microbiome as a Transporter of Antibiotic Resistance Genes between Continents

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ABSTRACT

Previous studies of antibiotic resistance dissemination by travel have, by targeting only a select number of cultivable bacterial species, omitted most of the human microbiome. Here, we used explorative shotgun metagenomic sequencing to address the abundance of >300 antibiotic resistance genes in fecal specimens from 35 Swedish students taken before and after exchange programs on the Indian peninsula or in Central Africa. All specimens were additionally cultured for extended-spectrum beta-lactamase (ESBL)-producing enterobacteria, and the isolates obtained were genome sequenced. The overall taxonomic diversity and composition of the gut microbiome remained stable before and after travel, but there was an increasing abundance of *Proteobacteria* in 25/35 students. The relative abundance of antibiotic resistance genes increased, most prominently for genes encoding resistance to sulfonamide (2.6-fold increase), trimethoprim (7.7-fold), and beta-lactams (2.6-fold). Importantly, the increase observed occurred without any antibiotic intake. Of 18 students visiting the Indian peninsula, 12 acquired ESBL-producing *Escherichia coli*, while none returning from Africa were positive. Despite deep sequencing efforts, the sensitivity of metagenomics was not sufficient to detect acquisition of the low-abundant genes responsible for the observed ESBL phenotype. In conclusion, metagenomic sequencing of the intestinal microbiome of Swedish students returning from exchange programs in Central Africa or the Indian peninsula showed increased abundance of genes encoding resistance to widely used antibiotics.

FOOTNOTES

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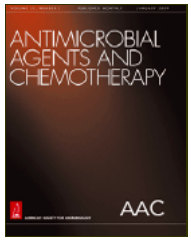

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