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

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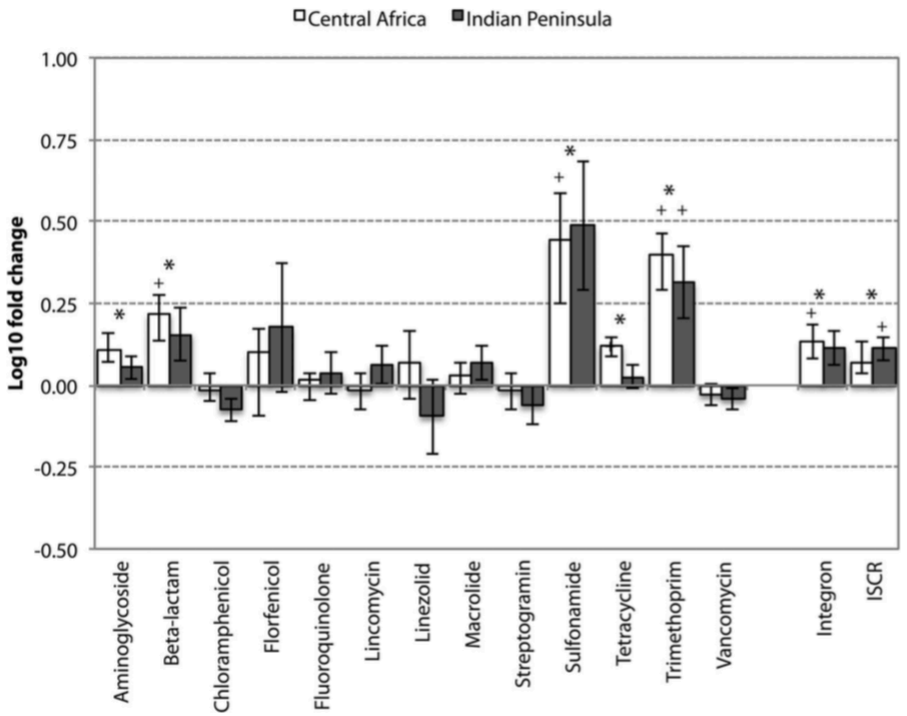
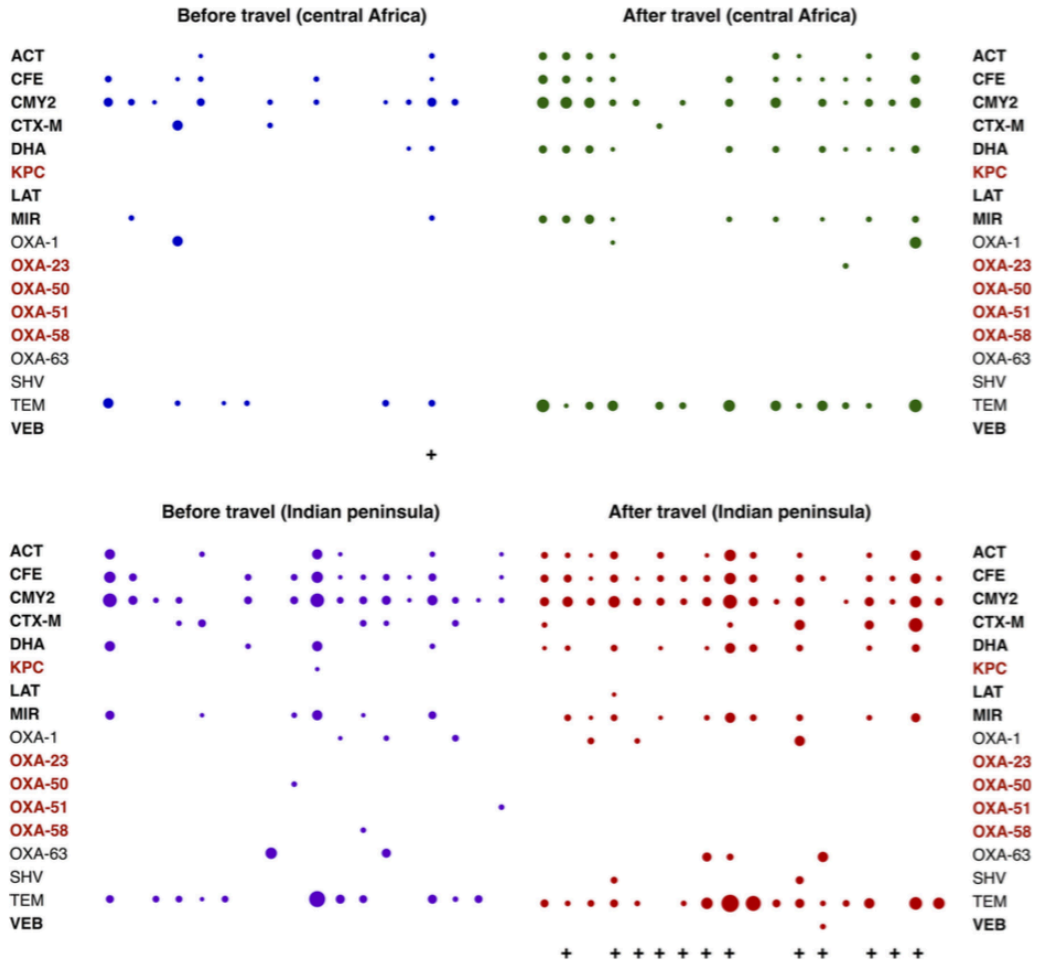
We have applied explorative shotgun metagenomic sequenc- ing to human feces from 35 students before and after travel from Sweden to the Indian peninsula or to Central Africa…

the study population was not exposed to antibiotic treatments



Average fold change of resistance gene categories after travel (log10 scale). Changes in the entire cohort significant after correction for multiple testing are indicated with an asterisk. Significance within the Indian peninsula or the Central Africa group is indicated with a plus sign.



Abundance of beta-lactam resistance genes in all specimens (before and after). Specimens with extended-spectrum betalactamase (ESBL)-positive isolates are indicated by a plus sign. ESBL resistance gene names are shown in bold, while carbapenemase gene names are indicated in red. The diameter of each dot represents the relative abundance of that gene in that specimen (log10 scale).

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 pro- grams on the Indian peninsula or in Central Africa**. All specimens were additionally cultured for extended-spectrum beta-lacta- mase (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 Proteobac- teria 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 meta- genomics 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.