

P0934 **Comparison of antimicrobial resistance-gene diversity in gut microbiome of healthy individuals from Turkey, Europe, America and China**

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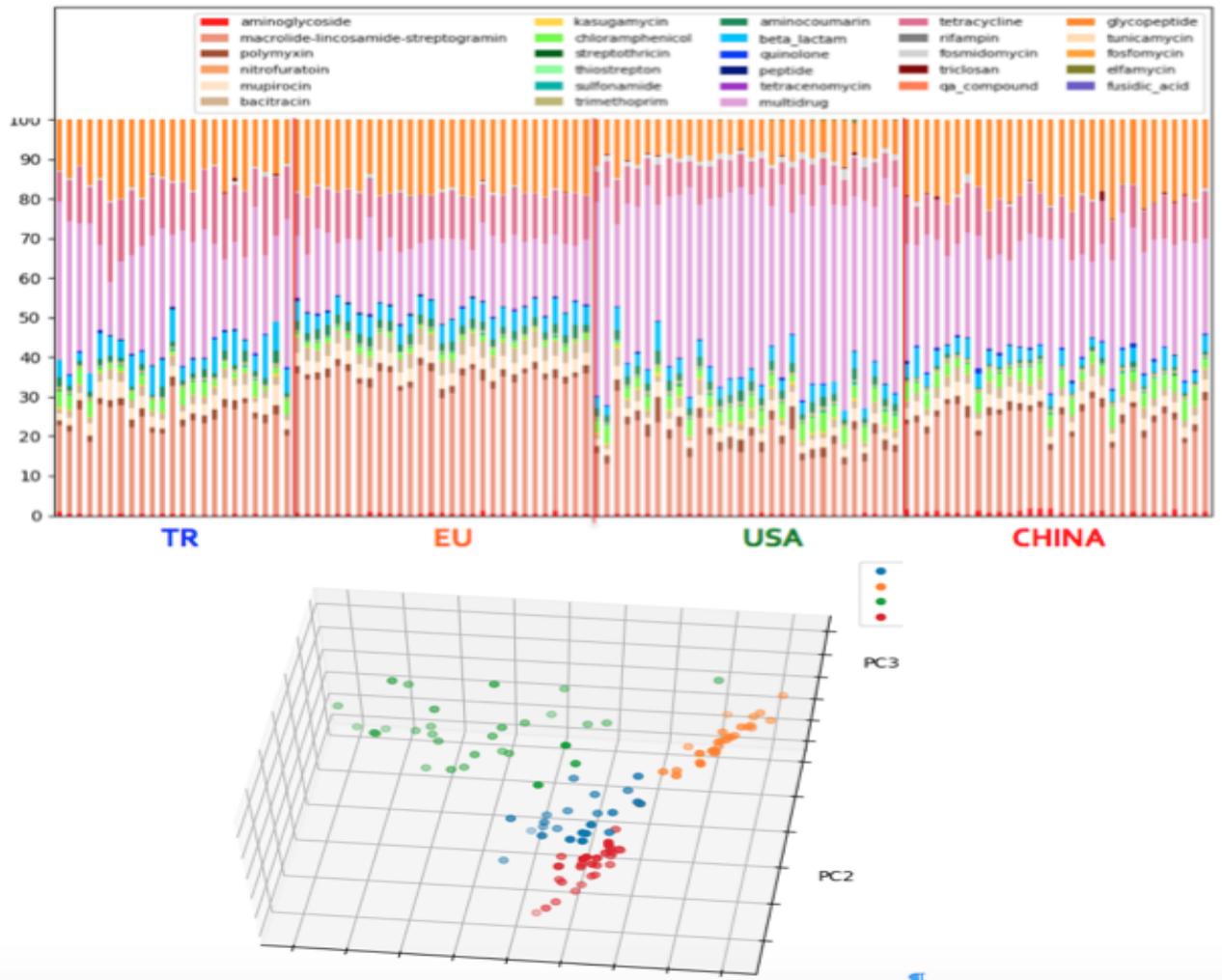
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Background: Human microbiome is among the main reservoirs of the resistome ecosystem, where clinically relevant Antimicrobial Resistance Genes (ARGs) might be transferred to human pathogens or even novel resistance might emerge. Therefore, profiling the ARGs harboured in human microbiome can be informative to reveal the potential antimicrobial resistance threats to public health. Turkey is the OECD country where the most antibiotics are transcribed. We have sequenced the gut microbiome of 23 healthy Turkish individuals and compared their ARG profiles to three other groups in different continents.

Materials/methods: Fecal samples from 23 healthy individuals in 50-65 years old range were collected and total DNA was extracted using commercial kits. Shotgun metagenomics sequencing was performed using Illumina NextSeq platform. Quality filtered reads were assembled by IDBA_ud program and open reading frames were obtained using MetaGeneMark and Prodigal gene prediction software. After clustering the genes to sequence similarity groups by CD-HIT program, the antimicrobial resistance genes were detected using DeepARG and HMMER programs employing CARD and ResFams databases respectively. Same bioinformatics pipeline is applied on publicly available gut metagenomes collected from healthy individuals from America, Europe, and China for quantitative comparison.

Results: Out of 263,413,179 sequencing reads 52,172 ARGs belonging to 60 different resistance gene ontology were detected. The figure below shows the ARG profiles of each group. The ARG diversity from Turkish gut metagenomes were highly similar to European gut resistome whereas the ARG relative abundances were lower than European and American gut resistomes similar to Chinese profiles. Multidrug resistance genes found mostly abundant in American resistomes and lowest in European. Macrolide resistance was the highest in Europe and the lowest in China. Glycopeptide resistance was the highest in Europe and the lowest in Turkey. All the detected ARGs were included in MetaHIT catalogue, revealing no novel or authentic resistance genes

Conclusions: The ARG profile of Turkish gut metagenomes exhibit a transitional characteristics between Chinese, European and American profiles in accordance with geographical distributions. We have seen that while the ARG diversity is high (European-like), the relative abundance of ARGs is relatively low (Chinese-like).



ARG profiles of Turkey(TR), Europe(EU), America(USA) and China